GAM-NAME GAM-SEQ  GAM-SEQ-ID DICER-SEQ  DICER-ID GAM-DRAW
GAM24
GAGGCAGGAGAATTGCTTGAACCCAGGAAGTGGAGGCTTCAGTGAGCTGAGAACACGCCACTGCACTCCAGTCC
TGGGCAACAGAGCAAGACTCTGTCTC 1 AACACGCCACTGCACTCCAGTCCT 2
    G  AA    GAA--    AG   GCTT   A - AGAA
GAGGCAG AG TTGCTT   CCCAGGA TGGAG   CAGTG GC TG
CTCTGTC TC AACGAG    GGGTCCT ACCTC   GTCAC CG AC
    - AG    ACAAC    G-   AC--   - C ----
GAM25   TCAGAGTGAACAGGCAACCTACAAAATGGGAGAAAATTTTCGCAACCTACTCATCTGA 11
TGAACAGGCAACCTACAAAATGGG 12
    G   AC  CAA------------   CA
TCAGA TGA AGG         CCTA  A
||||| ||| |||          ||||
AGTCT ACT TCC         GGGT  /
    -  CA  AACGCTTTTAAAAGA   AA
GAM26
TGTAAATTTGTTTAAGTTCCTTGTAGATGCTGGATATTAGACCTTTGTCAGATGGATAGAGTGCAAAAATTTTCTCC
CATTCTGTAGGTTGTCGGTTTACTCTGTTGATAGGTTCTTAATGCTGTGCA 36
TATTAGACCTTTGTCAGATGGATA 37
    AATTT -  TT TG--- TGC   ATTA   TTGT  T-- T   GC
TGTA   GT TTAAG CCT   TAGA  TGGAT   GACCT   CAGA   GGA AGAGT  A
||||   || ||||| |||   ||||  |||||   |||||   ||||   ||| |||||
ACGT   CG AATTC GGA   GTCT  ATTTG   TTGGA   GTCT   CCT TTTTA  A
   GT--- T   TT TAGTT  C--   GCTG   T---   TAC  C   AA
GAM27   AAAAAAGACTGAATTTCCTGGCTTACTTGCATATACAGACTGGGATTTTTTTTTTTTTT 46
GACTGGGATTTTTTTTTTTTTT 47
    CT  TT  TG - TACTTG
AAAAAAGA GAA TCC G CT    C
|||||||| ||| ||| | ||
TTTTTTTT TTT AGG C GA    /
     TT  TT  GT A CATATA
GAM28   AAACATCTCCAGGCTTTGATTTTTGTACCATGGAAATTGTATTTAACCATACAGGGTTTTGGTATGTTT 54
TATTTAACCATACAGGGTTTTGGT 55
    CT  -  - -- TT  C G
AAACAT CCAGG CTTTG AT TT GTAC AT G
|||||| ||||| ||||| || || |||| ||
TTTGTA GGTTT GGGAC TA AA TATG TA A
    T-  T  A CC TT  T A
GAM29   AAAGAACCTCGTCGTGACATTTCTCAGAAGCCATGACATGTCCCTGCGGCTGGAGGCCTTT 67
TGTCCCTGCGGCTGGAGGCCTTT 68
    AA  --  ---   T TCAGA
AAAG CCTC GTCGT  GACAT TC    A
|||| |||| |||||  ||||| ||
TTTC GGAG CGGCG  CTGTA AG    /
    C-  GT  TCC    C TACCG
GAM30
AAAGTCCTACGTGACTGATTTTAAACATTGTGATAAAATTAATTTTCAGTATAATAGTTGAATGTGTTAAGATAGGAT
TTT 97 TAATAGTTGAATGTGTTAAGATAG 98
    CG-  TGAT   AC   ATA  TT
AAAGTCCTA TGAC  TTTAA ATTGTG  AAA  A

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|||||||| |||| ||||| ||||| |||
TTTTAGGAT ATTG  AAGTT TAATAT TTT /
    AGA  TGT-  GA   GAC TA
GAM31  AAATATGCGCGAGAACCGCCGCGGTGTGACAAAAACCGCGCCGCCGGGGCTCTTATTATATTT 119
TATGCGCGAGAACCGCCGCGGTGT 120
   CGC- AA CC    ACA
AAATATG  GAG CCG GCGGTGTG  A
||||||| ||| ||| ||||||||
TTTATAT  CTC GGC CGCCGCGC  A
    TATT  GG  --    CAA
GAM32  AAATCACATTTCTTTTTATCATGTAAACTTGTACCAAAGACTTATGAATAGATTTATGAATT 134
TCACATTTCTTTTTATCATGTAAA 135
 A CATT  TTTTA  TAAA  GT
AA TCA  TCT   TCATG  CTT A
|| ||| |||  ||||| |||
TT AGT  AGA   AGTAT  GAA C
 A ATTT  TA---   TCA- AC
GAM33
AAGAAATAGTTTTAAGTAACTTTTTATAGCAAGATGATACAATGGTATGAGTGTAATCTAAACTTCCTTGTTGTATTA
CCTTGTATGCTGTTACTTTTATTTTATTCCTT 160 TAGCAAGATGATACAATGGTATGA 161
  A  TTTT-   TTTT  G  A    TG TAT  GTAA
AAG AATAG   AAGTAAC  TATA CAAG TGATACAA G  GAGT   T
 ||| |||||   |||||||  |||| |||| |||||||| |  ||||
TTC TTATT   TTCATTG  GTAT GTTC ATTATGTT T  TTCA   /
  C  TTATT   TC--  -  C    GT CC- AATC
GAM34  AAGAAGGTGATGCCGAAGCTGAGGTCGGAAATTACGAAGATCAGCTATCAAACTTGGAAATCATGTCTT
177 TCAGCTATCAAACTTGGAAATCAT 178
  AG  G-  -------  GG- GAA
AAGA GTGAT CCGA    AGCTGA TCG A
|||| ||||| ||||     |||||| |||
TTCT TACTA GGTT    TCGACT AGC /
  G- AA CAAACTA    AGA ATT
GAM35
AAGATGCTACCCAGCATCTTTAAACCAGCTTGGTGCGGATAGTCTGACTAGTTTAAGGAGACTGGCGAAGCGTCT
T 188 GACTAGTTTAAGGAGACTGGCGAA 189
    AC- CA    C C TG T GG
AAGATGCT  CCAG TCTTTAAAC AG T G GC A
||||||||| |||| ||||||||| || | | ||
TTCTGCGA  GGTC AGGAATTTG TC A C TG /
    AGC  AG    A - GT - AT
GAM36  AAGATGTAGCGGGTTTTCTGGTGGTGGATCCGAAGATGGGCCACAGAGATTCCACTTTCCTCTT 208
TAGCGGGTTTTCTGGTGGTGGATC 209
   TGT- C GT   G  GG  C
AAGA  AG GG  TTTCTG TGGT ATC G
||||   || || |||||| |||| |||
TTCT  TC CC AGAGAC ACCG  TAG A
   CCTT A TT    - GG  A
GAM37
AAGGCGGGGGTTTCACCATGTTGGCCAGGCTGGTCTCAAACTCCTGACCTCAAGTGGATATGCCTGCCTT 214
TGACCTCAAGTGGATATGCCTGCC 215
```

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        GT--    CA TT C   CT  CT
AAGGCGGG   TTCAC TG GG CAGG GGT C
||||||||   ||||| || || |||| |||
TTCCGTCC   AGGTG AC CC GTCC TCA /
     GTAT   A- T- A  -- AA
GAM38  AAGGGGATCTGAAAACCAGAGCGTCCCCGGCGCTCCCTTCTGTGCCGCCCGCTTAGGCAGGTTCCCTT
235 TCTGAAAACCAGAGCGTCCCCGGC 236
       AAAA A   TCCC    TCC
AAGGGGATCTG  CC GAGCG  CGGCGC  C
||||||||||| || ||||| |||||||
TTCCCTTGGAC  GG TTCGC  GCCGTG  T
       ---- A   CC--    TCT
GAM39
AAGGTGTCCAGGCCACAGTCTCAAGGGCTTTCTAGCAGCTTGGGGCTCCTGAAAGTCTGGCTGACTCTGCTTCT
CTCGGACACCTT 245 TGAAAGTCTGGCTGACTCTGCTTC 246
       ----- CAC  TCAA    T C  TT
AAGGTGTCC  AGGC AGTC  GGGCTTC AG AGC  G
||||||||   |||| |||| |||||||| || |||
TTCCACAGG   TTCG TCAG  TCTGAAAG TC TCG /
     CTCTC  TC- TCGG    - C  GG
GAM40
AATAAAAAGCTAACCTGGTTCAAAATGCTGATTAAGTTTCTACAAGCAAACACAAAACAGTGTTTTTTTTATT 259
TAAAAAGCTAACCTGGTTCAAAAT 260
     CT  - GTTCAAAA-  GATTAAG
AATAAAAAG AAC CTG      TGCT    T
||||||||| ||| |||      ||||
TTATTTTTT TTG GAC      ACGA    /
     --  T AAAACACAA  ACATCTT
GAM41  AATAAAATTTCTCAAACTATATCAATATCTAAAGTGCATATATTTTTTAAGAAAGATTATT 263
TAAAATTTCTCAAACTATATCAAT 264
   AA   C  CT  CAA  CT
AATAA TTTCT AAA ATAT  TAT A
||||| ||||| ||| ||||  |||
TTATT AAAGA TTT TATA  GTG /
   AG   A  TT  TAC  AA
GAM42
AATCCCATTTTGGGGTTTTCCATCCGGAATTTTTGTTTTTAATAAGGGTTCAGTTTCTTTTTCCCCAGGGATT 283
TAAGGGTTCAGTTTCTTTTTCCCC 284
    ATTT   TTTTCCATCCG       T
AATCCC  TGGGG       GAATTTTTGTT T
||||||  |||||       ||||||||||
TTAGGG  ACCCC       CTTGGGAATAA /
    ----   TTTTTCTTGA       T
GAM43  AATGACACCGTTGATTGAGCTTGTCAGCAGAGCTGAAAGAGACAGTCGACGGATGTGCATT 300
TGACACCGTTGATTGAGCTTGTCA 301
   - -    AG- G  A
AATG ACA CCGTTGATTG  CTT TCAGC G
|||| ||| ||||||||||  ||| |||||
TTAC TGT GGCAGCTGAC  GAA AGTCG /
  G  A     AGA - A
```

GAM44  AATGAGTTTCTTACTCGGGAGCTGGCTGAAGATGGCTACTCTGGAGTTGAGGTGCGAGTT 309
TGAGTTTCTTACTCGGGAGCTGGC 310
   GA  T  -  G   C   GA
AAT  GT TCTTA CTC GGAG TGGCT  A
|||  || ||||| ||| |||| |||||
TTG  CG GGAGT GAG TCTC ATCGG  G
   AG  T   T  G   -   TA
GAM45  AATTCTCAAAGGTGCTAGAACAAATCGTCCACTTCTACAGTGTTCTCGTATCCAACAGAGTT 337
TCAAAGGTGCTAGAACAAATCGTC 338
    CAAA   T   AATC  CCA
AATTCT  GGTGC AGAACA  GT  C
||||||  ||||| ||||||   ||
TTGAGA  CTATG TCTTGT  CA  T
    CAAC   C   GA-- TCT
GAM46
ACAAGGGGATGACTGGTGGGTCTCTCTTGGCCCGTGGTGGCGGTCCGGGGGGGGGCTTCTTCCTTACGTCCCTC
TGT 365 TGACTGGTGGGTCTCTCTTGGCCC 366
   AG    ACT T--      C  G
ACA GGGATG GG  GGGTCTCTCTTGG CCGT G
||| |||||| ||  ||||||||||||| ||||
TGT CCCTGC CC  TTCGGGGGGGGCC GGCG T
   CT   ATT TTC        T  G
GAM47  ACAGGCATGAGCCACTGCGCCCAGCCTGGAAGTTAATTTTTATGGTTGTGTATGTGTTGCTTGT 387
CATGAGCCACTGCGCCCAGCCTGG 388
    TGAGC  -  CC  -   T
ACAGGCA   CAC TGCGC AGCC TGGAAG T
|||||||   ||| ||||| |||| ||||||
TGTTCGT   GTG ATGTG TTGG ATTTTT A
    T---- T  -- T    A
GAM48  ACATGTGGTGTTTGGTTTCCTGCTCCTCTGTAAGTTTGCTGAGGATAATGGCTTCCAGCTTCATCCATGT
422 TGTGGTGTTTGGTTTCCTGCTCCT 423
   T  T--  TTT TGC-  T  A
ACATG GGTG  TTGG  CC  TCCTC GTA G
||||| ||||  ||||  ||  ||||| |||
TGTAC CTAC  GACC  GG  AGGAG CGT T
   -  TTC   TTC TAAT   T  T
GAM49
ACCCTAGCTAACATCCTACAGAATGGTGAAAGACTGAGTGTTTTTCCCCTATAATAGGAAACAAGCAAGGGT 429
TAACATCCTACAGAATGGTGAAAG 430
   A  AACA   CAGAAT  T    TG
ACCCT GCT  TCCTA    GG GAAAGAC  A
||||| |||  |||||    || |||||||
TGGGA CGA  AGGAT    CC CTTTTTG  /
   A  ACAA   AATAT- C   TG
GAM50  ACTAGAATGTTGACCTCGAGCCGAGGCCTACTTGCAGCGCACCGGAGGAGAGGTCTCTAGT 453
TAGAATGTTGACCTCGAGCCGAGG 454
   ATGTT    GAG-  AG  -  AC
ACTAGA   GACCTC  CCG  GC CT  T
||||||   ||||||  |||  || ||
TGATCT   CTGGAG   GGC  CG GA  T

```
         -----    AGGA  CA  C  CG
GAM51   ACTATTATGATCAAGGATATGGAAATTACAATAGTGCCTATGGTGGTGATCAAAACTATAGT 459
TATTATGATCAAGGATATGGAAAT 460
    TA---    AGGA    AA   C
ACTAT    TGATCA   TATGG  ATTA A
|||||    ||||||   ||||| ||||
TGATA    ACTAGT   GTATC  TGAT /
   TCAAA    GGTG    CG   A
GAM52   AGAGCCGGCTGGGAGAGGCGGCGTCAGGGTGGGTCCTGCGCCTGCCCTTTCCGCGCCGGCTTT 480
TGCGCCTGCCCTTTCCGCGCCGGC 481
      -   A  -  T   T
AGAGCCGGC TGGGAG GGC GGCG CAGGG G
||||||||| |||||| ||| |||| |||||
TTTCGGCCG GCCTTT CCG CCGC GTCCT G
      C    C  T  -   G
GAM53
AGAGGAAGCGGGAGGAGCTGAGCAACGTACTGGCCGCCATGAGGAAAGCTGCTGCCAATGAAAGACTGAGCCC
CTCCCCTGCCCTCT 522 GAAAGACTGAGCCCCTCCCCTGCC 523
    A- C     A  G  CAACG  C   C  CATGAG
AGAGG  AG  GGGAGG GCT AG    TA TGGC GC    G
||||| || |||||| ||| ||    || |||| ||
TCTCC  TC CCCTCC CGA TC    GT ACCG CG    /
   CG - C G AGAAA A  T TCGAAA
GAM54   AGATAAAAGGTTTCTAAAACATGACGGAGGTTGAGATGAAGCTTCTTCATGGAGTAAAAAATGTATTT
531 TAAAAGGTTTCTAAAACATGACGG 532
    AAAGG  C  AAA    C    GAG
AGATA    TTT TA  CATGA GGAGGTT  A
|||||    ||| ||  ||||| |||||||
TTTAT    AAA AT  GTACT TCTTCGA  /
   GTA-- A GAG    -    AGT
GAM55   AGATACCATACACATGATGAAGTTGCTGTTTGAAAGTACTGTTGAAGCACTGTACAAGTTTGTGGTTCT
545 TACCATACACATGATGAAGTTGCT 546
  T   C  A  A  T  GTTTGAAA
AGA ACCATA AC TG TG AGT GCT     G
||| |||||| || || || ||| |||
TCT TGGTGT TG AC AT TCA CGA     T
  -  T A - G - AGTTGTCA
GAM56   AGATCAGATGGTCGTAGTTGTGTGGCTTTATTTCTGAGTTCTCTTAACTGTTCCATTGGTCT 556
TCAGATGGTCGTAGTTGTGTGGCT 557
     A  TCG   TGT-   TAT
AGATCAG TGG  TAGTTG   GGCTT  T
||||||| ||| |||||| |||||
TCTGGTT ACC  GTCAAT  TTGAG  /
     - TT-   TCTC   TCT
GAM57   AGATGACGTTTATGATCGTATGCTGCTAGACTACTTCTTTTCTTATCATCAGTTCATCCATCT 561
TGACGTTTATGATCGTATGCTGCT 562
    ACGTTTA  C  TGCTGCT  CT
AGATG    TGAT GTA    AGA  A
|||||    |||| |||    |||
TCTAC    ACTA TAT    TCT  /
```

```
    CTACTTG   C  TCTTT-- TC
GAM58   AGATGAGGTCTCAGATGCGAGATCAACTCTAATACGAAATCCATCTGCAATCTGGGCCCCATTT 573
TGAGGTCTCAGATGCGAGATCAAC 574
    A   T   - G   CAAC- TA
AGATG GGTC CAGAT GC AGAT    TC A
IIIII IIII IIIII II IIII    II
TTTAC CCGG GTCTA CG TCTA    AG T
    C   -   A -  CCTAA CA
GAM59   AGCAATCAAAGGTTTTCGCAATTCTCCAGTGGGAGTAAACCACAGACTACGAGGGAGTTTGACAGCT
588 TCAAAGGTTTTCGCAATTCTCCAG 589
   AA   GG   CAAT  CCA   GAG
AGC TCAAA TTTTCG  TCT GTGG  T
III IIIII IIIIII  III IIII
TCG AGTTT GGGAGC  AGA CACC  /
  AC   GA   ATC- ---   AAA
GAM60
AGCATGACTGACACGTCTGACCCCTGAGAAGGTGGTCTCTGCCTTCCTAAAGGTGTCATCTGTGTTCAAGGACGA
AGCT 604 TGACACGTCTGACCCCTGAGAAGG 605
   ATGA-- --   TC  C  GA--   TG T
AGC    CT GACACG TGAC CCT   GAAGG G C
III    II IIIIII IIII III   IIIII I
TCG    GA TTGTGT ACTG GGA   CTTCC C /
  AAGCAG AC   CT  T AATC   GT T
GAM61   AGCATTCCAACAAAGGGTTTTAATGTAGATTTTTTTTTTTTGCACCCCATGCTGTTGATTGCT 617
TTCCAACAAAGGGTTTTAATGTAG 618
   TTC   AA-- TTTTAA    TTTT
AGCA  CAACA  GGG    TGTAGA   T
IIII  IIIII  III    IIIIII
TCGT  GTTGT  CCC    ACGTTT   /
  TA-   CGTA  C-----    TTTT
GAM62   AGCCAGTCATTCTAAGGGGCTTTGTATTGGTGCTATAAAGTCAACCTCAATTCCTTACAGTGGTCTGGTT
630 TAAAGTCAACCTCAATTCCTTACA 631
    -   C   ----------    TTG
AGCCAG TCATT TAAGG       GGCTTTGTA  G
IIIIII IIIII IIIII       IIIIIIIII
TTGGTC GGTGA ATTCC       CTGAAATAT  /
   T   C   TTAACTCCAA      CGT
GAM63
AGCCCTCGATGAGAACAAGGTCACGGTCAGCTGATTTACTTGAGCGTTCGGCTTACTCTGACCTGACACACTCCA
CAGAGCACTGGCT 652 TGAGAACAAGGTCACGGTCAGCTG 653
   ----  GAT- AACA--   C  C    TTTACT
AGCC  CTC  GAG    AGGTCA GGT AGCTGA     T
IIII  III  III    IIIIII III IIIIII
TCGG  GAG  CTC    TCCAGT TCA TCGGCT    /
   TCAC  ACAC  ACACAG    C  T   TGCGAG
GAM64   AGCCGGGTTGCGCCAGGCTGTCATAGTCCTTCTCGTGGAACACGGCGGCGCGGTCACCCAGGCT 673
ACACGGCGGCGCGGTCACCCAGGC 674
    -  ---   AG   CATAG  TTC
AGCC GGGT  TGCGCC  GCTGT    TCC  T
IIII IIII  IIIIII  IIII     III
```

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TCGG CCCA  GCGCGG CGGCA   AGG /
  A  CTG    --   CA--- TGC
GAM65  AGCCTCACAGCTCAGGTCTCTCTTTGCCTGTCACAGTGGAAGTCCCGTGCTGAGCCCAGGTT 697
TCACAGCTCAGGTCTCTCTTTGCC 698
   CACA    GTCTCT- GC  T
AGCCT  GCTCAG    CTTT CTG C
|||||  ||||||    |||| |||
TTGGA  CGAGTC    GAAG GAC /
  CC--    GTGCCCT  GT  A
GAM66  AGCCTGAGACTAGTTCGGACTCCCCTTCGGCAAGGTCGAAGGGGGTTCGGCTGGTCTCTGCT 721
TGAGACTAGTTCGGACTCCCCTTC 722
  CT    T   T     A
AGC  GAGACTAGT CGGAC CCCCTTCGGC A
|||  ||||||||| ||||| ||||||||||
TCG  CTCTGGTCG GCTTG GGGGAAGCTG /
  T-    -    -      G
GAM67
AGCCTTTATTGGGTCAGGGCTTGCTCCAGAGCTCAGGGGCCAGGTAGGTCAGGAGCCTTGGGATGGCT 737
TATTGGGTCAGGGCTTGCTCCAGA 738
   - ATT G AG    CCAGA  C
AGCC TTT  GG TC GGCTTGCT   GCT A
|||| |||  || || ||||||||   |||
TCGG AGG  CC AG CTGGATGG   CGG G
   T  GTT G GA    AC--- G
GAM68
AGCGGGATCGCTTCGGGTGCTCGACTCCTGTTGCGCATGCTCAGCGCGCTGCCCGGCTGGGGACCCGCGCAC
CTGCAGCGCCCGCT 748 GCCCGGCTGGGGACCCGCGCACCT 749
    AT  T    T A-- T  C  - TC
AGCGGG  CGCT CGGGTGC CG  CTCC GTTG GCA TGC A
||||||  |||| |||||||| ||  |||| |||| ||| |||
TCGCCC  GCGA GTCCACG GC  GGGG CGGC CGT GCG /
   -- C    C CCA T  C  C  CG
GAM69  AGCGGGATGGCTGCAGCCAAGGAGCTGGGGGAGGGCCGGGCTCAGGGCTAGCCCTTTCCGCT 782
TCAGGGCTAGCCCTTTCCGCT 783
    T- GC  AAG  G GG
AGCGGGA GGCT AGCC  GAGCT GG  A
||||||| |||| ||||  |||||| ||
TCGCCTT CCGA TCGG  CTCGG CC  G
   TC  --  GA-  G GG
GAM70
AGCTTCACGCTCTTTGTCATCCTGGACTTCTTCCCGCTCATCGCCCACTATTACCTCACCACTCTGGATGAGGCT
GATGAGGCAGGCAAGCGGATTTTTGGTCCCCGGGTGGGGAACGAGCTGTGCGAGGT 792
TGAGGCTGATGAGGCAGGCAAGCG 793
   G  -  -  - G   T-  TCTTC-  CA  -  CAC    -  - AC
A CTT CAC GCTC TTT TCATCC GGACT    CCGCT  TC GCC  TATTA CCTCA CC  T
| ||| ||| |||| ||| |||||| |||||    ||||| || ||  ||||| |||||| ||
T GAG GTG CGAG AAG GGTGGG  CCTGG    GGCGA GG CGG  GTAGT GGAGT GG /
  G  C  T  C  G    CC  TTTTTA  AC A  A--  C   A TC
GAM71
AGGAAAAACTTATGGCATGTATAGTGAGGTTAAGGACTTGCATGTCCCTCGCGATGGTTTCCTTCCCCTTATTCTT
ACTGCTCAGTGTCCT 818 TGGCATGTATAGTGAGGTTAAGGA 819
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   AAA  TAT  T  T-    TT  C----  ATGT
AGGA  ACT  GGCA GTA AGTGAGG AAGGA   TTGC   C
|||| ||| |||||| |||||||| |||||    ||||
TCCT  TGA  TCGT CAT TTATTCC TTCCT   AGCG  /
  G--  C--  -  TC    CC   TTGGT  CTCC
GAM72
AGGAAAATGTCTGTTGATGCTGGGCCCCAGGCAGCACCGTGAGAGCTGCAACGGGCTCACATTTGCCCCTAGTT
TTTCCT 835 TGTCTGTTGATGCTGGGCCCCAGG 836
    TGTCT-- T  C    CAG   ACCG
AGGAAAA    GT GATG TGGGCCC  GCAGC   T
|||||||    || |||| |||||||   |||||
TCCTTTT    CG TTAC ACTCGGG  CGTCG  /
    TGATCCC T  -    CAA    AGAG
GAM73  AGGACATGTGGGGTTTCTTGCTCACCCCCACTCTTGTGGGACGCGGCCTGTGCCCTGATTTTCCT 845
TGTGGGGTTTCTTGCTCACCCCCA 846
  CATG    TTCTT  CACC    T
AGGA  TGGGGT   GCT  CCCAC  C
|||| ||||||   ||   |||||
TCCT  GTCCCG   CGG  GGGTG T
   TTTA    TGTC-  CGCA    T
GAM74
AGGCTGACACTCTCAAAGGTCTTCTCGGATGGAAGTCTCCGGCTCCAGTCGTCTGTCCACTAAGCGAGAGGCGA
GTTGCGAGGGAGGCTGCGGGGGGCGGGCGGACGTATGTTGAGACCCTATGCAGCCT 862
TGGAAGTCTCCGGCTCCAGTCGTC 863
    A C----   AG---  T GA-- GA    GG  -  -   G CAC
AGGCTG CA    TCTCAA   GTCT CTCG   TG AGTCTCC  CTC CAG TCGTCT TC  T
|||||| ||    ||||||   |||| ||||   || |||||||  ||| ||| |||||| ||
TCCGAC GT    AGAGTT   CAGG GGGC   GC TCGGAGG  GAG GTT AGCGGA AG  A
   - ATCCC    GTATG  C  GGGG G-    -- C G   G CGA
GAM75
AGGGACGGGGTTTCTCCATGTTGGTCAGGCTGGTCTCGGGCTCCCGGCACTTTGGGGGGGCCGGGGCGGGCGG
ATCGCCTGAGGTCGGGAGTTTGAGACCGGCCTGGCCGGCATGGCGAAACCCCGTCTCT 876
TCGCCTGAGGTCGGGAGTTTGAGA 877
       T             A  T G GG  GGG
AGGGACGGGGTTTC CCATGTTGGTCAGGCTGGTCTCGGGCTCCCGGC CTT GG G  CCG   C
||||||||||||| ||||||||||||||||||||||||||||| ||| || | | |||
TCTCTGCCCCAAAG GGTACGGCCGGTCCGGCCAGAGTTTGAGGGCTG GAG CC C  GGC  /
       C              - T G TA  GGG
GAM76  AGGGAGGCTGGAGGTTGTGGTGGGTCACAGTGTTGCTGACACCTCTGGCCTCCAGCCCTGCATCCCT
905 TGACACCTCTGGCCTCCAGCCCTG 906
    -----        GT  T -  - AG
AGGGA   GGCTGGAGGTT GG GG GTCA C  T
|||||   ||||||||||| || || |||| |
TCCCT   CCGACCTCCGG  TC CC CAGT G  G
   ACGTC        -- T  A   C TT
GAM77
AGGGCGGCCGGGGAGCACCTGGTTTTATTTCCGTGCAGTGAGGGGATATCATCCTGGTGCCCTCGTCTTGGTTT
919 ATCATCCTGGTGCCCTCGTCTTGG 920
  G  - C   A   T TTT-  TT GTGC
AGG CG G CGGGG GCACC GG   TAT CC   A
```

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|||  ||  |  ||||  ||||| ||    |||  ||
TTT GT C GCTCC CGTGG CC   ATA GG   /
  G  T T    -    T TACT  GG AGTG
GAM78
AGGGGGCACACCACATCAAAATGAGGGGTGTGTTGCTGTTGCGAAATTAAAACCAATCGTTGTGTTTGTCCCCT
938 AAACCAATCGTTGTGTTTGTCCCC 939
    CAC   TCAAA   GG  GTG----  T
AGGGGGCA  CACA    ATGA  GGT    TTGC G
||||||||  ||||    ||||  |||     ||||
TCCCCTGT  GTGT    TGCT  CCA      AGCG T
     TT-  -----   AA  AAATTAA   T
GAM79  AGGGGGGGGCTCCAAATAGTGTTGGCCTTTAAATTGCTGGGAACGGGGAGGCCCAACCCT 952
TGGGAACGGGGAGGCCCAACCCT 953
   GG   -  AAATA  G- TG  CTTT
AGGG  GGGC TCC    GT T GC   A
||||  |||| |||    ||  |  |  ||
TCCC  CCCG AGG    CA  G  CG   /
   AA   G   GG--- AG GT  TTAA
GAM80
AGTCTCTGACCAGCCTGAACGTGTCTTATGTCACTTGTTTGGAAATGATGTGATTGAAGATTTCAGAGAGGTCATT
GGAGGCT 971 TGATTGAAGATTTCAGAGAGGTCA 972
      ---  AGC   CGT   AT   - TG  T
AGTCTCT  GACC  CTGAA  GTCTT  GTCAC T  TT G
|||||||  ||||  |||||  |||||  ||||| |  ||
TCGGAGG  CTGG  GACTT  TAGAA  TAGTG A  AA G
     TTA  AGA   ---   GT   T GT  A
GAM81
AGTGAGGGGCAGGATGAAATCATCTAGGGTAGGTATTTAGAGGGAGGGCGCCGTGCAAAATAAAATCCTCACT
997 AGGGGCAGGATGAAATCATCTAGG 998
       ---------  - A  AAA  A-    GTA
AGTGAGGG     GCA GG TG  TC  TCTAGG  G
||||||||     ||| || ||  ||  ||||||
TCACTCCT     CGT CC GC  AG  AGATTT  /
    AAAATAAAA  G  -  GGG  GG    ATG
GAM82
AGTGGACAATGTCATGTTTGGAGAAAGATAACAACACAAATAATGTAACCTTTCCTTAAAAGGCAGAACTCAATCC
ATT 1017 TGTCATGTTTGGAGAAAGATAACA 1018
    CAAT CA    ---- A   ATA  ACAC
AGTGGA  GT TGTTT   GG GAAAG  ACA   A
||||||  || |||||   || |||||  |||
TTACCT  CA ACGGA   TC CTTTC  TGT   A
    AACT AG   AAAT  -   CAA  AATA
GAM83  AGTTGATCAGATTTCAAGGTCTGGGGAGTATATCCACTGTGTACTGGGTCTTGAGCTCTAGAGAGCT
1037 TCAGATTTCAAGGTCTGGGGAGTA 1038
   GA  -  T   GT GGGG    CC
AGTT TC AGA TTCAAG CT   AGTATAT A
|||| || ||| |||||| ||    |||||||
TCGA AG TCT GAGTTC GG   TCATGTG /
   G- A  C   TG ----    TC
GAM84  ATAGAAGTATACTGAGAGTCTAAAATACATTCTAGTAGTGCATGTCTTGGTGTGCTTTTGT 1061
TAGAAGTATACTGAGAGTCTAAAA 1062
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          TG  GTCTAAAA  AT
ATAGAAGTATAC AGA      TAC T
|||||||||| |||      |||
TGTTTTCGTGTG TCT      ATG C
     GT  GTACGTG- AT
GAM85
ATATATGTTTTCTTTTTAAGCTAGCTAAAGAAAATACTCTTGATCGGGGTTAGTTCTTAAAGCAAAAAACAGAAGAA
AAGTATGTAT 1078 TAAGCTAGCTAAAGAAAATACTCT 1079
    -      TAAGCTA  A-   AAT   TG
ATATATG TTTTCTTTT    GCT AAGAA  ACTCT A
||||||| |||||||||    ||| ||||| |||||
TATGTAT AAAAGAAGA    CGA TTCTT TGGGG /
     G     CAAAAAA AA   GAT   CT
GAM86  ATATGGTCATGTGAATCAAATTTGATGTATAAAGTACTCACACAAGTTGTCTCAAAGATGATAT 1095
TATGGTCATGTGAATCAAATTTGA 1096
   G  ATG  AT  A   A  ATAAA
ATAT GTC  TGA  CAA TTTG TGT   G
|||| |||  |||  ||| |||| |||
TATA TAG  ACT  GTT GAAC ACA   /
   G  AA-  CT  -   -  CTCAT
GAM87  ATATGGTGTGAGAAATGGCTGTAGGAAACAACACTCAACGAAGTTATTCCATCATCCCGTGT 1111
TATGGTGTGAGAAATGGCTGTAGG 1112
     TG  GA-     GTAG- AAC
ATATGG TGA  AATGGCT   GA  A
|||||| |||  |||||||    ||
TGTGCC ACT  TTATTGA   CT  A
    CT  ACC     AGCAA  CAC
GAM88
ATCACAAGTGGGGTGTACTCCCCCTTGCATATTGGGAACAACATCACAAGTGGGGTGTACTGCCTCTGTGAT
1124 TCACAAGTGGGGTGTACTGCCTCT 1125
     AGT  -  T  -  C- A  G
ATCACA  GGGGT GTAC CCCC CTTG  AT TTG G
||||||  ||||| |||| |||| ||||  || |||
TAGTGT  CTCCG CATG GGGG GAAC  TA AAC A
     ---  T  T  T  AC C  A
GAM89  ATCACAGCTGTGCCAGTAATAAGGATGCTAACAATTAATTTTATCAAACCTAACTGTGACAGCTGTGAT
1140 TCACAGCTGTGCCAGTAATAAGGA 1141
      GC  AATAAG-  CTAACA
ATCACAGCTGT CAGT     GATG   A
||||||||||| ||||      ||||
TAGTGTCGACA GTCA     CTAT   T
     GT  ATCCAAA  TTTAAT
GAM90
ATCGTCAATGAAAGCCCTGGGCTGCTCTCCAGGATGTCACCATTGGGGGGTTCGGCTCGTCCGGTGGCCGGGGC
GGGTTTCCACCGGTGTGGCGCCTGGCCGCGTCCGGGGCTTCGGGCGAT 1159
TGTCACCATTGGGGGGTTCGGCTCG 1160
    AA  A     T TCT  A   C  -  TTC      -  T
ATCGTC  TGAA GCCCTGGGC GC  CCAGG TGTCAC ATTGG GGG  GGCTCGTCC GG G
|||||| |||| ||||||||| ||  |||||| ||||| |||| |||  ||||||||| ||
TAGCGG  GCTT CGGGGCCTG CG  GGTCC GCGGTG TGGCC CCT  TTGGGCGGG CC /
```

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       --   -     - CC-   -    - A ---      G G
GAM91  ATCGTGGGGCTTGTGGGAAATGGTGGGGAGTGCCAATGGCCGTAAATTATGTGTCGCGAT 1168
TGGCCGTAAATTATGTGTCGCGAT 1169
     G TT   GAA    GG-- A
ATCGTGG GC GTGG  ATGGT   GG G
IIIIIII II IIII  IIIII   II
TAGCGCT TG TATT  TGCCG   CC T
     G  --   AAA   GTAA  G
GAM92  ATGAGATTTGGGAGGGGCCAGGGGCAGAATGATATGGTTTGACTGTGTCCTCACCCAAATCTCAT 1171
TGAGATTTGGGAGGGGCCAGGGGC 1172
        A   C G GCA   GA
ATGAGATTTGGG GGGG CA GG   GAAT  T
IIIIIIIIIII IIII II II   IIII
TACTCTAAACCC CTCC GT TC   TTTG  A
       A   T G AG-   GT
GAM93  ATGAGGAACTCCTACAACTCAATAGTAAAACAAACAAAAACCCCTGATTCCTGGAGATCCTGAT 1196
TGAGGAACTCCTACAACTCAATAG 1197
  G   A  TACAAC  ATA  AAAACA
AT AGGA CTCC    TCA  GT    A
II IIII IIII    III  II
TA TCCT GAGG    AGT  CA    /
  G   A  TCCTT- CCC  AAAACA
GAM94  ATGCAGTATTTGGTTTCCTGTTCCTGTGTTAATTTGCTTAGGATAATGGCCTCCAGCTGCAT 1206
ATGCAGTATTTGGTTTCCTGTTCC 1207
     ATT  TTT TGT-   T TA
ATGCAGT TGG CC   TCCTG GT A
IIIIIII III II   IIIII II
TACGTCG ACC GG   AGGAT CG T
     ---  TCC TAAT    T TT
GAM95
ATGTGTTCGTGACACGGATCAACCTTTTTGTGCTTATCGAGGAGCAGAAAATCGTTGTGAAAGTGTTGAAGCCAC
GT 1220 TGACACGGATCAACCTTTTTGTGC 1221
     TTCG   GGAT-  CT  G   AT
ATGTG  TGACAC   CAAC TTTT TGCTT  C
IIIII  IIIIII   IIII IIII IIIII
TGCAC  GTTGTG   GTTG AAAA ACGAG  G
    CGAA   AAAGT  CT  G   GA
GAM96  ATTCAGAGTCCTGCACCAAGCCCCAGAGATGGTTTTGGTGGGTCTTGGTGGGGCCCAGGAAT 1227
TCAGAGTCCTGCACCAAGCCCCAG 1228
   AGA-  TG    C  GA TG
ATTC  GTCC  CACCAAG CCCA  GA  G
IIII  IIII  IIIIIII IIII  II
TAAG  CGGG  GTGGTTC GGGT  TT  /
   GACC  --     T  GG TT
GAM97  ATTCTTAATCTTAGTGAAATTCTGAAATACTTGATAATTCTTTAAAAGCTGTCTGGTTAAGAAT 1259
TAAAAGCTGTCTGGTTAAGAAT 1260
      T--  GAAATTCT  A CT
ATTCTTAATC TAGT     GAA TA T
IIIIIIIIII IIII     III II
TAAGAATTGG GTCG     CTT AT /
```

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          TCT   AAAATTT- A AG
GAM98
ATTTGTTTTTATTGGTGTAGTCGCTGCAGTTTTACCTGCCATGGTGGTGCTCAGGTATAACATAGATGGAAACAAG
T 1276 TATTGGTGTAGTCGCTGCAGTTTT 1277
          G   A CG  C T   TG
ATTTGTTTTTATT GTGT GT  CTG AGT TTACC  C
IIIIIIIIIIIII IIII II  III III IIIII
TGAACAAGGTAG TACA TA  GAC TCG GGTGG  C
          A   A TG  - T   TA
GAM99
CAAAGCCAGCAACGACATGTACCACAGCCGCGCGCTGCAGGTGGTGCGCGCCCGCAAGCAGATCGTAGCTGGG
GTG 1293 ACGACATGTACCACAGCCGCGCGC 1294
   AAG   A  CA  ACCACA C    C
CA  CCAGC ACGA TGT    GC GCGCGCTG A
II  IIIII IIII III    II IIIIIII
GT  GGTCG TGCT ACG    CG CGCGTGGT G
   GG-  A  AG  AACGCC  -    G
GAM100  CAATGGGAAGGTTGATGCTCGAAGTGACCGAACTGGGGAGGTCATCTTTAAGGACAATTTTTCTTCTG
1303 TGGGAAGGTTGATGCTCGAAGTGA 1304
   AT      ATG  CG  -   GAAC
CA  GGGAAGGTTG  CT AAG TGACC   T
II  IIIIIIIII  II III IIIII
GT  TCTTTTAAC  GA TTC ACTGG   G
   CT      AG- AT  T   AGGG
GAM101
CACAGAATCAGACCATGACTACCTTCACCTGGAACATCAACCACGCCCGGCTGATGGTGGTGGAGGAACCGATG
TGTTTACTGTG 1315 TGACTACCTTCACCTGGAACATCA 1316
    AATC  -  GACTA    TGGAA   A AC
CACAG  AGAC CAT   CCTTCACC   CATCA CC G
IIIII  IIII III   IIIIIIIII   IIIII II
GTGTC  TTTG GTA   GGAGGTGG   GTAGT GG  C
   A---  T  GCCAA    TG---   C CC
GAM102
CACAGAATCAGACCATGACTACCTTCACCTGGAACATCAACCACGCCCGGCTGATGGTGGTGGAGGAACGATGT
GTTTACTGTG 1327 TGACTACCTTCACCTGGAACATCA 1316
    AATC  -  GACTA    TGGAA   A AC
CACAG  AGAC CAT   CCTTCACC   CATCA CC G
IIIII  IIII III   IIIIIIIII   IIIII II
GTGTC  TTTG GTA   GGAGGTGG   GTAGT GG  C
   A---  T  GCAA-    TG---   C CC
GAM102
CACAGAATCAGACCATGACTACCTTCACCTGGAACATCAACCACGCCCGGCTGATGGTGGTGGAGGAACGATGT
GTTTACTGTG 1328 TGACTACCTTCACCTGGAACATCA 1316
    AATC  -  GACTA    TGGAA   A AC
CACAG  AGAC CAT   CCTTCACC   CATCA CC G
IIIII  IIII III   IIIIIIIII   IIIII II
GTGTC  TTTG GTA   GGAGGTGG   GTAGT GG  C
   A---  T  GCAA-    TG---   C CC
GAM102
CACAGAATCAGACCATGACTACCTTCACCTGGAACATCAACCACGCCCGGCTGATGGTGGTGGAGGAACGATGT
GTTTACTGTG 1329 TGACTACCTTCACCTGGAACATCA 1316
```

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    AATC  -  GACTA     TGGAA   A AC
CACAG  AGAC CAT   CCTTCACC   CATCA CC G
|||||  |||| |||   ||||||||   ||||| ||
GTGTC  TTTG GTA   GGAGGTGG   GTAGT GG C
   A---  T  GCAA-     TG---   C  CC
GAM102
CACAGAATCAGACCATGACTACCTTCACCTGGAACATCAACCACGCCCGGCTGATGGTGGTGGAGGAACGATGT
GTTTACTGTG 1330 TGACTACCTTCACCTGGAACATCA 1316
    AATC  -  GACTA     TGGAA   A AC
CACAG  AGAC CAT   CCTTCACC   CATCA CC G
|||||  |||| |||   ||||||||   ||||| ||
GTGTC  TTTG GTA   GGAGGTGG   GTAGT GG C
   A---  T  GCAA-     TG---   C  CC
GAM102
CACAGAATCAGACCATGACTACCTTCACCTGGAACATCAACCACGCCCGGCTGATGGTGGTGGAGGAACGATGT
GTTTACTGTG 1331 TGACTACCTTCACCTGGAACATCA 1316
    AATC  -  GACTA     TGGAA   A AC
CACAG  AGAC CAT   CCTTCACC   CATCA CC G
|||||  |||| |||   ||||||||   ||||| ||
GTGTC  TTTG GTA   GGAGGTGG   GTAGT GG C
   A---  T  GCAA-     TG---   C  CC
GAM102
CACAGAATCAGACCATGACTACCTTCACCTGGAACATCAACCACGCCCGGCTGATGGTGGTGGAGGAACGATGT
GTTTACTGTG 1332 TGACTACCTTCACCTGGAACATCA 1316
    AATC  -  GACTA     TGGAA   A AC
CACAG  AGAC CAT   CCTTCACC   CATCA CC G
|||||  |||| |||   ||||||||   ||||| ||
GTGTC  TTTG GTA   GGAGGTGG   GTAGT GG C
   A---  T  GCAA-     TG---   C  CC
GAM102
CACAGAATCAGACCATGACTACCTTCACCTGGAACATCAACCACGCCCGGCTGATGGTGGTGGAGGAACGATGT
GTTTACTGTG 1333 TGACTACCTTCACCTGGAACATCA 1316
    AATC  -  GACTA     TGGAA   A AC
CACAG  AGAC CAT   CCTTCACC   CATCA CC G
|||||  |||| |||   ||||||||   ||||| ||
GTGTC  TTTG GTA   GGAGGTGG   GTAGT GG C
   A---  T  GCAA-     TG---   C  CC
GAM102
CACAGAATCAGACCATGACTACCTTCACCTGGAACATCAACCACGCCCGGCTGATGGTGGTGGAGGAACGATGT
GTTTACTGTG 1334 TGACTACCTTCACCTGGAACATCA 1316
    AATC  -  GACTA     TGGAA   A AC
CACAG  AGAC CAT   CCTTCACC   CATCA CC G
|||||  |||| |||   ||||||||   ||||| ||
GTGTC  TTTG GTA   GGAGGTGG   GTAGT GG C
   A---  T  GCAA-     TG---   C  CC
GAM102
CACAGAATCAGACCATGACTACCTTCACCTGGAACATCAACCACGCCCGGCTGATGGTGGTGGAGGAACGATGT
GTTTACTGTG 1335 TGACTACCTTCACCTGGAACATCA 1316
    AATC  -  GACTA     TGGAA   A AC
CACAG  AGAC CAT   CCTTCACC   CATCA CC G
```

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||||| ||| |||  |||||||   ||||| ||
GTGTC  TTTG GTA   GGAGGTGG   GTAGT GG  C
   A---  T  GCAA-    TG---   C  CC
GAM103
CACAGACGAACAGGCAAGGGGCTAGGGAAGAAGAGGGGACCCATGTCTTCGGAAATACAAGGGACTTCTGCAAT
CCATGGAGAATGCCAAATAATGTG 1336 TACAAGGGACTTCTGCAATCCATG 1337
   GACGAACA  AGGGG  G  AGA-    GGA  A ---- T
CACA     GGCA   CTA GGA   AGAGG  CCC TG   TC T
||||      ||||    ||| |||   |||||  ||| || ||
GTGT     CCGT   GGT CCT   TCTTC  GGG AC   AG C
   AATAAA--  AAGA-  A  AACG   A--  A ATAA  G
GAM104  CACCTGCCCCAGCCCCTGCCTCTGCCCCAAGTGGGGCCAGCTGCCCTCACTTCTGGGGTGGATG
1347 ACCTGCCCCAGCCCCTGCCTCTGC 1348
  C TG   CCCCT--- CT  -   A
CA C CCCCAG      GC CTG CCCC A
|| | ||||||      || ||| ||||
GT G GGGGTC      CG GAC GGGG G
   A GT    TTCACTCC TC  C   T
GAM105  CACTAACAACTTCTGGCCGGGCCACGGGGCTCATGCCTTGTAATTCTCAGCCAGAGGGCGGGTG 1391
TAACAACTTCTGGCCGGGCCACGG 1392
   AACAA     C CC--     T
CACT   CTTCTGGC GGG   ACGGGGC C
||||   |||||||| |||   |||||||
GTGG   GGAGACCG CTC   TGTTCCG A
   GCG--     A TTAA     T
GAM106  CACTGGCCGAACTCTCGGTCTCGGGTCTTGAGTGGGGCCCGCAGCCGAAGAGTTGCAGGTG 1403
TGGCCGAACTCTCGGTCTCGGGTC 1404
   G CG    -  CT     G
CACT GC  AACTCT CGGT  CGGGTCTT A
|||| || |||||| ||||  ||||||||
GTGG CG  TTGAGA GCCG  GCCCGGGG G
   A  --   A  AC    T
GAM107  CACTTGTAATCCCCCCTGTACTTACCTACTCACATTGGAGAGTTCTGAGGCCGGAGTAACTGTG 1411
AGTTCTGAGGCCGGAGTAACTGTG 1412
   TTG A  CC  GT--   A TACT
CAC  TA TCC CCT   ACTT CC   C
|||  || ||| |||   |||| ||
GTG  AT AGG GGA   TGAG GG   A
   TCA G  CC  GTCT   A TTAC
GAM108  CAGAATGTCAGAGCTGAGTCTGGTGTTACTGACTAAGGAACAACCTGACTCAGGCTCTAGATGGCTG
1428 TGTCAGAGCTGAGTCTGGTGTTAC 1429
   AAT  -   -   T  -  A GA
CAG  GTC AGAGC TGAGTC GGT GTT CT  C
|||  ||| ||||| ||||||| ||| ||| ||
GTC  TAG TCTCG ACTCAG CCA CAA GA  /
   GG- A  G    T A G AT
GAM109
CAGAGATCAGAATACGAAGCTTCCTCTCAGCATCATGGGAGGAGATAAAATAATTCATTCTATGGTCTTTG 1443
GGAGGAGATAAAATAATTCATTCT 1444
      --  AC  GC-------    GC
```

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CAGAGATCA GAAT GAA      TTCCTCTCA A
||||||||| |||| |||      |||||||||
GTTTCTGGT CTTA CTT      GAGGAGGGT T
     AT  --  AATAAAATA      AC
GAM110
CAGCACCATAACACTAGACCCAGCCTAACTGTCCTGCAACAGGGGATGGGTAAAAGGGATGATGGCGCTG 1462
TAACACTAGACCCAGCCTAACTGT 1463
   A  AACA- AG-   G  AA   CC
CAGC CCAT   CT  ACCCA CCT CTGT T
|||| ||||   ||  ||||| ||| ||||
GTCG GGTA   GA  TGGGT GGG GACA G
   C  GTAGG  AAA   A  --   AC
GAM111 CAGCATCTGGTCCTTTTGCTGTGACCCACCCCATCCCGGAGCTGGTCGGGTCTGGCTGGATGTGCTG
1487 TCTGGTCCTTTTGCTGTGACCCAC 1488
     CTG  TTTT  T  -  ---- AT
CAGCAT GTCC  GCTG GACCC ACC  CC C
|||||| ||||  |||| ||||| |||   ||
GTCGTG TAGG  CGGT CTGGG TGG  GG /
     ---  T---  -   C  TCGA CC
GAM112 CAGCCCACGCCTGGGGAGCCTGCCTGGGGCCATGTGACCATGGCCTCTCCCTGGGAACGGGCTG
1494 TGGCCTCTCCCTGGGAACGGGCTG 1495
     ACG  TG   CCTGCCTG       T
CAGCCC  CC GGGAG      GGGCCATG G
|||||| || |||||      ||||||||
GTCGGG  GG CCCTC      TCCGGTAC A
    CAA  GT  --------      C
GAM113
CAGGCCCTAGGAGGGCGAGGGCTTAGTAGGTATCTTCAGGGTCAGAGCCTGAGTCCTCGCCTTGTTGGTTCTG
1515 TAGGAGGGCGAGGGCTTAGTAGGT 1516
   GC  T  G        AGT   A  TCA
CAG  CC AG AGGGCGAGGGCTT  AGGT TCT  G
|||  || || ||||||||||||  |||| |||
GTC  GG TT TTCCGCTCCTGAG  TCCG AGA  G
    TT  -  G          --- - CTG
GAM114 CAGTGTGCACGTGGGAACCTGTCCCCAGGCTGGAGCATAGGGGCATGATCCCAGCTCACTG 1525
TAGGGGCATGATCCCAGCTCACTG 1526
    T  ACG   ACC    CAG  T
CAGTG GC  TGGGA  TGTCCC  GC G
||||| ||  |||||  ||||||  ||
GTCAC CG  ACCCT  ACGGGG  CG G
    T  ---   AGT    ATA  A
GAM115 CATCTCACTAAGTGCTGATCAGTTTTGATTCAGTTGGAGTAGAGCACATAGGTTCTTTGGAGATG 1575
TCTCACTAAGTGCTGATCAGTTTT 1576
    ACT  T  GATCA     A  A
CATCTC  AAG GCT    GTTTTG TTC G
||||||  ||| |||    |||||| |||
GTAGAG  TTC TGG    CGAGAT AGG T
    GT-  T ATACA      G  T
GAM116
CATGAAAGAAGCCTGGTTACTGATTTGTATAAAATGTACTCTTAAAGTATAAAGTATAAGGTAAGGTAAATTTCATG
1589 TAAAGTATAAGGTAAGGTAAATTT 1590
```

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     GAA  GGT  GAT   AAAA    CT
CATGAAA  GCCT  TACT  TTGTAT   TGTACT  T
|||||||  ||||  ||||  ||||||   ||||||
GTACTTT  TGGA  ATGG  AATATG   ATATGA  /
    AAA  ---   ---   AA--     AA
GAM117 CATGACAACAGACACATTGACATGGGTGGGTTTACCCGCCAAGCGGTCGATGGTCTTCTGTGTG 1616
TGACAACAGACACATTGACATGGG 1617
   G  AC  A   ATG--    T
CAT ACA  AGAC CATTGAC   GGTGGG T
||| |||  |||| |||||||   ||||||
GTG TGT  TCTG GTAGCTG   CCGCCC T
 -  CT   -    GCGAA     A
GAM118 CATGACAACAGACACATTGACATGGGTGGGTTTACCGCCAAGCGGTCGATGGTCTTCTGTGTG 1643
TGACAACAGACACATTGACATGGG 1617
   G  AC  A   ATG--    GT
CAT ACA  AGAC CATTGAC   GGTGG T
||| |||  |||| |||||||   |||||
GTG TGT  TCTG GTAGCTG   CCGCC /
 -  CT   -    GCGAA     AT
GAM118 CATGACAACAGACACATTGACATGGGTGGGTTTACCGCCAAGCGGTCGATGGTCTTCTGTGTG 1644
TGACAACAGACACATTGACATGGG 1617
   G  AC  A   ATG--    GT
CAT ACA  AGAC CATTGAC   GGTGG T
||| |||  |||| |||||||   |||||
GTG TGT  TCTG GTAGCTG   CCGCC /
 -  CT   -    GCGAA     AT
GAM118 CATGACAACAGACACATTGACATGGGTGGGTTTACCGCCAAGCGGTCGATGGTCTTCTGTGTG 1645
TGACAACAGACACATTGACATGGG 1617
   G  AC  A   ATG--    GT
CAT ACA  AGAC CATTGAC   GGTGG T
||| |||  |||| |||||||   |||||
GTG TGT  TCTG GTAGCTG   CCGCC /
 -  CT   -    GCGAA     AT
GAM118 CATGACAACAGACACATTGACATGGGTGGGTTTACCGCCAAGCGGTCGATGGTCTTCTGTGTG 1646
TGACAACAGACACATTGACATGGG 1617
   G  AC  A   ATG--    GT
CAT ACA  AGAC CATTGAC   GGTGG T
||| |||  |||| |||||||   |||||
GTG TGT  TCTG GTAGCTG   CCGCC /
 -  CT   -    GCGAA     AT
GAM118 CATGACAACAGACACATTGACATGGGTGGGTTTACCGCCAAGCGGTCGATGGTCTTCTGTGTG 1647
TGACAACAGACACATTGACATGGG 1617
   G  AC  A   ATG--    GT
CAT ACA  AGAC CATTGAC   GGTGG T
||| |||  |||| |||||||   |||||
GTG TGT  TCTG GTAGCTG   CCGCC /
 -  CT   -    GCGAA     AT
GAM118 CATGACAACAGACACATTGACATGGGTGGGTTTACCGCCAAGCGGTCGATGGTCTTCTGTGTG 1648
TGACAACAGACACATTGACATGGG 1617
   G  AC  A   ATG--    GT
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CAT ACA  AGAC CATTGAC    GGTGG T
||| |||  |||| |||||||    |||||
GTG TGT  TCTG GTAGCTG    CCGCC /
  -  CT   -    GCGAA     AT
GAM118  CATGACAACAGACACATTGACATGGGTGGGTTTACCGCCAAGCGGTCGATGGTCTTCTGTGTG 1649
TGACAACAGACACATTGACATGGG 1617
   G  AC  A    ATG--   GT
CAT ACA  AGAC CATTGAC    GGTGG T
||| |||  |||| |||||||    |||||
GTG TGT  TCTG GTAGCTG    CCGCC /
  -  CT   -    GCGAA     AT
GAM118  CATGACAACAGACACATTGACATGGGTGGGTTTACCGCCAAGCGGTCGATGGTCTTCTGTGTG 1650
TGACAACAGACACATTGACATGGG 1617
   G  AC  A    ATG--   GT
CAT ACA  AGAC CATTGAC    GGTGG T
||| |||  |||| |||||||    |||||
GTG TGT  TCTG GTAGCTG    CCGCC /
  -  CT   -    GCGAA     AT
GAM118  CATGACAACAGACACATTGACATGGGTGGGTTTACCGCCAAGCGGTCGATGGTCTTCTGTGTG 1651
TGACAACAGACACATTGACATGGG 1617
   G  AC  A    ATG--   GT
CAT ACA  AGAC CATTGAC    GGTGG T
||| |||  |||| |||||||    |||||
GTG TGT  TCTG GTAGCTG    CCGCC /
  -  CT   -    GCGAA     AT
GAM118  CATGACAACAGACACATTGACATGGGTGGGTTTACCGCCAAGCGGTCGATGGTCTTCTGTGTG 1652
TGACAACAGACACATTGACATGGG 1617
   G  AC  A    ATG--   GT
CAT ACA  AGAC CATTGAC    GGTGG T
||| |||  |||| |||||||    |||||
GTG TGT  TCTG GTAGCTG    CCGCC /
  -  CT   -    GCGAA     AT
GAM118  CATGACAACAGACACATTGACATGGGTGGGTTTACCGCCAAGCGGTCGATGGTCTTCTGTGTG 1653
TGACAACAGACACATTGACATGGG 1617
   G  AC  A    ATG--   GT
CAT ACA  AGAC CATTGAC    GGTGG T
||| |||  |||| |||||||    |||||
GTG TGT  TCTG GTAGCTG    CCGCC /
  -  CT   -    GCGAA     AT
GAM118  CATGACAACAGACACATTGACATGGGTGGGTTTACCGCCAAGCGGTCGATGGTCTTCTGTGTG 1654
TGACAACAGACACATTGACATGGG 1617
   G  AC  A    ATG--   GT
CAT ACA  AGAC CATTGAC    GGTGG T
||| |||  |||| |||||||    |||||
GTG TGT  TCTG GTAGCTG    CCGCC /
  -  CT   -    GCGAA     AT
GAM118  CATGACAACAGACACATTGACATGGGTGGGTTTACCGCCAAGCGGTCGATGGTCTTCTGTGTG 1655
TGACAACAGACACATTGACATGGG 1617
   G  AC  A    ATG--   GT
CAT ACA  AGAC CATTGAC    GGTGG T
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|||·|||·||||·|||||||·····|||||
GTG TGT  TCTG GTAGCTG    CCGCC /
  - CT  -    GCGAA    AT
GAM118  CATGACAACAGACACATTGACATGGGTGGGTTTACCGCCAAGCGGTCGATGGTCTTCTGTGTG 1656
TGACAACAGACACATTGACATGGG 1617
   G  AC  A     ATG--   GT
CAT ACA  AGAC CATTGAC    GGTGG  T
|||·|||·||||·|||||||·····|||||
GTG TGT  TCTG GTAGCTG    CCGCC /
  - CT  -    GCGAA    AT
GAM118  CATGACAACAGACACATTGACATGGGTGGGTTTACCGCCAAGCGGTCGATGGTCTTCTGTGTG 1657
TGACAACAGACACATTGACATGGG 1617
   G  AC  A     ATG--   GT
CAT ACA  AGAC CATTGAC    GGTGG  T
|||·|||·||||·|||||||·····|||||
GTG TGT  TCTG GTAGCTG    CCGCC /
  - CT  -    GCGAA    AT
GAM118  CATGACAACAGACACATTGACATGGGTGGGTTTACCGCCAAGCGGTCGATGGTCTTCTGTGTG 1658
TGACAACAGACACATTGACATGGG 1617
   G  AC  A     ATG--   GT
CAT ACA  AGAC CATTGAC    GGTGG  T
|||·|||·||||·|||||||·····|||||
GTG TGT  TCTG GTAGCTG    CCGCC /
  - CT  -    GCGAA    AT
GAM118  CATGACAACAGACACATTGACATGGGTGGGTTTACCGCCAAGCGGTCGATGGTCTTCTGTGTG 1659
TGACAACAGACACATTGACATGGG 1617
   G  AC  A     ATG--   GT
CAT ACA  AGAC CATTGAC    GGTGG  T
|||·|||·||||·|||||||·····|||||
GTG TGT  TCTG GTAGCTG    CCGCC /
  - CT  -    GCGAA    AT
GAM118  CATGACAACAGACACATTGACATGGGTGGGTTTACCGCCAAGCGGTCGATGGTCTTCTGTGTG 1660
TGACAACAGACACATTGACATGGG 1617
   G  AC  A     ATG--   GT
CAT ACA  AGAC CATTGAC    GGTGG  T
|||·|||·||||·|||||||·····|||||
GTG TGT  TCTG GTAGCTG    CCGCC /
  - CT  -    GCGAA    AT
GAM118  CATGACAACAGACACATTGACATGGGTGGGTTTACCGCCAAGCGGTCGATGGTCTTCTGTGTG 1661
TGACAACAGACACATTGACATGGG 1617
   G  AC  A     ATG--   GT
CAT ACA  AGAC CATTGAC    GGTGG  T
|||·|||·||||·|||||||·····|||||
GTG TGT  TCTG GTAGCTG    CCGCC /
  - CT  -    GCGAA    AT
GAM118  CATGACAACAGACACATTGACATGGGTGGGTTTACCGCCAAGCGGTCGATGGTCTTCTGTGTG 1662
TGACAACAGACACATTGACATGGG 1617
   G  AC  A     ATG--   GT
CAT ACA  AGAC CATTGAC    GGTGG  T
|||·|||·||||·|||||||·····|||||
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GTG TGT  TCTG GTAGCTG    CCGCC /
 - CT  -    GCGAA    AT
GAM118  CATGACAACAGACACATTGACATGGGTGGGTTTACCGCCAAGCGGTCGATGGTCTTCTGTGTG 1663
TGACAACAGACACATTGACATGGG 1617
  G  AC  A     ATG--    GT
CAT ACA  AGAC CATTGAC    GGTGG  T
||| ||| |||| |||||||    |||||
GTG TGT  TCTG GTAGCTG    CCGCC /
 - CT  -    GCGAA    AT
GAM118  CATGACAACAGACACATTGACATGGGTGGGTTTACCGCCAAGCGGTCGATGGTCTTCTGTGTG 1664
TGACAACAGACACATTGACATGGG 1617
  G  AC  A     ATG--    GT
CAT ACA  AGAC CATTGAC    GGTGG  T
||| ||| |||| |||||||    |||||
GTG TGT  TCTG GTAGCTG    CCGCC /
 - CT  -    GCGAA    AT
GAM118  CATGACAACAGACACATTGACATGGGTGGGTTTACCGCCAAGCGGTCGATGGTCTTCTGTGTG 1665
TGACAACAGACACATTGACATGGG 1617
  G  AC  A     ATG--    GT
CAT ACA  AGAC CATTGAC    GGTGG  T
||| ||| |||| |||||||    |||||
GTG TGT  TCTG GTAGCTG    CCGCC /
 - CT  -    GCGAA    AT
GAM118  CATGACAACAGACACATTGACATGGGTGGGTTTACCGCCAAGCGGTCGATGGTCTTCTGTGTG 1666
TGACAACAGACACATTGACATGGG 1617
  G  AC  A     ATG--    GT
CAT ACA  AGAC CATTGAC    GGTGG  T
||| ||| |||| |||||||    |||||
GTG TGT  TCTG GTAGCTG    CCGCC /
 - CT  -    GCGAA    AT
GAM119
CATGCTTGAGCAAAACAACAGACATTGGTGAGGGCTGGGTCGCCTGGACCACAAGTTTGACTGATGTTTGCCAG
GCGTG 1667 AACAACAGACATTGGTGAGGGCTG 1668
    A   ACAA---   AT-  GA   TG
CATGCTTG GCAAA    CAGAC  TGGT  GGGC  G
|||||||| |||||      |||||   |||| ||||
GTGCGGAC CGTTT     GTTTG  ACCA  TCCG  G
   -    GTAGTCA   AAC   GG   CT
GAM120  CATGTGATGATAATGGTCTTCTCGCCATCCCAAGATGGGTTGGCAGCCATGATCTTTGCATG 1684
TGTGATGATAATGGTCTTCTCGCC 1685
  TG T  A   T TCTC  T  AA
CATG  A GAT ATGG CT   GCCA CCC  G
|||| | ||| |||| ||    |||| |||
GTAC  T CTA TACC GA   CGGT GGG  /
  GT T  G  -  ----   T  TA
GAM121  CATGTTATACCTGGAAAGGACCGTGGGCACTAATCTGCACTTTGTTCCAGGTAATCCATG 1699
TGTTATACCTGGAAAGGACCGTGG 1700
  TTA     AG  CC TG  CA
CATG  TACCTGGAA GA  G  GG  C
|||| ||||||||| || | ||
```

GTAC  ATGGACCTT TT C CT T
   CTA      GT CA GT AA
GAM122
CATGTTATAGATTATTTGGAAAGACTGTATTTCCCATTGTCACAAAGCAAGTTTATTTCAAATGCTTTATCACATG
1702 TGTTATAGATTATTTGGAAAGACT 1703
   T   T     -  - ATTTCCCA
CATGT ATAGA TATTTGGAA AGACT GT     T
||||| ||||| ||||||||| ||||| ||
GTACA TATTT GTAAACTTT TTTGA CG      T
    C   C     A   A AAACACTG
GAM123  CATTCCTGAGGGGTTGGCCTCATGACCCAAAGACACCCATTAGGCCCCAGCTCCAACATTGGGATG
1722 TTAGGCCCCAGCTCCAACATTGGG 1723
   TGA---   --  C ACCCAA
CATTCC   GGGGTT GGCCT ATG    A
||||||     |||||| ||||| |||
GTAGGG   CCTCGA CCGGA TAC   /
   TTACAA   CC   T CCACAG
GAM124
CATTCTGGATTTGGTCGATTGCTTCTTTTTAGTATCTTTAACTTATTAGATCTCAAACTCAGCTGCACATCAGAATG
1734 TTAGATCTCAAACTCAGCTGCACA 1735
    ATTT- C -- CT- TTTT ATC
CATTCTGG  GGT GA TTG TCT  AGT T
||||||||   ||| || ||| |||   |||
GTAAGACT  TCG CT AAC AGA   TCA /
    ACACG A CA TCT TTAT ATT
GAM125
CCAACAGGATGCCACGCTGGGCCGAGCGACTATTTCCTGCCAATGTTGCTCACTCGGTGTACGTCCTGGAGG
1741 ACTCGGTGTACGTCCTGGAGG 1742
  AA   CC     CC    TATTTC
CC CAGGATG ACGCTGGG GAGCGAC    C
|| ||||||| |||||||| |||||||
GG GTCCTGC TGTGGCTC CTCGTTG    T
  AG   A-   A-    TAACCG
GAM126
CCAACCACATGGCACATCGGGCTATTTGAACACGGTGACTGTCTCTCCCAGATGGATCCCTCTGTGCTTCTTGGA
CGG 1770 TGGCACATCGGGCTATTTGAACAC 1771
  AA  CAT   TC  --    AACAC T CT
CC CCA  GGCACA GGG CTATTTG   GG GA G
|| ||| |||||| ||| |||||||   || ||
GG GGT  TCGTGT CCC GGTAGAC   CC CT /
  CA TCT   CT TA    ----- T CT
GAM127
CCAACCAGAGCAGTTCGACTGGGCCATCAATGACCGCATCAATGAGATGGTCCACTTCGACCTGCCAGGGCAGG
 1780 TGAGATGGTCCACTTCGACCTGCC 1781
  AA AGA  T  C-    AA-- CC
CC CC  GCAG TCGA TGGGCCATC   TGA G
|| || |||| |||| |||||||||   |||
GG GG  CGTC AGCT ACCTGGTAG   ACT /
  AC GAC  C  TC     AGTA AC
GAM128
CCAAGACCAACAGGATGCCACGCTGGGCCGAGCGACTATTTCCTGCCAATGTTGCTCACTCGGTGTACGTCCTG

GAGGACTCTATTGTGG 1786 GCTCACTCGGTGTACGTCCTGGAG 1787
 ---- -- AA    CC    CC    TATTTC
CCA  AGA CC CAGGATG ACGCTGGG GAGCGAC   C
||| ||| || |||||||| |||||||| ||||||
GGT  TCT GG GTCCTGC TGTGGCTC CTCGTTG    T
  GTTA CA AG    A-    A-    TAACCG
GAM129
CCAAGTTCATTGAGGTATCTAAAGAGGCCCGGAAGCGGTTCCTGGGCCCCCTGCACCCCTCCTTCAACCTGG
1803 TGAGGTATCTAAAGAGGCCCGGAA 1804
 A  CATT  TATCTAA A-   -  G
CCA GTT  GAGG    AG GGCCC GGAA C
||| |||   ||||     || ||||| ||||
GGT CAA   CTCC     TC CCGGG CCTT G
  C  CTTC  CCACG-- CC   T  G
GAM130
CCAATGGCACATGGACTGGTGTTAGCAAGGAAGGGACCCTTTGTTTAGAACGGGTCAGATGGGCCGTGGG 1812
TGGCACATGGACTGGTGTTAGCAA 1813
 A  A G- G GTT-   AAG
CC ATGGC CAT GACT GT  AGCAAGG  G
|| ||||| ||| |||| ||  |||||||
GG TGCCG GTA CTGG CA  TTGTTTC  G
 G  G GA  G AGAT    CCA
GAM131
CCAATGGGAGGTTTGTGTACAGTCAGTGAAATTGAAGAACATTTATGTCATTAATGGACTTACATAGCTATTGG
1825 TGTCATTAATGGACTTACATAGCT 1826
    GAGGT    C  ----   AAT  GA
CCAATGG   TTGTGTA AGTC   AGTGA  TGAA  A
|||||||   |||||||| ||||   ||||| ||||
GGTTATC   GATACAT TCAG   TTACT  ATTT  /
   -----      - GTAA   GT- AC
GAM132
CCACCCCATGATTTTAGCATTCATTGATGATTCTTGTGTGAACGTTTAATACATTTGTGATTATGGAATTTTAACGT
GG 1842 TTAGCATTCATTGATGATTCTTGT 1843
  CCCAT    GCAT  T  - CT-  G
CCAC   GATTTTA  TCAT GATG ATT  TGT T
||||   |||||||  |||| |||| |||  |||
GGTG   TTAAGGT  AGTG TTAC TAA  GCA G
  CAATT    ATT-  T  A TTT  A
GAM133
CCACCTGCCGGGAGCATGCCTCTGCGCCACTGGGGGATGGCCAGGGCAGTAAGCCCGTTGGGGATGG 1857
TGGCCAGGGCAGTAAGCCCGTTGG 1858
 -- GC  AGCA-  T  C  - TG
CCA CCT CGGG    TGCC CTG GCCA C  G
||| ||| ||||    |||| ||| |||| |
GGT GGG GCCC    ACGG GAC CGGT G  /
  AG  TT  GAATG  -  -  A GG
GAM134 CCACGCCTGGCTAATTTTTGTATTTTTAATAAAGATGCAGTGTCACCATATTGGCCAGGCTGG 1880
TGCAGTGTCACCATATTGGCCAGG 1881
 C    TT-------     A
CCA GCCTGGCTAAT     TTGTATTTTT A

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||| |||||||||     ||||||||||
GGT CGGACCGGTTA     GACGTAGAAA /
 -      TACCACTGT      T
GAM135
CCACGGGCACCTACCACGGGGACAGCGACCTGCAGCTGGAACGCATCAACGTGTACTACAATGAGGCCACCGG
CGGCAGTACGTGCCCCGCGCCGTGCTCGTGG 1887 TGAGGCCACCGGCGGCAGTACGTG 1888
      CTACCA   A G AC  A   AAC A  AC  T
CCACGGGCAC    CGGGG CA CG CTGC GCTGG  GC TCA  GTG A
|||||||||||     ||||| || || |||| |||||  || ||| |||
GGTGCTCGTG    GCCCC GT GC  DACG CGGCC  CG AGT  CAT /
     CCGC--  - - AT  G   AC- G  AA  C
GAM136
CCACTGCTTCATGAGCTCAAATCTGTTTTTTCTAGCTAAGAGACCACAGGCCAAAGAACTAAAGGGCAAGCAGGG
1898 TGAGCTCAAATCTGTTTTTTCTAG 1899
 A   CATGA  AAATCT    CTA  AAGAG
CC CTGCTT  GCTC   GTTTTTT  GCT   A
|| ||||||   ||||    |||||||  |||
GG DACGAA   CGGG   CAAGAAA  CGG   /
 -   -----  AAAT--   C--  ACACC
GAM137
CCAGCTTCTAGATGACATAGAATGACATGTAATGCTAAATTTCATTTTGGCTTTGCAAGTCATGAAGCTTAGG 1907
TGACATAGAATGACATGTAATGCT 1908
 --   TAGATGACATAGA   A   T    TT
CC  AGCTTC         ATGAC TGTAA GCTAAA  T
|| ||||||          ||||| ||||| ||||||
GG  TCGAAG         TACTG ACGTT CGGTTT  C
 AT  -------------  A   T    TA
GAM138
CCAGGATCAGGAGGACCCCGAGGAGTTCTACGTGCTGAGCGAGACCACCTTGGCCCAGCCCCAGAGCCTGG
1922 TCAGGAGGACCCCGAGGAGTTCTA 1923
    A A A ACC--   AGT  A  GC
CCAGG TC GG GG   CCGAGG  TCT CGT  T
||||| || || ||   ||||||  ||| |||
GGTCC AG CC CC   GGTTCC  AGA GCG  /
   G A - GACCC    ACC - AG
GAM139
CCAGGCCGGGCCACCGCCGGCCCCCTGGGCTGTCCGCGGGAGCCGACTGCCTGAACAGCTTTACCGCCGGGG
TGCCTGGCTTCGTGCTGG 1947 AACAGCTTTACCGCCGGGGTGCCT 1948
    ------   C  G   CCCCT    C  C  G  C
CCAG    GCCGGGC ACC CCGGC   GGGCTGT CG GG AG C
||||    |||||||| ||| |||||    ||||||| || || ||
GGTC    CGGTCCG TGG GGCCG    TTCGACA GT CC TC G
   GTGCTT   - -  CCAT-   A - G A
GAM140
CCATCCCCCAGCTGGCATACTGTGTAGTGCAGTTTTTAGGAAAGAGGACCGCACCCTCAGGGAACCAGTGGTGA
TGG 1954 TGGCATACTGTGTAGTGCAGTTTT 1955
   C  CA   CATA  TGTA  A   AG
CCATC CC GCTGG   CTG  GTGC GTTTTT  G
|||||| || |||||   |||   |||| ||||||
GGTAG GG TGACC   GAC   CACG CAGGAG  A
```

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     T --    AAGG  TCC-   C    AA
GAM141  CCATGACACAGTTCTGTCTTGGCCAGGGACCTGGCTGGTGGAGAGGTGGAAGTTGCATGG 1967
TGACACAGTTCTGTCTTGGCCAGG 1968
    ACA----  G   G  - TG    G
CCATG     CA TTCT TC T  GCCAG  G
|||||     || |||| || |  |||||
GGTAC     GT GAGA GG G  CGGTC  A
   GTTGAAG  G   - T GT    C
GAM142  CCATGGAGTAGATTACAGCGTGTTGGACAAGGACATTCCCCCGCGTGAAGGCACACTCCATGG 1983
TGGAGTAGATTACAGCGTGTTGGA 1984
      AGATTACA    TT  CAAG
CCATGGAGT     GCGTG  GGA   G
|||||||||     ||||| |||
GGTACCTCA     TGCGC  CCT   /
      CACGGAAG    CC  TACA
GAM143
CCCAATTAACATCGAGGTCTCAGCAAACAATTACCACATTTAACATATATGGAGTTAAAGTAGATTGGATTTGCTG
AAAATCGGTGCTGGG 1992 TCTCAGCAAACAATTACCACATTT 1993
    ATTAA    GGTC     --   ACC  A    ATAT
CCCA    CATCGA   TCAGCAAA  CAATT  AC TTTAAC   A
||||    ||||||   |||||||| |||||  || ||||||
GGGT    GTGGCT   AGTCGTTT  GTTAG  TG AAATTG   /
   C----   AAA-    AG   A-- -    AGGT
GAM144
CCCAGGATGAGTTCTACCGCAGCGGCTGGGCCCTGAACATGAAGGAGCTGAAGCTGCTGCAGACCATCGGG
2008 TGAGTTCTACCGCAGCGGCTGGGC 2009
   AG   A T ACC     G- - GAA
CCC GATG GT CT  GCAGCGGCT GGC CCT  C
||| |||| || ||  ||||||||| ||| |||
GGG CTAC CA GA  CGTCGTCGA TCG GGA  A
   --  - - ---     AG  A  AGT
GAM145  CCCCATCTAAACTGGAGAAGCCCCCAACACTTTTAAGCTATGTGGAGGGGTGGGAGTTTGGGAGGGG
2020 TCTAAACTGGAGAAGCCCCCAACA 2021
    AT    GGAGAA   CAA  TTTTA
CCCC CTAAACT   GCCCC  CAC   A
|||| |||||||   ||||| |||
GGGG GGTTTGA   TGGGG  GTG   /
   AG    GGG---  AG- TATCG
GAM146  CCCCTTCCCATCCCCCCACCCGCCTGCCCATGGGCCAGTCCTAGGAGCAGCTGGGGATGAAGGGG
2040 TAGGAGCAGCTGGGGATGAAGGGG 2041
    CC    CCACCC  C - AT  C
CCCCTTC ATCCCC    GC TGC CC GGG C
||||||| ||||||    || ||| || |||
GGGGAAG TAGGGG    CG ACG GG CCT A
     --    T----- - A AT  G
GAM147  CCCGGCAGCACCCCTAGCAAATAGGTCTGTATCAAAGATTCTGTACAGCTGGTTTTGGGGGGTGAAGGG
2112 CAGCTGGTTTTGGGGGGTGAAGGG 2113
   GGCAG    GC  A T   T AAG
CCC   CACCCCTA AAAT GG CTGTA CA  A
|||   |||||||| |||| || ||||| ||
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GGG    GTGGGGGT  TTTG  TC  GACAT  GT  /
 AA---        --  G  -   -  CTT
GAM148
CCCGGCCCGGAATGGAATGGGATTCACGCGACTGCACCAGGTGGGCAATTTGTTGATCTCAGGGCACGTGG
2125 TGGAATGGGATTCACGCGACTGCA 2126
 - -  GGAATGGAA    C  C  C  A  A
CC CG GCCC      TGGGATT  ACG  GA  TGC  CC  G
|| || ||||       |||||||| |||  || |||  ||
GG GC CGGG      ACTCTAG  TGT  TT  ACG  GG  G
 T A  ---------     T  -  A  -  T
GAM149
CCCGGCCTCGTTGCCCCCTGGCGACCCTCAGCTCATCGCTATCATCGTGGGGCAGCTCAAGAGCAGGG 2132
TATCATCGTGGGGCAGCTCAAGAG 2133
 G  -  C--      CTG    CCCTC   TC
CCC GC CT  GTTGCCCC  GCGA    AGC  A
||| || || ||||||||  ||||     |||
GGG CG GA  CGACGGGG  TGCT    TCG  /
 A  A ACT        ---   ACTA-  CT
GAM150
CCCGGGGACTGAGAGTTAAGGAGAGTTGGAGGCTTTACTGGGCCACAGGGTTCCTACTCGCCCCTGGG 2141
TGAGAGTTAAGGAGAGTTGGAGGC 2142
    ACTGA   TA   AG  GA    T
CCCGGGG    GAGT  AGGAG  TTG  GGCTT  A
|||||||    |||| ||||| ||| |||||
GGGTCCC    CTCA  TCCTT  GAC  CCGGG  C
    CG---   --  GG  A-   T
GAM151  CCCTCATACCAACTGTGGACTTGGAATATCAGCAGAGTAGTAGGCACAGTTGTAAAAGGG 2157
TACCAACTGTGGACTTGGAATATC 2158
  CATAC     GA  TGGAATA  A
CCCT   CAACTGTG  CT    TC  G
||||   |||||||| ||     ||
GGGA   GTTGACAC  GA    AG  C
  AAAAT     G- TGATG--  A
GAM152  CCCTGGCAGACTTCACACCTCATTGCTTTACCCCCTGGGCCTGGGGAAATGTCTGTACTTTGGG 2170
TGGCAGACTTCACACCTCATTGCT 2171
 TG---    TTCACA   TT  TAC
CCC   GCAGAC    CCTCA  GCTT  C
|||   ||||||      ||||| ||||
GGG   TGTCTG    GGGGT  CGGG  C
 TTTCA    TAAA--   C-  TCC
GAM153
CCGCCCCGTGCCCCGCCGCGCCCCCTGCGGGGGCGAGGTCGGGCCTGGCGCTGCGGGCCTGTCGCCCTCGG
CGGGGGGTGCGGGTGCGGACGGGCGG 2182 TGTCGCCCTCGGCGGGGGGTGCGG 2183
    C  G  C  -      -    GGT     GC
CCGCCC GT CC CGCC GCGCCCCTGC GGGGGCGA  CGGGCCTG  G
|||||| || || |||| |||||||||| ||||||||  ||||||||
GGCGGG CA GG GTGG CGTGGGGGGCG CTCCCGCT  GTCCGGGC  C
    - -  C  G      G     ---     GT
GAM154  CCGCGAGAAGACGTGGAACATCTCGTTCGCGGGCTGCGGCTTCCTCGGCGTCTACTACGTCGG 2194
TGCGGCTTCCTCGGCGTCTACTAC 2195
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   - - A     ---  ---- T  T
CCG CG AG AGACGT  GGAA   CA CTCG T
||| || || |||||| ||||   || ||||
GGC GC TC TCTGCG  CCTT   GT GGGC C
  T A A     GCT  CGGC  C   G
GAM155
CCGCGGGTGGAGGTCGATGGCAGCATCATGGAAGGGGGCGGCCAGATCCTGAGAGTCTCTACGGCCTTGAGCT
GTCTCCTAGGCCTCCCCTTGCGG 2204 TGGCAGCATCATGGAAGGGGGCGG 2205
     T   GAT--   A T AA--   GGC  A
CCGCGGG GGAGGTC   GGCAGC TCA GG   GGGGGC  CAG T
||||||| |||||||   |||||| ||| ||   ||||||  |||
GGCGTTC CCTCCGG   CTGTCG AGT CC   TCTCTG  GTC /
     C   ATCCT  - T GGCA   AGA  C
GAM156
CCGCTTCACTGGCACCATGGATGCCTTCGTGAAGATCGTGAGGCACGAGGGCACCAGGACCCTCTGGAGCGG
2227 TGGCACCATGGATGCCTTCGTGAA 2228
      CT CA A  A     AAGA  G
CCGCTTCA GG  CC TGG TGCCTTCGTG   TC T
|||||||| ||  || ||| ||||||||||   ||
GGCGAGGT CC  GG ACC ACGGGAGCAC   GG G
      CT CA - -       ---- A
GAM157
CCGGATGGAACGTACTCTGTGCTTATATCATCACAGAGCTTGGATGAAAGAGAGCGAGAAGAGTTCTATAGG
2240 TGAAAGAGAGCGAGAAGAGTTCTA 2241
 GG    GTAC  G  ATA-   A A
CC ATGGAAC   TCT TGCTT   TCATC CAG G
|| |||||||   ||| |||||   ||||| |||
GG TATCTTG   AGA GCGAG   AGTAG GTT /
 A-    AGA-  -  AGAA   - C
GAM158 CCGGGGCGCAATGCGAGCGGCTGGCGTAGGCTTGGTGGACTGTCACTGCCACCTCTCCGCCCCGG
2266 TGCCACCTCTCCGCCCCGG 2267
     CAATGC  C C   TA TTGG
CCGGGGCG   GAG GG TGGCG GGC   T
||||||||   ||| || ||||| |||
GGCCCCGC   CTC CC ACCGT CTG   G
     ------  T -   CA TCAG
GAM159 CCTAACGCCTCGGTCAGCAACGGAGCTACCTTCCTGGAGTCCCCCACGTGCGCCGGGGCTGGG 2277
TAACGCCTCGGTCAGCAACGGAGC 2278
  AC    CA AC--- AG A TT
CCTA GCCTCGGT GCA   GG CT CC C
|||| |||||||| |||   || || ||
GGGT CGGGGCCG CGT   CC GA GG /
  --     -- GCACC CT - TC
GAM160 CCTCCACTACTGGTTGTGGAGTCCCAGAAGGATCCCGAGAACAGCCCTGTGGTGCTTTGG 2290
TCCCGAGAACAGCCCTGTGGTGCT 2291
 TC--   T-  ---- AG  CA
CC   CACTAC GGTTGT  GG TCC G
||   |||||| ||||||  || |||
GG   GTGGTG CCGACA  CC AGG /
 TTTC   TC   AGAG CT AA
```

GAM161
CCTCCTGACACCCTTCTCCCACTCTCCTAGGCATTCTGGACCTCTGGGTTGGGATCAGGGGTAGGAATGG 2295
TGACACCCTTCTCCCACTCTCCTA 2296
 --   A A  TC   CT  CT  CATT
CC  TCCTG C CCCT  TCCCA  CTC  AGG   C
|| ||||| | |||| ||||| ||| |||
GG  AGGAT G GGGA  AGGGT  GGG  TCC   /
 TA   - -  CT   T-  TC  AGGT
GAM162
CCTGAAGCCGACCATCTGCTCCGACCAGGACAACTACTGCGTGACTGTGTCTGCTAGTGCCGGCATTGGG 2312
GACTGTGTCTGCTAGTGCCGGCAT 2313
 TG A   AC  CT  TCC  -  GACA  TA
CC  A GCCG  CAT  GC  GAC CAG   AC  C
|| | |||| ||| || ||| |||   ||
GG  T CGGC  GTG  CG  CTG GTC   TG  T
 GT A   C-  AT  T--  T  AG--  CG
GAM163
CCTGCGCACGCGTCGCAGCCATCTCCGCGCACAGTGGTGGCCACCGCGACTGGTGCTGAAGTGTCGGCGTGTG
CCGGG 2328 TCGCAGCCATCTCCGCGCACAGTG 2329
   C      CAGC  TC  C   A   G   C
CCTG  GCACGCGTCG   CA  TC GCGC CAGT GTGG C
|||| |||||||||   ||  || |||| |||| ||||
GGGC  CGTGTGCGGC   GT  AG CGTG GTCA CGCC /
   -      T---  GA  T  -   G   A
GAM164  CCTGGCACCTGTGTTCCAGCCCACATCCCACATGCGGCTCGGGCTTCGGAACACGGAGTGGCCGGG
2345 TGGCACCTGTGTTCCAGCCCACAT 2346
   - -      --   ACATC  AC
CCTGGC AC CTGTGTTCC  AGCCC    CC  A
|||||| || ||||||||| |||||    ||
GGGCCG TG GGCACAAGG  TCGGG    GG  T
    G  A      CT    CTC--  CG
GAM165
CCTGGCAGACAGGCGGGCAAACAGTGAGCGCCCACCCAGACCGGCTGCTGCGCCCCCTCCTGCCAGG 2363
TGGCAGACAGGCGGGCAAACAGTG 2364
    AC  C  AAA  G  GCCCAC
CCTGGCAG  AGG  GGGC  CAGT  AGC    C
||||||||| ||| |||| |||| |||
GGACCGTC  TCC  CCCG  GTCG  TCG    C
    C-  -  C--  -  GCCAGA
GAM166  CCTTTATTAGTCCACCCCTTGGAGCTAGACATCCTGTACTTAGTCACGGGGATGGTGGAAGAGG 2389
TATTAGTCCACCCCTTGGAGCTAG 2390
   ATTAG     --   GA   - -  AT
CCTTT   TCCACC  CCTTG  GCTA G AC  C
||||||   |||||| ||||| |||| | | ||
GGAGA    AGGTGG  GGGGC  TGAT C TG  /
   -----    TA   AC   T A  TC
GAM167  CCTTTGCCCGCATGCTGATCGCGCAAGAGGGGCTGCTGTGCGGTGGCAGTGCTGGCAGCACGG 2400
GTGCGGTGGCAGTGCTGGCAGCAC 2401
 T--   C  -  G    AG  G
CC  TTGCC  GCA  TGCT  ATCGCGCA  AG  G

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||  |||| ||| |||| |||||||| ||
GG   GACGG CGT ACGG TGGCGTGT TC /
 CAC   T  G   -     CG  G
GAM168  CCTTTTATATGATGATCTGGAGAATTCTGCTCTTTGATAACAACTCAGGATTTTTTTGATCACGTTTGG
2422 TATGATGATCTGGAGAATTCTGCT 2423
 TTTTAT  A   TG      CTCT  A
CC    ATG TGATC  GAGAATTCTG   TTG T
||    ||| ||||| |||||||||| |||
GG    TGC ACTAG  TTTTTAGGAC   AAC  A
 TT---- -  TT       TC-- A
GAM169  CGACCCTCGACTGCGGGGCCCGGGCGGCGGCGCTAGCAGATCCAGCGGATGAAGCGGTCG 2434
TAGCAGATCCAGCGGATGAAGCGG 2435
   - - A  -  GCCCG-  G
CGACC CT CG CTGC GGG    GGCG C
||||| || || |||| |||    ||||
GCTGG GA GT GGCG CCT     TCGC G
  C A  A   A AGACGA   G
GAM170
CGAGATTGAGCAATAACAGGTCTGTGATGCCCTTAGTTGTCCGGCCCGGACAACGACAGGATTGACAGATTGATA
GCTCTTTCTCG 2448 TAACAGGTCTGTGATGCCCTTAGT 2449
   TT  AATAACA    - G CTTA     G
CGAGA GAGC    GGTCTGT GAT CC   GTTGTCCG C
||||| ||||      ||||||| ||| ||   ||||||||
GCTCT CTCG      TTAGACA TTA GG   CAACAGGC /
   TT  ATAG---    G  - ACAG      C
GAM171  CGCAGCCCTGCTCGTGGGTCCAAGAGCTGCTTACTTCTGGGGGCACCCATGCTGAGGGGGCTGCG
2458 GGGGGCACCCATGCTGAGGGGGCT 2459
    G  ---    ---- AG CTG
CGCAGCCCT CTC  GTGGGT  CCA AG  C
|||||||||| ||| |||||||   ||| ||
GCGTCGGGG GAG  TACCCA   GGT TC /
   - TCG     CGGG   CT ATT
GAM172
CGCGTGCCCCGCCCGCTGGAGCACCTGCCACCGAGGCGCGCGTGGGGCCACTGCCGTGGCGGCGGCTGCCC
TCCTCACACTCGGCTCCGCGCCGCCTCCGGCCACCGTGCGCTCCCGCGTGGGGCGCCTCG 2477
TCACACTCGGCTCCGCGCCGCCTC 2478
  C-    CC T  -- CT-- ACC   C     ACTGCC  C C C
CG GTGCCCCGC GC GGAGC AC  GCC  GAGGCG GCGTGGGGCC    GTGG GG GG T
|| ||||||||| || ||||| ||   ||| |||||| ||||||||||    |||| || ||
GC CGCGGGGTG CG CCTCG TG  CGG  CTCCGC CGCGCCTCGG    CACT CC CC G
 TC     -- C  CG CCAC  C--  -      CTCA-- - T C
GAM173  CGCTTTCGCTCCGCGTTCGCGCTTTCGACCAGAGGGGGGGGGGGGCGCACCTCGCTTACCGAAAGTG
2516 TCGCTCCGCGTTCGCGCTTTCGAC 2517
    CTCC  TTC-   TT GA  A
CGCTTTCG  GCG  GCGCT C CC G
|||||||| ||| ||||| | ||
GTGAAAGC  CGC  CGCGG G GG A
   CATT  TCCA   GG GG  G
GAM174
CGGGGGGAGTTGTGGTGCTTCTGGGTCTCTGGGCCCCGCCTGCTGGCCTGGGATGCCCTCATGTTGGGAAGCAT
TCCGTGCCCCCCG 2524 GGGATGCCCTCATGTTGGGAAGCA 2525
```

```
   A - TG    G TCTCT -- -- T
CGGGGG GT TG GTGCTTCT GG   GGGC CCC GCC G
|||||| || || |||||||| ||   |||| ||| |||
GCCCCC CG GC TACGAAGG TT   CCCG GGG CGG C
   - T CT    G GTACT  TA TC  T
GAM175
CGTGAGCCAATTCTCCCTAATAAACTCCCTTATATATGTAGTCATATATCCTACTAGTTCTGTTCCTCTGGAGAATC
ATG 2532 TATCCTACTAGTTCTGTTCCTCTG 2533
   GCCAA    CT--- - CCCTT-   T
CGTGA    TTCTCC   AATA AACT    ATATATG A
|||||    ||||||   |||| ||||    |||||||
GTACT    AAGAGG   TTGT TTGA    TATATAC G
   -----    TCTCC  C TCATCC    T
GAM176 CTACCCTCACCCCATCACAGCACCCTGAGAATCACGGGTCCAACTGTGTGGGAGGGGGCTGTGG
2540 TACCCTCACCCCATCACAGCACCC 2541
   -- AC  T  C--- - AG
CTAC CCTC CCCA CACAG   ACCC TG A
|||| |||| |||| |||||   |||| ||
GGTG GGGG GGGT GTGTC   TGGG AC /
   TC  GA  -  AACC   C TA
GAM177
CTATAAACACGGAAGCCAAATTTGGGAAAGGTGTGTTATTAAGAATATGTTGCGACAAGCGTGGTCCGTGCTTTG
AG 2564 TGTTGCGACAAGCGTGGTCCGTGC 2565
  A  -  AA  AA  GGAAA TG  AT
CT TAAA CACGG GCCA TTTG   GG TGTT T
|| |||| ||||| |||| ||||   || ||||
GA GTTT GTGCC TGGT GAAC   TT ATAA A
  - C  --  GC  AGCG- GT  GA
GAM178 CTATCATCATCTAGCACCTGTCCGGTTCCCCACGTGAGCCTTGGGCAGGACGCTGCAGTGTTGATGG
2583 TATCATCATCTAGCACCTGTCCGG 2584
   T  C- A-   --   CCC
CTATCA CAT TAGC CCTGTCC GGTTC  A
|||||| ||| |||| ||||||| |||||
GGTAGT GTG GTCG GGACGGG CCGAG /
   T AC  CA   TT  TGC
GAM179 CTATTTTTTATTTGCAACTACATGATTTCACACAATTCTCTTAAACAACGACATAAAATAG 2595
CTTAAACAACGACATAAAATAG 2596
   TTAT  CAACTACAT- TTTCA
CTATTTT TTG      GA   C
||||||| |||      ||
GATAAAA AGC      CT  /
   TAC- AACAAATTCT TAACA
GAM180 CTCCAGAGCTCCTATAGGGCAAGACACTGTTTCTCATATATTTCTGGATCCTTGGAGCTTAGCTCGGAG
2600 ATTTCTGGATCCTTGGAGCTTAGC 2601
   - --- TAT  CA- CAC TTC
CTCC AG AGCTCC AGGG AGA TGT T
|||| || |||||| |||| ||| |||
GAGG TC TCGAGG TCCT TCT ATA /
   C GAT  T-- AGG TT- TAC
GAM181 CTCCCACCCTGCCGGCCTCAGGAACAGCTGGCTCCAGATGGGGGGGTGGCAGGCAGTGAAGTGGGAG
2619 TGGGGGGTGGCAGGCAGTGAAGTG 2620
```

```
       -------      G   AGGAACAG  G
CTCCCAC      CCTGCCG CCTC     CTG C
|||||||      ||||||| ||||     |||
GAGGGTG      GGACGGT GGGG     GAC T
    AAGTGAC       G  GTA----- C
GAM182
CTCTCTCTTCCAGCTGCAGATGCCACACTGTCCTCTGCTTCCCGGGGACGAGGGGGTGGGCGGGACTGGGTAC
AGGTTGGGAGGGGAG 2643 TGCCACACTGTCCTCTGCTTCCCG 2644
    T    GCAGA  A CT   -- TG   - G
CTCTC CTTCCAGCT   TGCC CA GTCCT  C CTTCC CG G
||||| |||||||||   |||| || ||||| | ||||| ||
GAGGG GAGGGTTGG   ATGG GT CAGGG  G GGGGG GC G
    -      AC---   - --   CG GT    A A
GAM183
CTCTGACAACAGTGGCTGGACTGAAATCCGCCGGGAAGCCTGGGTCTCCTCTAGCTTATTGGTGTCTCCAGAG
2666 ACAACAGTGGCTGGACTGAAATCC 2667
    ---  A  -   CT A   CC G
CTCT  DACA CAGTG GCTGGA GA ATCCG  GG A
||||  |||| ||||| |||||| || ||||| ||
GAGA  CTGT GTTAT CGATCT CT TGGGT CC A
  CCT  G   T   C- C   -- G
GAM184
CTCTGCACAGCAGCCCAGCAGGGATGTCCTCTCTAGAGATGGTTTATCAAGGGTACCCCATGAGAGGGCAGCTC
CTGATGCAGCTGCCGGAAGAG 2682 TGAGAGGGCAGCTCCTGATGCAGC 2683
    GCACA  C- G  A-    TAGAG  TT CA
CTCT   GCAGC CA CAGGG TGTCCTCTC   ATGG TAT A
||||   ||||| || ||||| |||||||||   |||| |||
GAGA   CGTCG GT GTCCT ACGGGAGAG   TACC ATG /
   AGGC-  AC A  CG      -----   CC GG
GAM185 CTGACACATGAGGCAAAAGGCTCCGACGATGCTCCAGACGCGGACACGGCCATCATCAATGCAG 2692
TGACACATGAGGCAAAAGGCTCCG 2693
  A C--  - AAAAGGC  A ATGC
CTG CA ATGA GGC     TCCG CG   T
||| || |||| |||       |||| ||
GAC GT TACT CCG     AGGC GC   C
  - AAC   A GCAC---  - AGAC
GAM186 CTGACTTGTTGGACGGGAATCTGGTTATTTGGCACCGCCCTTCTGTTCATAACAGGTTGG 2706
TGACTTGTTGGACGGGAATCTGGT 2707
 TG   --     ATC  TAT
C ACTTGT TGGACGGGA TGGT  T
| |||||| ||||||||| ||||
G TGGACA ACTTGTCTT GCCA  T
 GT    AT    CCC  CGG
GAM187 CTGAGAATTTCTCTTGCATGCCTTAGCTTTACAGCTTTTGCATTCCTGTGGATTATTCTCAG 2715
TGAGAATTTCTCTTGCATGCCTTA 2716
    T- CTTGC- CTT  T
CTGAGAAT TCT   ATGC AGCT T
|||||||| |||   |||| ||||
GACTCTTA AGG   TACG TCGA A
    TT TGTCCT  TTT  C
```

GAM188 CTGCACATATCATCGCGGAATTCATTCGGCTTCCAGCAAGCTGACACTCCATGATACAAGCGG 2734
TATCATCGCGGAATTCATTCGGCT 2735

```
   ACA    CGC  ATTCAT     CC
CTGC  TATCAT GGA    TCGGCTT A
||||  |||||| |||    |||||||
GGCG  ATAGTA CCT    AGTCGAA /
   AAC    ---  CAC---    CG
```

GAM189
CTGCATCAAAGGTAGACTTTCGCACAGGTTGTGAGGTTGGAGTCACAGTGTTATTTGTTGTACCTGATGTAG 2737
TCAAAGGTAGACTTTCGCACAGGT 2738

```
      AA  -  TTTC-  AGGT   GGT
CTGCATCA  GGTA GAC   GCAC  TGTGA  T
|||||||| |||||| |||    ||||  |||||
GATGTAGT  CCAT TTG    TGTG  ACACT  G
       --  G  TTTAT  ----    GAG
```

GAM190 CTGCCAATGTCGATTGGCCTTAATTTGGCAAAAAAAAAAATGGGGGGCCGAAATAAATGGGCGG 2744
TGGGGGGCCGAAATAAATGGGCGG 2745

```
   AATGTCGA     A-  GGCAA
CTGCC     TTGGCCTT ATTT   A
|||||     |||||||| ||||
GGCGG     AGCCGGGG TAAA   /
   GTAAATAA     GG  AAAAA
```

GAM191 CTGCCAGTATGCTGTTAGTCAAGAGTCCTCAGTAGGAGAACTTGAGTGAAACGTACACCCAG 2753
TGCCAGTATGCTGTTAGTCAAGAG 2754

```
  CCA   CTG  G   AG-  C
CTG  GTATG  TTA TCAAG  TCCT A
|||  |||||  ||| |||||  ||||
GAC  CATGC  AGT AGTTC  AGGA G
  CCA   AA-  G   AAG   T
```

GAM192 CTGCGAGCCATTCACCCAGCTGGTCCCTCCAAGACAGAGCCGGGGCCAGCGGCAGACTCCCAG 2763
TGCGAGCCATTCACCCAGCTGGTC 2764

```
  C  CCAT AC A     TCCAAG
CTG GAG   TC CC GCTGGTCCC    A
||| |||   || || |||||||||
GAC CTC   AG GG CGACCGGGG    C
  C  ---- AC -     CCGAGA
```

GAM193 CTGCTGCGCCCTGTCCTCCGTCGGCTCTGCGGGCTCCCGGGCCTACAGCGGCTGCGGCAG 2783
TCCCGGGCCTACAGCGGCTGCGGC 2784

```
    -  -  CC-  TC  CT
CTGCTGC GCC CTGT  TCCG GGCT G
||||||| ||| ||||  |||| ||||
GACGGCG CGG GACA  GGGC TCGG /
    T  C  TCC  CC  GC
```

GAM194
CTGGGAATATAATGGCCTATTCACCAGGCACCAGTTAAGGGTGCCACTAATTGGCCGTGAACTTCCCAG 2794
TATAATGGCCTATTCACCAGGCAC 2795

```
     TATA    T  CACCA     AGT
CTGGGAA  ATGGCC ATT   GGCACC  T
||||||||  |||||| |||    ||||||
GACCCTT  TGCCGG TAA    CCGTGG  /
```

```
       CAAG    T TCA--    GAA
GAM195
CTGGGATGGGGACCGCGGAAGTTCCCACCGATGCGGCCGGCGGGGCCCAGCCTTGGTCCCCAGCTCCGG
2807 TGGGATGGGGACCGCGGAAGTTCC 2808
    A-     C AAGT-  A  ATG
CTGGG TGGGGACCG GG   TCCC CCG  C
||||| ||||||||| ||    |||| |||
GGCCT ACCCCTGGT CC   GGGG GGC  /
   CG     T GACCC   C  CGG
GAM196
CTGGGCTTTGGGCCTGGTGGTTGGGAGTCACCTACTGACATCGGGACTGACATTCCTGAACCCCTGGTATGAGG
CCAG 2826 TGACATTCCTGAACCCCTGGTATG 2827
   G TGG  T T  -  --   CCTA  A
CTGG CTT  GCC GG GGTT GGGA GTCA   CTG C
|||| |||   ||| || |||| |||| ||||    |||
GACC GAG   TGG CC CCAA TCCT CAGT   GGC A
   G TA- T -  G  TA  CAG- T
GAM197
CTGGGGTGTTTATGGCAAGTCACTTTGACAGACATTATTGTGGGCAAATGTTGTCTGACTTACTGTTTCAACAAAC
CAG 2846 TGGCAAGTCACTTTGACAGACATT 2847
   GG  T--  C  CTTT   A  AT T
CTGG TGTT  ATGG AAGTCA   GACAG CATT  TG G
|||| ||||  |||| ||||||    ||||| ||||  ||
GACC ACAA  TGTC TTCAGT   CTGTT GTAA  AC G
    AA  CTT  A    ----    -  -- G
GAM198
CTGGTGCATCAGTTGTTCCCGGCGCAGGCCCCCGTTGATCGTGGCGCTGGTGCTGCTGACGGAGCTGCTGGTT
CTGCTGCCAG 2858 TCAGTTGTTCCCGGCGCAGGCCCC 2859
    - ---  T  -----    A - C TT
CTGGT GCA  TCAGT GTTCC   CGGCGC GGC CC CG  G
||||| |||  ||||| |||||    |||||| ||| || || ||
GACCG CGT  GGTCG CGAGG   GTCGTG TCG GG GC  /
    T CTT   T  CAGTC    G  C T TA
GAM199 CTGGTTAACTTCTTGAGCTATTTCGTGGAACTTGGAACACAGCCTGCCACCCAGTGAAGTGTCCAG
2874 CACCCAGTGAAGTGTCCAG 2875
    TTA   TTGA  ATTTC  AAC-  GA
CTGG  ACTTC  GCT   GTGG  TTG A
||||  |||||  |||    ||||   |||
GACC  TGAAG  TGA   CACC   GAC /
   TG-   ----  CC---  GTCC  AC
GAM200
CTGTCCCCAAGCGCATGCCATCTGCAGCCAGCAGTCTTGGAACTTTGGTTGGTGGCACCAGGGGACAG 2880
TGGTTGGTGGCACCAGGGGACAG 2881
     AAGCGCA    CTG    C  CT
CTGTCCCC    TGCCAT  CAGCCAG AGT  T
||||||||    ||||||  |||||||  |||
GACAGGGG    ACGGTG  GTTGGTT TCA  G
    ACC----     ---     -  AG
GAM201 CTGTCTGTTCATATGTTGGTTATGACTTTTACATTAAAATATCATTTAAACGAATGAGCAATCAG 2898
CATTTAAACGAATGAGCAATCAG 2899
```

```
   TC    A  GGTT   CT  AC
CTG TGTTCAT TGTT   ATGA TTT A
||| ||||||| ||||   |||| |||
GAC ACGAGTA GCAA   TACT AAA T
   TA    A  ATT-   AT  AT
GAM202  CTGTGAACAGAGAGGCCATGGGAAGATTCGAAATTATTCACGAAAAATCCTAAGATTTCAGTTCAGAG
2921 TGAACAGAGAGGCCATGGGAAGAT 2922
  G    A  GGCCA    AGA   AAAT
CT TGAAC GAGA    TGGGA  TTCG   T
|| ||||| ||||    |||||  ||||
GA ACTTG CTTT    ATCCT  AAGC   A
  G    A  AGA--   AAA   ACTT
GAM203  CTGTGATGGCGCAATTAACGTTTCCTAGCCTCCCATGTAATCCTAGGACGTGTACGCTTCGTCAGAG
2946 TGTGATGGCGCAATTAACGTTTCC 2947
  G    C AATTA  TT    CCTCCC
CT TGATGG GC    ACG  TCCTAG    A
|| |||||| ||    |||  ||||||
GA ACTGCT CG    TGC  AGGATC    T
  G    T CATG-  --    CTAATG
GAM204
CTGTGGACCACTGTTTCTCCATCAAAGGCCTAAGGGCACTGTGAGTGACAGGGGACCAGTCCTTTGCAG 2953
TGTGAGTGACAGGGGACCAGTCCT 2954
   TG CC  T   --- -  A - T
CTG GA ACTG TTCTC  CA TCA AG GCC A
||| || |||| |||||  || ||| || |||
GAC TT TGAC AGGGG  GT AGT TC CGG A
   GT CC  C   ACA G  G A G
GAM205  CTGTGTTCTGGCGGCCCCATTCGTAGCCACTGGGGGTCAGCTTGTAGGCCGTCAGTGTACAG 2967
TGTTCTGGCGGCCCCATTCGTAGC 2968
    TT     CC TC A-  AC
CTGTG CTGGCGGCC AT GT GCC T
||||| ||||||||| || || |||
GACAT GACTGCCGG TG CG TGG G
    GT     A- TT AC  GG
GAM206
CTGTTGGTTCTTTCTCCTGACTCCTGTGGTTTTGCTAATGGCACTTTACAGACTCCATGGAGATGTCAGGTGGACC
ATCTTCTAGGGCCCAGCAGGAGTAGGGAATGTGCCAACAG 2973 TGTCAGGTGGACCATCTTCTAGGG 2974
     TCT T  A    --    CTA-  --   T  GA  C
CTGTTGGT  TTC CCTG CTCCTGT  GGTTTTG   ATGG  CACTT ACA  CTC A
||||||||  ||| |||| |||||||  |||||||   ||||  ||||| |||  ||| 
GACAACCG  AAG GGAT GAGGACG  CCGGGAT   TACC  GTGGA TGT  GAG T
     TGT  - -  AC    CTTC   AG   C A-  G
GAM207  CTTAGGGAGGAAGGACTAGGAGGGAAAACTGGGAAAACGTACGGTGGGCTCTGTCTTGCGTCTTGAG
3004 TTAGGGAGGAAGGACTAGGAGGGA 3005
    AGGA   TAGG   AAA   GGAA
CTTAGGG  AGGAC  AGGG  ACTG   A
|||||||  |||||  ||||  ||||
GAGTTCT  TTCTG  TCTC  TGGC   A
    GCG-  ----   GGG   ATGC
GAM208
CTTCAGCAATGTCAGTAAAATGATCTTCCGATGCTGACGCCAGCATTTTCCCATCATGGCTGAAACTGAGG 3021
```

```
TGTCAGTAAAATGATCTTCCGATG 3022
    CAATG   AAA   CTTCC    A
CTTCAG   TCAGT  ATGAT   GATGCTG C
||||||   |||||  |||||   |||||||
GGAGTC   AGTCG  TACTA   TTACGAC G
   AA---  G--   CCCTT     C
GAM209
GAAAATATAAGAACATTCTAGAAGGTTGTGAGACATAAGGTACAAAAACCTTCTAGCATAATTTCAAAAAATTTTC
3030 TAAGAACATTCTAGAAGGTTGTGA 3031
    ATAA- C-- T      GTGAG AT
GAAAAT   GAA  AT CTAGAAGGTT   AC A
||||||   |||  || |||||||||||   ||
CTTTTA   CTT  TA GATCTTCCAA   TG /
    AAAAA  TAA  C       AAACA GA
GAM210
GAAATGAGGTCGGGTTTATATGCACTTATTGGTATTGGAATTTCTGGTGCAACTTATAGGTTTGATTTTAATTT
3043 TGAGGTCGGGTTTATATGCACTTA 3044
   A    GG   ---   TATT  AT
GAA TGAGGTCG  TTTATA  TGCACT   GGT  T
||| ||||||||  ||||||  ||||||   |||
TTT ATTTTAGT  GGATAT  ACGTGG   TTA  G
   A     TT   TCA     TCT-  AG
GAM211
GAAGACAAATTGAAGGGAGAGATGATGGATCTCCAACATGGCAGCCTTTTCCTTAGAACACCAAAGATTGTCTC
3049 TGGCAGCCTTTTCCTTAGAACACC 3050
  A  A--  -------      ------  A A
GA GACAA  TTG     AAGGGAGAG    ATG TGG T
|| |||||  |||     |||||||||    ||| |||
CT CTGTT  AAC     TTCCTTTTC    TAC ACC C
   -   AGA  CACAAGA      CGACGG  A T
GAM212  GAAGCTGTCCGCATTTATGTGGCATCGGTCCAAGCATCCCTGGGCCAGTCGTGCGACAGACTC 3069
TGTCCGCATTTATGTGGCATCGGT 3070
  AG   C   TTATGT  ATC    AGC
GA CTGTC GCAT    GGC  GGTCCA  A
|| ||||| ||||    |||  ||||||
CT GACAG CGTG    CTG  CCGGGT  T
  CA   -  ------  A--    CCC
GAM213  GAATCCAGATGGCATGGTTGCTCTATTGGACTACCGTGAGGATGGTGTGACCCCATATATGATTT 3075
TGGCATGGTTGCTCTATTGGACTA 3076
   CAG-  CAT  TG T  TGGACTA  G
GAATC  ATGG  GGT C CTAT    CC T
|||||  ||||  ||| | ||||    ||
TTTAG  TACC  CCA G GGTA    GG G
   TATA   ---  GT T  -------  A
GAM214  GAATGAGCTGCTAAATCCTGAAGATGACCTCTTACCAGGGAAGATTCGAGACAGCAATCGTTC 3081
TGAGCTGCTAAATCCTGAAGATGA 3082
    GC   AAA  C   GATGA  CT
GAATGA  TGCT  TC TGAA    CCT T
||||||  ||||  || ||||    |||
CTTGCT  ACGA  AG GCTT    GGA A
```

```
      A-  C-- A   AGAAG  CC
GAM215
GAATTCTGATCATACCAGTTTCCATCAGGATTTATCAGATCTGAAACATCCTGCAGATAAGCTGGTTGACAATCCC
ACAGCAGTTC 3101 TACCAGTTTCCATCAGGATTTATC 3102
   - A------- T    CCAT-  TTA  G
GAATT CTG    TCA ACCAGTTT   CAGGAT  TCA A
IIIII III    III IIIIIIII   IIIIII III
CTTGA GAC    AGT TGGTCGAA   GTCCTA  AGT T
   C ACCCTAAC -    TAGAC   CAA  C
GAM216
GACACCGGTGTCCTTCCTCGAGTAACCGACCTTCCAGTTCCAGCCCTCCAAGTCCCACGGCTCGGAAGAGCGAC
TACCATCGTC 3118 TCCAAGTCCCACGGCTCGGAAGAG 3119
 ACC  -  - CC   AACC-  CTTCCA- T
GAC  GGT GTC CTT  TCGAGT   GAC    GT C
III  III III III IIIIII   III     II
CTG  CCA CAG GAG  GGCTCG   CTG    CG C
  CTA  T  C  AA   GCACC   AACCTCC A
GAM217 GACCCGGGGCTGGACGCCAGCCTCTGTGATGAGTTCTGGCTGTGTCCACGCTCCTGGCTC 3132
TGGCTGTGTCCACGCTCCTGGCTC 3133
  C  - -  --- C- TG
GA CCGGG GC TGGAC  GCCAG CTC T
II IIIII II IIIII  IIIII III
CT GGTCC CG ACCTG  CGGTC GAG G
  C  T C  TGT   TT  TA
GAM218 GACTATGGCAAGGACCTGATGGAGAAGGTCAAGAGCCCAGAGCTTCAGGCCGAGGCCAAGTC 3172
TGGCAAGGACCTGATGGAGAAGGT 3173
  A  AA- A   T AGAA-  CA
GACT TGGC  GG CCTGA GG   GGT A
IIII IIII  II IIIIII II    III
CTGA ACCG  CC GGACT TC   CCG /
  -  GAG -  -  GAGAC  AG
GAM219
GACTGAAGGAGGAATATCAGTCCCTTATCCGGTATGTGGAGAACAACAAGAATGCTGACAACGATTGGTTCCGAC
TGGAGTC 3204 TATCAGTCCCTTATCCGGTATGTG 3205
  GA GA  AT    CCTTATC    G-- GAG
GACT AG GGA ATCAGTC     CGGTAT TG A
IIII II III IIIIIIII    IIIIII II
CTGA TC CCT TGGTTAG     GTCGTA AC A
  GG AG  --    CAACA--  AGA AAC
GAM220
GACTTCAGGCAAATCATTTATTTTTTGGGGCATCAGTGTCACAAACTATAACATCAGAGAATAAACCAAATGACCT
CATGTC 3210 TAACATCAGAGAATAAACCAAATG 3211
  TTC  - AATCA       GGCATC  GTC
GAC  AGG CA   TTTATTTTTTGG   AGT  A
III  III II   IIIIIIIIIIII    III
CTG  TCC GT   AAATAAGAGACT   TCA  /
  TAC  A AAACC        ACAATA  AAC
GAM221 GACTTTGCTTCCGGTACAAACAGGCCACCTGAGCACTGGTGGTGGCCTGCTCCGGCTGCTTGTC 3247
ACTTTGCTTCCGGTACAAACAGGC 3248
  TTT TT  TACAAA     TGAGC
```

```
GAC GC CCGG   CAGGCCACC   A
||| || ||||   |||||||||
CTG CG GGCC   GTCCGGTGG   /
 TT- TC TC----     TGGTC
GAM222 GAGAGCATTAGACCCAAGACCATTGTGGAGAAGATTGACTTGACAGTGTGTCCAGCATAATGCTCTC
3266 CAGTGTGTCCAGCATAATGCTCTC 3267
      GACCCAA  -   G  AAG
GAGAGCATTA    GAC CATTGT GAG  A
||||||||||    ||| |||||| |||
CTCTCGTAAT    CTG GTGACA TTC  T
     ACGAC-- T   G  AGT
GAM223 GAGAGCGCTATAGGATCCCTTTTACAAGGGCACTAATCCCACTCATGATCTAATTAGCTCTC 3279
CCCACTCATGATCTAATTAGCTCT 3280
   GCT A   CCTTTTACAA  CA
GAGAGC  AT GGATC     GGG  C
||||||  || |||||       |||
CTCTCG  TA TCTAG     CCT  T
  AT- A   TACTCAC--- AA
GAM224
GAGATGAAATGTTTTACTTCTGACTGTGGGACTAATGTGTTCCTACAGGTTGCAACATAAAACGGATTTCTC 3287
TGAAATGTTTTACTTCTGACTGTG 3288
   TGAAA    CTTCTGA--    - TA
GAGA   TGTTTTA      CTGTGGGA C  A
||||   |||||||      |||||||| |
CTCT   GCAAAAT      GACATCCT G  T
  TTAG-   ACAACGTTG     T TG
GAM225 GAGATGAGACATTTTGCCTAGCTGATGACCACTTAGTTCTCAAGAAGCAACTATCTCTTTC 3306
TGAGACATTTTGCCTAGCTGATGA 3307
   T  CATT  CTAG - T  CA
GAGA GAGA   TTGC   CT GA GAC  C
|||| ||||   ||||   || || |||
CTTT CTCT   AACG   GA CT TTG  T
  -  ATC-  AA-- A  C  AT
GAM226 GAGATGGGATTTCACCATGTTGGCCAGGCCTGTCTTGAACTCTTGACCTCAAGTGATCCACCCACCTC
3315 TGGGATTTCACCATGTTGGCCAGG 3316
  A  ATT-  CA TT C  CCT CT
GAG TGGG   TCAC  TG GG CAGG  GT  T
||| ||||   |||| || || ||||  ||
CTC ACCC   AGTG AC CC GTTC  CA  /
  C  ACCT  A- T- A  T-- AG
GAM227 GAGATGGGGTTTCACCATGTTGGCCAGGCTCGTCTCGAACTCCTGACTTCAGGTGATCCACCCATCTC
3343 TGGGGTTTCACCATGTTGGCCAGG 3344
     GTT-  A TT C  C-- T
GAGATGGG   TCACC TG GG CAGG   TCG C
||||||||   ||||| || || ||||   |||
CTCTACCC   AGTGG AC TC GTCC   AGC /
    ACCT   - T- A  TCA  T
GAM228
GAGCGGCAGCGCCGCGATGCCAGGCGCGTCCCTACAGCGGGCCTGCCGCCTGCTCGTGGCCGTCTGCGCTC
3350 TGCCGCCTGCTCGTGGCCGTCTGC 3351
```

```
    G - -   T C   C --- TA
GAGCG CAG CG CCGCGA GC AGGCG GT  CCC  C
||||| ||| || |||||| || ||||| ||   |||
CTCGC GTC GC GGTGCT CG TCCGC CG  GGG  A
  - T C   - -  - TCC  CG
GAM229
GAGCGGGCGTGCATATGCGGTGGCGGGTGGGGTGGAAGGGGGAGATCCTGCTGCACTGGCCGCCAAGTATGA
GGGGCGAGCTC 3375 TATGCGGTGGCGGGTGGGGTGGAA 3376
  GG GTG-  GC   G  G GGA  GG
GAGC GC  CATAT GGTGGC GGTG GGT  AGGG  A
|||| ||   ||||| |||||| |||| |||   ||||
CTCG CG   GTATG CCGCCG TCAC TCG  TCCT /
   AG GGGA  AA   G  G  ---  AG
GAM230  GAGCGGTCGGTGACAGCCTCAAGGGCTTCAGCACCGCGCCCATGGCAGAGCCAGACCGACTC 3409
TGGCAGAGCCAGACCGACTC 3410
  -  - GACA  TCAA  TTCAG
GAG CGGTC GGT  GCC  GGGC   C
||| ||||| |||  |||   ||||
CTC GCCAG CCG  CGG  CCCG   /
   A  A  AGA- TA--  CGCCA
GAM231  GAGCTAACAGCACGAGAAGCCAGTTGGGGACTGCCCCCTCCTGGAGCAGCTCCTGGGCTGTGCTC
3419 TAACAGCACGAGAAGCCAGTTGGG 3420
   TA  AC-- AAG--  TT  AC
GAGC ACAGC  GAG   CCAG GGGG  T
|||| |||||   |||    |||| ||||
CTCG TGTCG  CTC   GGTC CCCC /
   -- GGTC  GACGA  CT  CG
GAM232
GAGGAACGAGATGGCGGTTCTCTGGAGGCTGAGTGCCGTTTGCGGTGCCCTAGGAGGCCGAGCTCTGTTGCTT
C 3431 TGGCGGTTCTCTGGAGGCTGAGTG 3432
   -  - ATGG  TC   A  TGAGT  T
GAGG AAC GAG   CGGT  TCTGG GGC   GCCG T
|||| ||| |||   |||| ||||| |||    ||||
CTTC TTG CTC   GCCG GGATC CCG   TGGC T
   G  T GA--  GA   -  -----   G
GAM233  GAGGATGAAAGAGGACCTGGGAGCGGCAACTTTGTTCTGGTTTGTTGTTTTCTCTTCCCTACCTC 3449
TGAAAGAGGACCTGGGAGCGGCAA 3450
   ATGAA  A  CCT GG      - TTG
GAGG   AG GGA  G AGCGGCAA CT  T
||||    || |||  | |||||||| ||
CTCC   TC CCT  C TTGTTGTT GG  /
   A---- - TCT TT      T  TCT
GAM234
GAGGATTTTATTTCAAGATAAAACATAACTTCTACCCATACTATTGATTCCAAAGGTTAGAAAAAGTGTTTTTCCTC
ATCTTATCCTT 3465 TTCAAGATAAAACATAACTTCTAC 3466
    TTTATTTCA AT    AAC   C ATACTATT
GAGGAT     AG AAAACAT TTCTA CC     G
||||||      || |||||||| ||||| ||
TTCCTA      TC TTTTGTG AAGAT GG      /
    TTCTAC--- CT    AAA   T AAACCTTA
```

GAM235

GAGGCGGGCGGATCACCGGAGGTCGGGAGTTTGAGACCAGCCTGACCAACATGGAGAAACCCCATCTC 3469
TGACCAACATGGAGAAACCCCATC 3470

```
  GC  CGGA A  GA--     AGT  A
GAG GGG  TC CCG   GGTCGGG  TTG G
||| |||   || |||   |||||||| |||
CTC CCC  AG GGT   CCAGTCC  GAC A
  TA  CAA- A  ACAA      ---  C
```

GAM236

GAGGGATAGCATTCGAAGGACTCGGGGATATCTAACAGCAATACCTGATCACTACTTCGCACTAGTTTCTC 3494
TCACTACTTCGCACTAGTTTCTC 3495

```
  GG - CATT   GAC---    GATATCTA
GAG AT AG  CGAAG    TCGGG      A
||| || ||   |||||     |||||
CTC TG TC   GCTTC    AGTCC      /
  TT A AC--   ATCACT    ATAACGAC
```

GAM237

GAGGGTGTTATCTCCAATGTCAATAAGAATTGATGAATAAGAATGTATATCAATATGGAGGAGATAGGTGGAGAAA
GACGTGTTT 3506 ATCAATATGGAGGAGATAGGTGGA 3507

```
  GG  A-  A-  AATAAGA-    A A
GAG TGTT TCTCCA TGTC      ATTGATG ATA G
||| |||| |||||| ||||      |||||||| |||
TTT GCAG AGAGGT ATAG      TAACTAT TGT A
  GT  AA   GG  AGGAGGTA     A A
```

GAM238

GAGGTGCCGGTGGGCCTGTGTTGCTGCGATTTTAGTCTGTGCTGGGAGGCAGGGCTCCGCTGCGCCTC 3522
TGGGAGGCAGGGCTCCGCTGCGCC 3523

```
    C  -  TGTGTTG  GA     C
GAGGTGC GGTGG GCC    CTGC TTTTAGT T
|||||||| ||||| |||     |||| |||||||
CTCCGCG TCGCC CGG     DACG AGGGTCG G
    -  T -------  G-   T
```

GAM239 GAGGTGGGAGGTCACCCGAGGTCAGGTGTCTGTGACCAGGCCGGCCAACATGGTGAAACCCCGTCTC
3543 TGGGAGGTCACCCGAGGTCAGGTG 3544

```
  GT  AGG   CGA--  A GT  T
GAG GGG  TCACC   GGTC GGT CTG G
||| |||  |||||    |||| ||| |||
CTC CCC  AGTGG   CCGG CCG GAC A
  TG  CAA   TACAA  -  --  C
```

GAM240

GAGTCCACTGGTGCCCAGTAACACCCTCCGTGGGACCACCTTGGGAAGCATGTGCCGCGGAGTCCACCACGGG
GGGTCCTGGGTCCCGGGAGGGCTC 3570 TAACACCCTCCGTGGGACCACCTT 3571

```
   A-  TG  TAAC       --  CA  T  GAAG
GAGTCC CTGG CCCAG  ACCCTCCGTGG GAC CC TGG   C
|||||| |||| ||||   ||||||||||| ||| || |||
CTCGGG GGCC GGGTC  TGGGGGGCACC CTG GG GCC   A
   AG  CT  C---     AC  A-  C  GTGT
```

GAM241 GAGTCGATAACTGTTGTCCTACTCACCGGTGGTTTCAGTGGCTAATTAGAACTGTGGTATTGATTC 3578
TAACTGTTGTCCTACTCACCGGTG 3579

```
    A TG T  C  CTCA-  G G
```

```
GAGTCGATA C T GT CTA    CCG TG T
|||||||||| | | || |||      ||| ||
CTTAGTTAT G  G CA GAT    GGT AC T
      - GT T  A  TAATC  G  T
GAM242  GAGTGCCTCGCTCGGTAACTGCTTGGTCCTGAACATTCTCTCGTTTCAGGAACTGATGAGGTTCTC
3584 CAGGAACTGATGAGGTTCTC 3585
   T    C   AACTGCTTGG      - ATT
GAG GCCTCG TCGGT      TCCTGAA C  C
||| |||||| |||||         ||||||| |
CTC TGGAGT AGTCA        AGGACTT G  T
   T    -   ----------     T CTC
GAM243
GAGTTGCGAGGGAGGCTGCGGGGGCGGGCGGACGTATGTTGAGACCCTATGCAGCCTCCTGCTCTCCCGAGG
GCTCCTGCGGCTC 3593 GCAGCCTCCTGCTCTCCCGAGGGC 3594
      GA   G  G  --   C  AC   TTGA
GAGTTGC  GGGAG CT CGGG G GCGGG GG  GTATG   G
||||||| ||||| || |||| | ||||| || |||||
CTCGGCG  TCCTC GG GCCC C CGTCC CC  CGTAT   /
      --    G  A   TT   T GA    CCCA
GAM244  GATAAGGACCTGTTTGGGGCAGCAGGGAGCAAAATCTCCTTTAACAACCAAGCAGTTCCTCATTC 3622
TAAGGACCTGTTTGGGGCAGCAGG 3623
  TA- C      GGCAGC     CA
GA  AGGA CTGTTTGG     AGGGAG  A
||  |||| |||||||||      ||||||
CT  TCCT GACGAACC      TTCCTC  A
   TAC  T      AACAAT    TA
GAM245  GATAAGGACCTGTTTGGGGCAGCAGGGAGCAAAATCTCCTTTAACAACCAAGCAGTTCCTCATTC
3643 TAAGGACCTGTTTGGGGCAGCAGG 3623
  TA- C-     GGCAGC     CA
GA  AGGA CTGTTTGG     AGGGAG  A
||  |||| |||||||||      ||||||
CT  TCCT GACGAACC      TTCCTC  A
   TAC  TT      AACAAT    TA
GAM245  GATAAGGACCTGTTTGGGGCAGCAGGGAGCAAAATCTCCTTTAACAACCAAGCAGTTCCTCATTC
3644 TAAGGACCTGTTTGGGGCAGCAGG 3623
  TA- C-     GGCAGC     CA
GA  AGGA CTGTTTGG     AGGGAG  A
||  |||| |||||||||      ||||||
CT  TCCT GACGAACC      TTCCTC  A
   TAC  TT      AACAAT    TA
GAM245  GATAAGGACCTGTTTGGGGCAGCAGGGAGCAAAATCTCCTTTAACAACCAAGCAGTTCCTCATTC
3645 TAAGGACCTGTTTGGGGCAGCAGG 3623
  TA- C-     GGCAGC     CA
GA  AGGA CTGTTTGG     AGGGAG  A
||  |||| |||||||||      ||||||
CT  TCCT GACGAACC      TTCCTC  A
   TAC  TT      AACAAT    TA
GAM245  GATAAGGACCTGTTTGGGGCAGCAGGGAGCAAAATCTCCTTTAACAACCAAGCAGTTCCTCATTC
3646 TAAGGACCTGTTTGGGGCAGCAGG 3623
  TA- C-     GGCAGC     CA
```

```
GA  AGGA  CTGTTTGG    AGGGAG  A
||  ||||  ||||||||    ||||||
CT  TCCT  GACGAACC    TTCCTC  A
  TAC  TT    AACAAT    TA
GAM245  GATAAGGACCTGTTTGGGGCAGCAGGGAGCAAAATCTCCTTTAACAACCAAGCAGTTTCCTCATTC
3647 TAAGGACCTGTTTGGGGCAGCAGG 3623
  TA-  C-    GGCAGC    CA
GA  AGGA  CTGTTTGG    AGGGAG  A
||  ||||  ||||||||    ||||||
CT  TCCT  GACGAACC    TTCCTC  A
  TAC  TT    AACAAT    TA
GAM245  GATAAGGACCTGTTTGGGGCAGCAGGGAGCAAAATCTCCTTTAACAACCAAGCAGTTTCCTCATTC
3648 TAAGGACCTGTTTGGGGCAGCAGG 3623
  TA-  C-    GGCAGC    CA
GA  AGGA  CTGTTTGG    AGGGAG  A
||  ||||  ||||||||    ||||||
CT  TCCT  GACGAACC    TTCCTC  A
  TAC  TT    AACAAT    TA
GAM245  GATAAGGACCTGTTTGGGGCAGCAGGGAGCAAAATCTCCTTTAACAACCAAGCAGTTTCCTCATTC
3649 TAAGGACCTGTTTGGGGCAGCAGG 3623
  TA-  C-    GGCAGC    CA
GA  AGGA  CTGTTTGG    AGGGAG  A
||  ||||  ||||||||    ||||||
CT  TCCT  GACGAACC    TTCCTC  A
  TAC  TT    AACAAT    TA
GAM245  GATAAGGACCTGTTTGGGGCAGCAGGGAGCAAAATCTCCTTTAACAACCAAGCAGTTTCCTCATTC
3650 TAAGGACCTGTTTGGGGCAGCAGG 3623
  TA-  C-    GGCAGC    CA
GA  AGGA  CTGTTTGG    AGGGAG  A
||  ||||  ||||||||    ||||||
CT  TCCT  GACGAACC    TTCCTC  A
  TAC  TT    AACAAT    TA
GAM245  GATAAGGACCTGTTTGGGGCAGCAGGGAGCAAAATCTCCTTTAACAACCAAGCAGTTTCCTCATTC
3651 TAAGGACCTGTTTGGGGCAGCAGG 3623
  TA-  C-    GGCAGC    CA
GA  AGGA  CTGTTTGG    AGGGAG  A
||  ||||  ||||||||    ||||||
CT  TCCT  GACGAACC    TTCCTC  A
  TAC  TT    AACAAT    TA
GAM245  GATAAGGACCTGTTTGGGGCAGCAGGGAGCAAAATCTCCTTTAACAACCAAGCAGTTTCCTCATTC
3652 TAAGGACCTGTTTGGGGCAGCAGG 3623
  TA-  C-    GGCAGC    CA
GA  AGGA  CTGTTTGG    AGGGAG  A
||  ||||  ||||||||    ||||||
CT  TCCT  GACGAACC    TTCCTC  A
  TAC  TT    AACAAT    TA
GAM245  GATAAGGACCTGTTTGGGGCAGCAGGGAGCAAAATCTCCTTTAACAACCAAGCAGTTTCCTCATTC
3653 TAAGGACCTGTTTGGGGCAGCAGG 3623
  TA-  C-    GGCAGC    CA
GA  AGGA  CTGTTTGG    AGGGAG  A
```

```
       ||  |||| |||||||||    ||||||
       CT  TCCT GACGAACC    TTCCTC A
        TAC  TT    AACAAT    TA
GAM245 GATAAGGACCTGTTTGGGGCAGCAGGGAGCAAAATCTCCTTTAACAACCAAGCAGTTTCCTCATTC
3654   TAAGGACCTGTTTGGGGCAGCAGG 3623
        TA-  C-    GGCAGC    CA
       GA  AGGA CTGTTTGG    AGGGAG A
       ||  |||| |||||||||    ||||||
       CT  TCCT GACGAACC    TTCCTC A
        TAC  TT    AACAAT    TA
GAM245 GATAAGGACCTGTTTGGGGCAGCAGGGAGCAAAATCTCCTTTAACAACCAAGCAGTTTCCTCATTC
3655   TAAGGACCTGTTTGGGGCAGCAGG 3623
        TA-  C-    GGCAGC    CA
       GA  AGGA CTGTTTGG    AGGGAG A
       ||  |||| |||||||||    ||||||
       CT  TCCT GACGAACC    TTCCTC A
        TAC  TT    AACAAT    TA
GAM245 GATAAGGACCTGTTTGGGGCAGCAGGGAGCAAAATCTCCTTTAACAACCAAGCAGTTTCCTCATTC
3656   TAAGGACCTGTTTGGGGCAGCAGG 3623
        TA-  C-    GGCAGC    CA
       GA  AGGA CTGTTTGG    AGGGAG A
       ||  |||| |||||||||    ||||||
       CT  TCCT GACGAACC    TTCCTC A
        TAC  TT    AACAAT    TA
GAM245 GATAAGGACCTGTTTGGGGCAGCAGGGAGCAAAATCTCCTTTAACAACCAAGCAGTTTCCTCATTC
3657   TAAGGACCTGTTTGGGGCAGCAGG 3623
        TA-  C-    GGCAGC    CA
       GA  AGGA CTGTTTGG    AGGGAG A
       ||  |||| |||||||||    ||||||
       CT  TCCT GACGAACC    TTCCTC A
        TAC  TT    AACAAT    TA
GAM245 GATAAGGACCTGTTTGGGGCAGCAGGGAGCAAAATCTCCTTTAACAACCAAGCAGTTTCCTCATTC
3658   TAAGGACCTGTTTGGGGCAGCAGG 3623
        TA-  C-    GGCAGC    CA
       GA  AGGA CTGTTTGG    AGGGAG A
       ||  |||| |||||||||    ||||||
       CT  TCCT GACGAACC    TTCCTC A
        TAC  TT    AACAAT    TA
GAM245 GATAAGGACCTGTTTGGGGCAGCAGGGAGCAAAATCTCCTTTAACAACCAAGCAGTTTCCTCATTC
3659   TAAGGACCTGTTTGGGGCAGCAGG 3623
        TA-  C-    GGCAGC    CA
       GA  AGGA CTGTTTGG    AGGGAG A
       ||  |||| |||||||||    ||||||
       CT  TCCT GACGAACC    TTCCTC A
        TAC  TT    AACAAT    TA
GAM246 GATAAGGACCTGTTTGGTGCAGCAGGGAGCAAAATCTCCTTTAACAACCAAGCAGTTCCTCATTC 3660
       TAAGGACCTGTTTGGTGCAGCAGG 3661
        TA-  C    GCAGC    CA
       GA  AGGA CTGTTTGGT    AGGGAG A
       ||  |||| |||||||||    ||||||
```

```
CT  TCCT GACGAACCA    TTCCTC A
 TAC  T      ACAAT    TA
GAM247 GATACAAGACAGGCAAGAACAAGTGGTTCTTCCAGAAACTGCGGTTTTAGATGCTTTGTTTTGATC 3675
TACAAGACAGGCAAGAACAAGTGG 3676
  A    -  ---   AA TG  - TT
GAT CAAGACAG GCA  AGAAC G GTT C  C
||| |||||||| |||  ||||| | ||| |
CTA GTTTTGTT CGT  TTTTG C CAA G  /
  -     T AGA    G- GT  A AC
GAM248 GATACCAGCCTCCCACTGTGGTGCCTGGTGGAGAACTGGCCAAGGTACAAGGAAGGCTGTGTT 3696
TACCAGCCTCCCACTGTGGTGCCT 3697
   C  C ACTGTG    -  GGAG
GATAC AGCCT CC    GTGCCT GGT   A
||||| ||||| ||     |||||| |||
TTGTG TCGGA GG    CATGGA CCG   /
  -   A AA----    A  GTCA
GAM249 GATCACATAGAATCTAGGGAAGAAATGAGAAATTCTGGGATTTTTTTTTTTAACAGAAGTGTTGTGATC
3709 TAGAATCTAGGGAAGAAATGAGAA 3710
    TAGAA  AGG    AAT     C
GATCACA    TCT  GAAGA  GAGAAATT T
|||||||    |||  |||||  ||||||||
CTAGTGT    AGA  TTTTT  TTTTTTAG G
   TGTGA   CAA    ---      G
GAM250
GATCTCGGCGTTGTGCATGTCGGGCGACTGCTCCATGATCTTGCGCCGCTCGATCTGCGACCACACCATGAAGG
CGTTCATGGGTCGCTTGATGTGCCCACTCGGGGTC 3717 TGAAGGCGTTCATGGGTCGCTTGA 3718
     C T T        TGCT   TCTT   GC  ATC  CG
GATCTCGG GT G GCATGTCGGGCGAC  CCATGA  GCGCC TCG  TG  A
|||||||| || | |||||||||||||   |||||  ||||| |||  ||  ||
CTGGGGCT CA C CGTGTAGTTCGCTG  GGTACT  TGCGG AGT  AC  C
    - - C         ----    ----   A-  ACC AC
GAM251
GATGCTCCCAAACATCCTATATGCATCCATGGAAATTTAAAGATCCTGGAATAGCGTCTTCCATGTGGGACATC
3735 GAATAGCGTCTTCCATGTGGGACA 3736
   C  AA  CCTAT  A--  T AATT
GATG TCCC ACAT   ATGC  TCCA GGA   T
|||| |||| ||||    |||| |||| |||
CTAC AGGG TGTA   TGCG  AGGT CCT   A
  -  -- CCTTC   ATA  -  AGAA
GAM252
GATGGAACACATGAAATCTTTGGTTCACAGACTATTTACAATCTTGCATTTAGAAGAGTCTCAGAAAAAGAGAGAG
CACCATT 3745 TGAAATCTTTGGTTCACAGACTAT 3746
   AACACA AAA   GG AC   A  ACAATCT
GATGG   TG TCTTT TTC AGACT TTT    T
|||||   || ||||| ||| ||||| |||
TTACC   AC AGAGA AAG TCTGA AAG     /
   ------ GAG   AA AC   G  ATTTACG
GAM253
GATGGAATAGTTCAGAAGGAATGGTACCAGTTCCTCCTTGTACCTCTGGTAGAATTCGGCTGTGAATCCATC 3761
TGGAATAGTTCAGAAGGAATGGTA 3762
```

```
   ATAGTT  AAG   GG    TTCCTCC
GATGGA    CAG  GAAT TACCAG    T
||||||    |||  |||| ||||||
CTACCT    GTC  CTTA ATGGTC    /
   AAGT-- GG-  AG   TCCATGT
GAM254  GATGGACTCTTTCTTTTTAATGTGTCCAGCTCTTGTTCTTTTTCATTTCTTAGCCTGCAGAGTTCATC
3779 TGGACTCTTTCTTTTTAATGTGTC 3780
     TT--- TTTT  TGTCC- T
GATGGACTCT  CT  AATG    AGC C
||||||||||  ||  ||||    |||
CTACTTGAGA  GA  TTAC    TTG T
     CGTCC TTCT  TTTTC  T
GAM255
GATGGTTTTAGATGATAACCACAGGTCTACAAGAGCGTTTTTAGTAAAGTGCCTGTGTTCATTGTGGACAAAGTTA
TTATTTTGCAACATC 3815 TAACCACAGGTCTACAAGAGCGTT 3816
   GTTTT     CACAG    -  TTTT TAA
GATG   AGATGATAAC  GTCTACAA GAGCG  TAG  A
||||   |||||||||   ||||||||  |||||  |||
CTAC   TTTATTATTG  CAGGTGTT CTTGT  GTC  G
   AACGT     AAA--    A  ---- CGT
GAM256  GATGTAAACACAAAAGAAAGTGTCTCAGCAGGGCTGAGCCCTCCTTCTCGTGTCTGCATT 3848
TGTAAACACAAAAGAAAGTGTCTC 3849
     A  AAA  -- T T    A
GATGTA ACAC  AGAA  AG G CTCAGC G
|||||| ||||  ||||  || | ||||||
TTACGT TGTG  TCTT  TC C GAGTCG /
   C  C--   CC C -    G
GAM257
GATGTCAATGCTGCCATTGCCACCATCAAAACAAGCGCAGCATCCAGTTTGTGGATTGGTGCCCCACTGGCTTCA
AGGTGGCATC 3858 CATTGCCACCATCAAAACAAGCGC 3859
     A-- CT  T C--   TCAAA    GCAG
GATGTCA  TG GCCA TG  CACCA   ACAAGC   C
|||||||  || |||| ||  |||||    ||||||
CTACGGT  AC CGGT AC  GTGGT   TGTTTG  A
     GGA TT  C CCC    TAGG-    ACCT
GAM258  GATTAGCTCATTTGAAGAATACCACAACAGTGGTTTTAAACATTTTTGAATTGACTAGTC 3884
TAGCTCATTTGAAGAATACCACAA 3885
     C  T G   -------   A
GATTAG TCA TT AAGAAT    ACCAC A
|||||| ||| || ||||||      |||||
CTGATC AGT AA TTTTTA    TGGTG C
     -  T G   CAAATTT    A
GAM259  GATTGACCTCCCTGAAGCCCAAGCCAATCTGTCCCAGCTCCGGGATCACTTGGGACAGGAGGTCATC
3899 TCACTTGGGACAGGAGGTCATC 3900
    T   C AAG    CCAATCT   AG
GAT GACCTCC TG  CCCAAG     GTCCC  C
||| |||||||| ||  ||||||       |||||
CTA CTGGAGG AC  GGGTTC     TAGGG  T
    -   - A--  AC-----    CC
GAM260
GATTTGACACTGCAGGCAGATGAGGTCTTGGGATGCCTCTTGCGTTCCCCCCTTCTGTGGGAGCAGGTGCCTTCC
```

CAACCTCAGCACTCAGTCCCAATC 3909 TGAGGTCTTGGGATGCCTCTTGCG 3910

```
  T AC   C - AGA    CT   T- CT   GT   CCT
GATT G ACTG AG GC  TGAGGT TGGGA GC CTTGC TCCC  T
|||| | |||| || ||  |||||| ||||| || ||||| ||||
CTAA C TGAC TC CG  ACTCCA ACCCT CG GGACG AGGG  C
  - CC   - A ---    --    TC T-   --   TGT
```

GAM261
GCAAGACACTAGGCTGTCCCGAACCCCTGGTAATAGAATTGTTTACCTTTATACCAAGAAGAGTTGGGAAAGCAC
CAAAATCTGC 3917 TACCAAGAAGAGTTGGGAAAGCAC 3918

```
 A CACTAG- G   ACCCC--  A ATTG
GCA GA    GCT TCCCGA    TGGTA TAGA   T
||| ||    ||| ||||||    ||||| ||||
CGT CT    CGA AGGGTT    ACCAT ATTT   T
 - AAAACCA A   GAGAAGA   - CCAT
```

GAM262 GCAAGTCTTCTTAGAGCTGGGGCCAAGTGACTTCTCCTTGACTCCTCTGAGCAAAGCCCAGC 3922
CAAGTCTTCTTAGAGCTGGGGCCA 3923

```
 AA- TC -   GCT  C  T C
GC  G TT CTTAGA  GGGG CAAG GA T
|| | || ||||||  |||| |||| ||
CG  C AA GAGTCT  CCTC GTTC CT T
 ACC GA C    ---  A  - C
```

GAM263 GCAAGTGCCTCCGGACATGTGGATCACAGGCTACTAGAAACCACGAGTTCCCTCCATTTGT 3947
AGAAACCACGAGTTCCCTCCATTT 3948

```
    CCTCC  A   ATCAC G
GCAAGTG   GGAC TGTGG   AG C
|||||||   |||| |||||   ||
TGTTTAC   CTTG GCACC   TC T
    CTCC-  A   AAAGA A
```

GAM264 GCAATGCCAGGTTCAGTAGCCGTCCCCCCGGAAAGGGGTGACCTTTATGCTCGTGCTTGATGTTGC
3961 TGCCAGGTTCAGTAGCCGTCCCCC 3962

```
   GC   TC-  GCC-- C  GG
GCAAT CAGGT  AGTA   GTC CCCC  A
||||| |||||  ||||   ||| ||||
CGTTG GTTCG  TCGT   CAG GGGG  /
   TA   TGC  ATTTC T  AA
```

GAM265 GCAATGTAATTTGAAATCAGTTGAATTTCCTGTTTTTCTCTCATAGGTTCAACTACTCAATTTCATGC
3977 TGTAATTTGAAATCAGTTGAATTT 3978

```
 A T T  AATC    TTT  TTTT
GCA TG AA TTGA  AGTTGAA  CCTGT   C
||| || || ||||  |||||||  |||||
CGT AC TT AACT  TCAACTT  GGATA   /
 - - T  CA--    ---   CTCT
```

GAM266
GCACTTTTAACTTTTCGCCATGGAACAACGACCCTAAAGAAAGGATAAAAGGGGGCAGTTGCCATGCTGGAACGT
GAAAAGGC 3988 TTTAACTTTTCGCCATGGAACAAC 3989

```
 A   A T   C   AA  GA  AAAGAAA
GC CTTTT AC TTTCG CATGG  CAAC  CCCT    G
|| ||||| || ||||| ||||| ||||  ||||
CG GAAAA TG AAGGT GTACC  GTTG  GGGG     G
 -   G C   C   --  AC  GAAAATA
```

GAM267

GCAGAATTGAAGATGGGAAGTTCATTGGGACTGTGTCTTGGAAAAGCACCAAGTTCGTCTCAGTTGTTCCTGTTTT
TTGC 4007 TGGGAAGTTCATTGGGACTGTGTC 4008

```
    TTGAA      GTTC     T TGT   AAA
GCAGAA   GATGGGAA   ATTGGGAC G CTTGG  A
||||||   ||||||||   |||||||| | |||||
CGTTTT   TTGTCCTT   TGACTCTG C GAACC  /
    -----      GT--     - TT-   ACG
```

GAM268

GCAGAGCTTGTGTAGGAAGAATGAAATCTGCAATTTGACTTTTAGGAGTGTCGTTTTCCGGGTCAGGCAGATTGG
TATTCAGCGCTGGCTCTGC 4018 TGAAATCTGCAATTTGACTTTTAG 4019

```
       T AGGAA  A-   AAT    TTA  TGT
GCAGAGCT GTGT   GAATG AATCTGC TTGACTT GGAG  C
|||||||| ||||   ||||| ||||||| ||||||| ||||
CGTCTCGG CGCG   CTTAT TTAGACG GACTGGG CCTT  /
       T A----  GG    ---    --- TTG
```

GAM269  GCAGCCGCTTTGGATGCTCTTCGGCCTGCACGGGACCATCACGCAGATCCGCATCCTCGGTGAGTGC
4038 TCACGCAGATCCGCATCCTCGGTG 4039

```
  GC  TT   TCTTC GC  ACG A
GCA CGCT GGATGC  G CTGC GG C
||| |||| ||||||  | |||| ||
CGT GTGG CCTACG  C GACG CT C
  GA  CT   C---- TA  CA- A
```

GAM270

GCAGGAGCGGGGGGGAATCATTGACCTTGAGGCTGAGCGAAACCGATACTTCATCAGCCTTCAGCAGCCTCCTG
CCCCTGC 4052 TCAGCCTTCAGCAGCCTCCTGCCC 4053

```
    A     GAATCA  AC T    GC  ACC
GCAGG GCGGGGGG    TTG CT GAGGCTGA GAA  G
||||| ||||||||    ||| || |||||||| |||
CGTCC CGTCCTCC    GAC GA TTCCGACT CTT  A
    C     ------  -- C    A-  CAT
```

GAM271  GCAGGATGATTGAGGATGCAATTCGAAGTCACAGCGAATCAGCCTCACCTTCAGCCCTGT 4068
TCAGCCTCACCTTCAGCCCTGT 4069

```
    A- T--  A CA   AAGT
GCAGG TGA  TGAGG TG ATTCG   C
||||| |||  |||||| || |||||
TGTCC ACT  ACTCC AC TAAGC  /
    CG TCC   G  --   GACA
```

GAM272

GCAGTGGAGGGGGCAGGACCTCCTGCTGGTGCAGCACCAGCTGCTGTGAGCAGGTCCACCGGCCCCTACACTG
C 4104 TGTGAGCAGGTCCACCGGCCCCTA 4105

```
    GA   A ACCT   GGT-  A
GCAGTG GGGGGC GG   CCTGCT   GCAGC  C
|||||| |||||| ||   |||||| |||||
CGTCAC TCCCCG CC   GGACGA   CGTCG  C
    A-   G ACCT   GTGT  A
```

GAM273  GCATATGAGGACGGCCATTATTGTTGGGGGCAAATGGAAATGCTCTAGGCGGGGCCGCGTAGC 4125
TATGAGGACGGCCATTATTGTTGG 4126

```
  A  AGGA    ATTA  TG    AAT
GC TATG   CGGCC   TTGT GGGGCA  G
```

```
      II IIII   IIIII   IIII IIIIII
      CG ATGC   GCCGG   GGCG TCTCGT  G
       -   ----   ----   GA    AAA
GAM274  GCATCAGAGTAATCTTCAGTGTGGAATGTTAAATAACGCTTTTATACTGTATTTTGTACTATGATGT 4137
TCAGAGTAATCTTCAGTGTGGAAT 4138
       G   ATCTT--      -   A
GCATCA AGTA      CAGTGTGGAA TGTT A
IIIIII IIII      IIIIIIIIII IIII
TGTAGT TCAT      GTCATATTTT GCAA A
       A  GTTTTAT        C   T
GAM275  GCATCTAATGTGATAAGGCTGCACGTTTTATATCGATGGTCATTCTTTATTGTATTGGTGC 4142
TCTAATGTGATAAGGCTGCACGTT 4143
      T    TG    C- CA   TTA
GCA CTAATG ATAAGG TG CGTT  T
III IIIIII IIIIII II IIII
CGT GGTTAT TATTTC AC GTAG  /
     -  GT    TT TG   CTA
GAM276  GCATGAGGAAGATAATCCTTTGAAACATCATTAATTGAAGTGATTTAAATAGGATTTCCTTTTGT 4157
TGAGGAAGATAATCCTTTGAAACA 4158
      T   GATA   TTG-  C   AA
GCA GAGGAA  ATCCT   AAA ATCATT  T
III IIIIII  IIIII   III IIIIII
TGT TTCCTT  TAGGA   TTT TAGTGA  T
      T   ----   TAAA  -    AG
GAM277
GCATGGCCAGGGAGGGCAAATGGAAAGGCAACCACTCTCTGCCGGTCCTGGGCTTATCCCTGCAATGTGC 4177
TGGCCAGGGAGGGCAAATGGAAAG 4178
      GC-   -  AAAT  AA  ACCA
GCATG CAGGGA GGGC   GGA GGCA   C
IIIII IIIIII IIII   III IIII
CGTGT GTCCCT TTCG   CCT CCGT   /
      AAC    A  GGT-  GG  CTCT
GAM278
GCCAATTAGAGGTTAAATAAATTGCTTAAAAGTGTTCTCAAAACTTGCAGTTTCTTCAATCTTATGAAATTGGC
4202 TTAGAGGTTAAATAAATTGCTTAA 4203
       A---   A T    TTAA   GTTC
GCCAATT  GAGGTT AA AAATTGC  AAGT   T
IIIIIII  IIIIII II IIIIIII  IIII
CGGTTAA  TTCTAA TT TTTGACG  TTCA   /
       AGTA    C C    ----   AAAC
GAM279  GCCACCACTCGGGTACGGAGGCTCAGAGACTACTATAGCAGCCGGAGTCAGAGTGGTGGC 4234
TAGCAGCCGGAGTCAGAGTGGTGG 4235
        G TA-  AG  CAG  A
GCCACCACTC GG  CGG  GCT  AG  C
IIIIIIIIII II  III  III  II
CGGTGGTGAG CT  GCC  CGA  TC T
        A GAG  GA  TA-  A
GAM280  GCCACCCTACGCCGTAGCCGTCCAGAGACTGGCAGGCCTCGGCTAAAGGTCTGGAGGGTGAGC 4245
TGGCAGGCCTCGGCTAAAGGTCTG 4246
      -   AC---------  TA  GT   A
```

```
GC CACCCT       GCCG GCC CCAG G
|| ||||||        |||| ||| ||||
CG GTGGGA       CGGC CGG GGTC /
 A   GGTCTGGAAAT  TC  AC   A
GAM281
GCCAGCAAAGACTGCCTCTTCGCCATCGTGGGGAACAAAGTGGACCTCACTGAGGAGGGGGCCTTGGCGGGC
4261 TCACTGAGGAGGGGGCCTTGGCGG 4262
  A  A  A  G     CCATC    AA AA
GCC GC AAG CT CCTCTTCG   GTGGGG  C A
||| || ||| || ||||||||    ||||||  |
CGG CG TTC GG GGAGGAGT   CACTCC  G /
  G  G  C  G     -----     AG TG
GAM282  GCCATCACTGCCACCCAGAAGACTGTTGGATGGCCCCTCCGGGAAAACTGTGGCGTGATGGC 4276
TCACTGCCACCCAGAAGACTGTTG 4277
    T   CCAGAAGA  TT AT
GCCATCAC GCCAC     CTG GG G
|||||||| |||||      ||| ||
CGGTAGTG CGGTG     GGC CC G
    -   TCAAAAG-  CT CC
GAM283
GCCATGGCGGCCATGAGTTGTTGCGGCGGGTTTCGGTTACTGCGGTGGCAGCTCTGTCTGGCCGGCCCCTTGG
C 4290 TGGCGGCCATGAGTTGTTGCGGCG 4291
   T-- -  T---     TG G  GTTT
GCCA  GGC GGCCA   GAGTTGT C GCGG   C
||||  ||| |||||   |||||||| | ||||
CGGT  CCG CCGGT   CTCGACG G CGTC   G
  TCC  G   CTGT     GT G  ATTG
GAM284
GCCCAGCCCATGGCTGCCATGGGAGGCCTGAAGGTGCTTCTGCACTGGGCTGGTCCAGGCGGCGGGGAGCCC
TGGGT 4301 TGGCTGCCATGGGAGGCCTGAAGG 4302
    ----  ATG    A  A-  GAA   T
GCCCAG  CCC  GCTGCC TGGG GGCCT  GGTGC T
||||||  |||  |||||| |||| |||||  |||||
TGGGTC  GGG  CGGCGG ACCT TCGGG  TCACG C
   CCGA  G--  -  GG  ---   T
GAM285  GCCCCAACCTCCTGGCTTGGTCTCCGCTTGTTGTTGGCTACCTAGTTCCAGGTTGAGGGC 4318
TACCTAGTTCCAGGTTGAGGGC 4319
   -   CCT  T  CT - TT
GCCC CAACCT  GGCT GGT CCG C  G
|||| ||||||  |||| ||| ||| |
CGGG GTTGGA  TTGA CCA GGT G /
  A   CC-  T  TC  T TT
GAM286
GCCCCGCCCCTGCCGCCGGAATCCTGAAGCCCAAGGTCTGCCCGGGGGGCGGTCCGGCGGCGCCGGCGATGG
GGC 4328 TGCCGCCGGAATCCTGAAGCCCAA 4329
   --- CC      AT TGAA  AA TC
GCCCC GCC TGCCGCCGGA CC  GCCC GG T
||||| ||| ||||||||| ||  |||| ||
CGGGG CGG GCGGCGGCCT GG  CGGG CC /
  TAG CC       -- ----  GG CG
```

GAM287

GCCCCTCAAGTCGGGTATGAAGGAGCTGGCCGTGTTCCGGGAGAAGGTCACTGAGCAGCACCGGCAGATGGGC
 4344 TCGGGTATGAAGGAGCTGGCCGTG 4345

    C AA    GTA AAGG C   GTG  C
GCCC TC GTCGG  TG  AG TGGCC  TTC G
|||| || ||||| || || ||||| |||
CGGG AG CGGCC  AC  TC ACTGG  GAG /
  T A-    ACG GAG- -   AA- G
GAM288

GCCCTCCCTTTGGTCTCCCTGTTCTTCTATGTGGTGACAGATGGCAAGGAAGTCCTACTACCAGAGGTTGGGGC
4353 TGGCAAGGAAGTCCTACTACCAGA 4354

    C-    CTCCCTG--  -  G G
GCCCT CCTTTGGT      TTCTT CTAT TG T
||||| ||||||||      ||||| |||| ||
CGGGG GGAGACCA      AGGAA GGTA AC G
   TT    TCATCCTGA   C   G A
GAM289

GCCCTCGCCCGGCCTGTCAGCGCTGCTCTCCGCCGCAGCTTCAGCACCTCGGCCCAGAACAATGCTAAAGTAG
CTGTGCTAGGGGC 4369 TGTCAGCGCTGCTCTCCGCCGCAG 4370

    C- C  -- GTC  C C CC  CA-- T
GCCCT GC CGGC CT  AGCG TG TCT GCCG   GC T
||||| || |||| || |||| || ||| ||||   ||
CGGGG CG GTCG GA  TCGT AC AGA CGGC   CG C
   AT T  AT AA-  A A CC   TCCA A
GAM290  GCCGCATCTTCTTTTGCGTCGCCAGCCGAGCCACATCGCTCAGACACCATGGGGAAGGTGAAGGT
4378 CGCTCAGACACCATGGGGAAGGTG 4379

  G-      - C- GCC  C GC
GCC CATCTTCTTT TG GTC  AGC GA C
||| |||||||||| || |||  ||| || ||
TGG GTGGAAGGGG AC CAG  TCG CT A
   AA     T CA AC- - AC
GAM291  GCGCCGCCTCCTTGAAACTTAGCGCTCTGACCCAGAGTCTGACCAGGGTACGGCAGGCGC 4400
GTCTGACCAGGGTACGGCAGGCGC 4401

   - T-- AAAC  C   A
GCGCC GCC  CCTTG   TTAG GCTCTG C
||||| ||| ||||| |||| ||||||
CGCGG CGG  GGGAC   AGTC TGAGAC /
   A CAT   C--- -    C
GAM292  GCGCTCACTTGTCTTCAGGAAGCTCGGAGCCTTTGGTGGAGCCGGGGAGAGGAAGGGTGGGTGC
4429 TCACTTGTCTTCAGGAAGCTCGGA 4430

     TG   AGGAAG   AG TT
GCGCTCACT TCTTC    CTCGG CC T
||||||||| |||||    ||||| ||
CGTGGGTGG AGGAG    GGGCC GG G
     GA    AG----   GA TG
GAM293

GCGGGAGCTGGGGGTGTGCCTCCAGGAGCTGCTGATGGCTGACGGGCGGCCCGGGACTGGTGGATCTCCCGG
CTGACCGT 4449 TGGGGGTGTGCCTCCAGGAGCTGC 4450

    G-    - G -- A A   GA GC
GCGG AGCTGGG GGT TGCC  TCC GG GCTGCT  TG T

```
|||| |||||||| ||| |||| ||| || |||||| ||
TGCC  TCGGCCC CTA GTGG  AGG CC CGGCGG  GC /
   AG     T  G   TC  G -    -- AG
GAM294
GCGGGCAGCCACAGTTACCAAGAAGACTTATGAGATCTGGCATCGACGGCATGACTACTGGCTGCTAGC 4458
TGGCATCGACGGCATGACTACTGG 4459
  G      C-    -- AA- ---- - T
GC GGCAGCCA AGTTA CC  GA   AGA CT A
|| |||||||| ||||| ||  ||   ||| ||
CG TCGTCGGT TCAGT GG  CT   TCT GA T
  A     CA   AC CAG ACGG  A G
GAM295
GCGGGGCCCGGGCGGCGGCGCTAGCAGATCCAGCGGATAAAAGCGGTCGAAGAAGCCGGGTTGCGC 4462
TAAAAGCGGTCGAAGAAGCCGGGT 4463
   G    G GG--- - AGCAG   A
GCG GGCCCGG C  CGGC GCT   ATCC G
||| |||||| |   |||| |||    ||||
CGC TTGGGCC G   GCTG CGA   TAGG /
   G    - AAGAA   G AAA-- C
GAM296
GCGGTAATGATCAGAGACCGAGGCTGCACCGGCAGAGGCTGCGGGGCGGACGCGCGGGCCGGCGCAGCCAT
GGTGAAGATTAGCTTCCAGC 4473 TCAGAGACCGAGGCTGCACCGGCA 4474
  - TAA-  AGAG   A   A   AGAG  T  GGG
GC GG   TGATC  ACCG GGCTGC CCGGC  GC GCG  C
|| ||   |||||  |||| |||||| |||||  || |||
CG CC   ATTAG  TGGT CCGACG GGCCG  CG CGC  /
  A TTCG   AAG- A   C   GG-- - AGG
GAM297
GCGTTTTTGAAGTTATTGAGATTCTACATTGCATTGACTGGGATTCCAGTAGCAATTTTCATAACTCTGGTGAATG
T 4488 AGCAATTTTCATAACTCTGGTGAA 4489
    T GA   T  TTCTAC  ATTG   G
GCGTTT TT AGTTAT GAGA   ATTGC  ACTGG A
|||||| || |||||| ||||    |||||   |||||
TGTAAG GG TCAATA CTTT    TAACG   TGACC T
    T TC    -  ------   A---   T
GAM298
GCTATGGCGGATATGATTATACTGGGTATAACTATGGGAACTATGGATATGGACAGGGATATGCAGACTACAGTG
GC 4508 TATGATTATACTGGGTATAACTAT 4509
   GGC ATA AT A- GG  A    G
GCTAT GG  TG TAT CTG TATA CTATGG A
||||| ||  || ||| ||| |||| ||||||
CGGTG  TC  AC ATA GAC GTAT GGTATC /
   ACA AG- GT GG AG  A    A
GAM299  GCTATTCCAAGAACATGAATGGAGGAATGTTGGGCCGAATTACAGCGTGGTTGTGCATGGGAGTGGT
4521 TTCCAAGAACATGAATGGAGGAAT 4522
     AAGAA  A TG AGGA    GGCC
GCTATTCC   CATG A G  ATGTTG  G
||||||||   |||| | |  ||||||
TGGTGAGG   GTAC T T  TGCGAC  A
    ----- G GT GG--   ATTA
```

GAM300
GCTCCGCCTTTTCTGGGTACTTACGGTCCTGAGTCTCAAGTTCGTCTTCGAGATGCTGTTGTGCCAGAAGCTGGC
GGAGC 4544 TCTGGGTACTTACGGTCCTGAGTC 4545

```
     T-    G  TT   CCTGA   -  TT
GCTCCGCC TTTCTGG TAC ACGGT   GTCTC AAG C
|||||||| |||||||| ||| |||||    ||||| |||
CGAGGCGG GAAGACC GTG TGTCG   TAGAG TTC /
     TC    - T-  -----   C  TG
```

GAM301 GCTGACATTAACTACAATTATGGGAAATGCAAAGCTGTTTGGATATGGTAGTGTGTGGT 4556
TGACATTAACTACAATTATGGGAA 4557

```
  G  TA   AAT  GG  AT A
GCT ACAT ACTAC  TAT GAA GC A
||| |||| |||||  ||| ||| ||
TGG TGTG TGATG  ATA TTT CG A
  -  --  GT-  GG  GT A
```

GAM302 GCTGACCATGCAGCAACTGAACTGGCTCTGTACCATCAGAGCCTTTCCCGGCGATCTGGCTCAGC
4578 TGACCATGCAGCAACTGAACTGGC 4579

```
  - TGCA AACT  CT    TA
GCTGA CCA  GC  GAA GGCTCTG C
||||| |||  ||   ||| ||||||||
CGACT GGT  CG  CTT CCGAGAC C
   C  CTAG GCC- T-    TA
```

GAM303
GCTGACGCCGGCTAGGGAGGAGCAGCCCCCACAACATCGATCCAAGAGGGGGAGCTCAGTGGGCGGCGTGTG
C 4591 TGACGCCGGCTAGGGAGGAGCAGC 4592

```
  TG   G  GGGAG  AG   ACAACATC
GC ACGCCG CTA   GAGC CCCCC     G
|| |||||| |||    |||| |||||
CG TGCGGC GGT   CTCG GGGGG     /
  TG   G  GA---  A-   AGAACCTA
```

GAM304 GCTGACGTGGGTGTGATCGCTAGCAGCTTCGAGATCGGGAACCTGGCGCTCATCCTCTTCGTGAGC
4618 TGACGTGGGTGTGATCGCTAGCAG 4619

```
  G  T-  TG  T    CAG  T A
GCT ACG  GGG  TGA CGCTAG  CT CG G
||| ||| ||| ||| |||||||  || ||
CGA TGC  CTC  ACT GCGGTC  GG GC A
  G  TT  CT  C    CAA  - T
```

GAM305
GCTGAGAAGCAGTGACCCGCAGATGCCGGCTGAATGGACTGCTCCGGTCTTGGAGTCACTGCTACTCAGC 4627
TGAGAAGCAGTGACCCGCAGATGC 4628

```
    A    -  C AT   CTGAAT
GCTGAG AGCAGTGAC CCG AG  GCCGG    G
|||||| ||||||||| ||| ||  |||||
CGACTC TCGTCACTG GGT TC  TGGCC    G
    A    A - --   TCGTCA
```

GAM306
GCTGCATCAAAGGTAGACTTTCGCACAGGTTGTGAGGTTGGAGTCACAGTGTTATTTGTTGTACCTGATGTAGT
4647 TCAAAGGTAGACTTTCGCACAGGT 2738

```
    AA  - TTTC- AGGT  GGT
GCTGCATCA GGTA GAC  GCAC  TGTGA T
```

```
|||||||||| |||| |||    |||| |||||
TGATGTAGT CCAT TTG   TGTG   ACACT  G
    --  G TTTAT ----    GAG
GAM306
GCTGCATCAAAGGTAGACTTTCGCACAGGTTGTGAGGTTGGAGTCACAGTGTTATTTGTTGTACCTGATGTAGT
4648 TCAAAGGTAGACTTTCGCACAGGT 2738
     AA  - TTTC- AGGT   GGT
GCTGCATCA GGTA GAC   GCAC   TGTGA  T
|||||||||| |||| |||    |||| |||||
TGATGTAGT CCAT TTG   TGTG   ACACT  G
    --  G TTTAT ----    GAG
GAM306
GCTGCATCAAAGGTAGACTTTCGCACAGGTTGTGAGGTTGGAGTCACAGTGTTATTTGTTGTACCTGATGTAGT
4649 TCAAAGGTAGACTTTCGCACAGGT 2738
     AA  - TTTC- AGGT   GGT
GCTGCATCA GGTA GAC   GCAC   TGTGA  T
|||||||||| |||| |||    |||| |||||
TGATGTAGT CCAT TTG   TGTG   ACACT  G
    --  G TTTAT ----    GAG
GAM306
GCTGCATCAAAGGTAGACTTTCGCACAGGTTGTGAGGTTGGAGTCACAGTGTTATTTGTTGTACCTGATGTAGT
4650 TCAAAGGTAGACTTTCGCACAGGT 2738
     AA  - TTTC- AGGT   GGT
GCTGCATCA GGTA GAC   GCAC   TGTGA  T
|||||||||| |||| |||    |||| |||||
TGATGTAGT CCAT TTG   TGTG   ACACT  G
    --  G TTTAT ----    GAG
GAM306
GCTGCATCAAAGGTAGACTTTCGCACAGGTTGTGAGGTTGGAGTCACAGTGTTATTTGTTGTACCTGATGTAGT
4651 TCAAAGGTAGACTTTCGCACAGGT 2738
     AA  - TTTC- AGGT   GGT
GCTGCATCA GGTA GAC   GCAC   TGTGA  T
|||||||||| |||| |||    |||| |||||
TGATGTAGT CCAT TTG   TGTG   ACACT  G
    --  G TTTAT ----    GAG
GAM307
GCTGGACGAGCTGACCTTGGAAGGGGTGGCCCGGTACATGCAGAGCGAACGCTGTCGCAGAGTCATCTGTTTG
GT 4652 TGACCTTGGAAGGGGTGGCCCGGT 4653
 TG  G C  C - A G G- CCG A
GC  GAC AG TGAC TTG GA GG GT  GC   GT C
|| ||| || |||| ||| || || || || || || ||
TG  TTG TC ACTG GAC CT TC CA  CG   CG A
 GT  - T  A  G G  AG AGA  T
GAM308  GCTGGATAGCTCTGGAGCAGCTTAGTGTGTCTGGGGCAGACCGACCACCTTCTATCTTGAGTGCCAGC
4667 TAGCTCTGGAGCAGCTTAGTGTGT 4668
   ATA  T  GC  CTTA  T  T GG
GCTGG  GCTC GGA AG   GTG GTC GG  C
||||| |||| ||| ||   ||| ||| ||
CGACC  TGAG TCT TC   CAC CAG CC  A
  G--  T  A- TTC-  - - AG
```

GAM309
GCTGTGACTGCCTGCAGGGTTTCCAGCTGACCCACATCCCTGGGTGGGGGGACTGGGTCTGGGATGGGTACCC
TCATCATCAGC 4680 TGCAGGGTTTCCAGCTGACCCACA 4681
　　- CTGCC　C　　T　G- -　　CA-　　G
GCTG TGA　　TG AGGGT TCCA　CT GACCCA　TCCCT G
|||| |||　　|| ||||| ||||　|| |||||| 　||||||
CGAC ACT　　AC TCCCA GGGT　GG CTGGGT　GGGGG G
　　T　-----　-　　T　AG T　　CAG　　T
GAM310　GCTTCCTTCGTCTACCACTCTGTGCCAGCTCCAACAGACCTGGCAACTAATAGGACTAGAAGGAGGC
4701 GGCAACTAATAGGACTAGAAGGAG 4702
　　　-- ACCACTCTG　　C CA
GCTTCCTTC GTCT　　　TGCCAG TC　A
||||||||| ||||　　　|||||| ||
CGGAGGAAG CAGG　　　ACGGTC AG　/
　　　AT　ATAATCA--　　C AC
GAM311
GCTTCTTGCTGATCAGAGCTTGGTTGGCACAGCCGGGGTCCTCGCCCTCGGCCCTGCTGTTCTCCCGGATCGCT
CTGATCCAGCCCAGC 4719 TCAGAGCTTGGTTGGCACAGCCGG 4720
　　TCTT　-　　　---　TT C　　C　T TCG
GCT　GCTG ATCAGAGC　TTGG　GG ACAGC GGGG CC　C
|||　|||| ||||||||　||||　|| ||||| |||| ||
CGA　CGAC TAGTCTCG　GGCC　CT TGTCG TCCC GG　C
　CC-- C　　CTA　CT -　- - CTC
GAM312
GCTTGCACGCAGAGGCGGGCGGCAGACGGTGCCCGGCGGAATCTCCTGAGCTCCGCCGCCCAGCTCTGGTGC
CAGC 4738 GAGCTCCGCCGCCCAGCTCTGGTG 4739
　　T　G　GC　　AGAC T　C　C A
GCT GCAC CAGAG GGGCGGC　GG GC CGG GG A
||| |||| ||||| |||||||　|| || ||| ||
CGA CGTG GTCTC CCCGCCG　CC CG GTC CT T
　　C　- GA　　---- T A　- C
GAM313
GCTTGGCCTATGACAGGTCACCGTGTGTAAATCTTTCCCAATAAAGTGTTGCACAAAGGCATCCTGTCCGTGCAG
GT 4771 TGACAGGTCACCGTGTGTAAATCT 4772
　　- CTAT　　TCA G-　　AT　CC
GCTTG GC　GACAGG　CC TGTGTAA CTTT C
||||| ||　|||||| || ||||||| ||||
TGGAC TG　CTGTCC GG ACACGTT GAAA A
　　G C---　　TAC AA　　GT　TA
GAM314
GCTTTTAACTTGGACTAGTGTAACTCCTTCATGCAATAAACTGAAAAGAGCCATGCTGTCTAGTCTTGAAGT 4781
AAAAGAGCCATGCTGTCTAGTCTT 4782
　　TAAC　T　AA C-　TGCA
GCTTT　TTGGAC AGTGT CTC TTCA　A
|||||　|||||| ||||| ||| ||||
TGAAG　GATCTG TCGTA GAG AAGT　T
　　TTCT　-　CC AA　CAAA
GAM315
GCTTTTCTAGTTTGCAACTTCTAATCTGCTGTGAGTCAGGAAAACATATGGCAGAGTTAAATTGTGCTTTTGGTTA
GGT 4798 TGGCAGAGTTAAATTGTGCTTTTG 4799

```
  TT  TTT  ACTTCTAA-     A CAG
GCTT CTAG GCA      TCTGCTGTG GT  G
|||| |||| |||       |||||||| ||
TGGA GGTT CGT      AGACGGTAT CA  /
  TT  TT- GTTAAATTG     A AAA
GAM316
GGAAATGGTTATTGAATCAGATAGACCAGTTCTGTTGAGGGTCTTAAAGAGTCTCAATTTTCTCATCTATAAAACCA
ATACCTTTCC 4812 TCAGATAGACCAGTTCTGTTGAGG 4813
   T T  AATCAG   CC TTCT    G TT
GGAAA GGT ATTG    ATAGA AG  GTTGAGG TC  A
||||| ||| ||||     ||||| ||  ||||||| ||
CCTTT CCA TAAC    TATCT TC  TAACTCT AG  /
   - -  CAAAA-   AC TTT-    G AA
GAM317 GGAACATGACAGCAGGCACACTCATGGAATACAATGGGTTTTCCATGCACCCTGTCATCCTCAGTCC
4819 TGACAGCAGGCACACTCATGGAAT 4820
  ACAT- CA   CACACT    T AA
GGA   GA GCAGG    CATGGAA AC  T
|||   || |||||     ||||||| ||
CCT   CT TGTCC    GTACCTT TG  /
  GACTC AC   CAC---    T GG
GAM318 GGAAGACCGTAATTGTGGCTGCACTGGATGGGACCTTCCAGAGGAAGCCATTTGGGGCCATCC 4843
AGACCGTAATTGTGGCTGCACTGG 4844
  AGA G TT   GCA-   TGG
GGA  CC TAA GTGGCT  CTGGA  G
|||  || ||| ||||||   |||||
CCT  GG GTT TACCGA  GACCT  A
  ACC G -- AGGA    TCC
GAM319
GGAAGCCGTCAGCCAAGTCGCCACATTTCTCTGCAAAATGTCATAGCTTATATTAATGTACAGTATTCCATGGTAT
GCTGCCTTCCGTTGTAAGTAGCAGATCTCTCCGTGACTTGACACGGCTACT 4858
TGTCATAGCTTATATTAATGTACA 4859
  A  CAGC    CACATTTC  AAAATGTCATA   TTAATGTA   TCC
GG AGCCGT  CAAGTCGC    TCTGC     GCTTATA    CAGTAT  A
|| ||||||  ||||||||     |||||     |||||||     ||||||
TC TCGGCA  GTTCAGTG    AGACG     TGAATGT    GTCGTA  T
  A  CA--   CCTCTCT-  A----------   TGCCTTCC   TGG
GAM320
GGAAGCTCTTTGCCCCACAGCAGATTCTGCAATGCAGGCCTGACAACTGAGGGAACTGCGAGGGCCGCC 4873
TGACAACTGAGGGAACTGCGAGGG 4874
  AA T   ---- A ---- AT  A
GG GC CTTTGC  CCC CAG  CAG TCTGC A
|| || ||||||   ||| |||   ||| |||||
CC CG GGAGCG  GGG GTC  GTC GGACG /
  GC -   TCAA A AACA C-  T
GAM321 GGAAGGCAGCCAAGAGGAAGTGGGCGGCACAGACCATCCGGCGGCTCATCCGAGGCTTCATCC 4918
AGGCAGCCAAGAGGAAGTGGGCGG 4919
  A C  AAGA AG   G ACA AC
GGA GG AGCC  GGA TGGGC GC  G C
||| || ||||  |||  ||||| ||   |
CCT CT TCGG  CCT ACTCG CG  C /
```

```
   A  -   AG--  --   G  GC- TA
GAM322  GGAATAAAAATAACAACTCTTTGTGGGCGCGGCGTTTTGGGCCCGAGAAGAGGTTTTTTTAAACC 4923
TAAAAATAACAACTCTTTGTGGGC 4924
  AA   T AA   G   G  C
GG  TAAAAA AAC  CTCTTT TGGGC CGG G
||  |||||| |||  |||||| ||||| |||
CC  ATTTTT TTG  GAGAAG GCCCG GTT T
  AA   -  --    A   G  T
GAM323
GGAATCTCGAAGCTGCTAAATGAGTTCCACGAAGAACTTGCCTCCAATTAAAAGGCGCGTATTTATATACCTTTCA
TAGGGCGGGGGGAGATTTT 4942 AATGAGTTCCACGAAGAACTTGCC 4943
       GAAG   AA   TTCCACG-  A  T   CCAA
GGAATCTC   CTGCT ATGAG     AAG AC TGCCT   T
||||||||   ||||| |||||      ||| || |||||
TTTTAGAG   GGCGG TACTT     TTT TG GCGGA   /
      GGG-   GA   TCCATATA A  C   AAAT
GAM324  GGAATGAGAATACCTGAAACCAAACCGTTAACAAGGAATGGTAGTGAAGTTAAGGAGTTAGCTCATTCT
4958 TGAGAATACCTGAAACCAAACCGT 4959
       AAT - GA  -- A-   AAC
GGAATGAG  AC CT AAC CA ACCGTT  A
||||||||  || || ||| || ||||||
TCTTACTC  TG GG TTG GT TGGTAA   /
     GAT A AA  AA GA    GGA
GAM325
GGACACCATCTTTATAAAAGTAAAACTTCTAGATCCTGAAATGTACTACAGTAGAGTCTATAGTTTACACTTTTAAT
CACAGATTGGAATTC 4970 TAAAAGTAAAACTTCTAGATCCTG 4971
  CA  -  TTA--    A-   TC   TC  AAA  TA
GGA CCA TCT   TAAAAGT AAACT TAGA CTG  TG C
||| ||| |||   ||||||| ||||| |||| |||  ||
CTT GGT AGA   ATTTTCA TTTGA ATCT GAT  AC /
  AA  T CACTA     CA  T-  GA  G-- AT
GAM326  GGACCAACTGATACCTCGCTATGTAGCTTTACTCCTTTATCCTCTAGGTGGCGTATTAGAATGGTGCC
4974 GTGGCGTATTAGAATGGTGCC 4975
  -  A-    CTC   G  CTTTACTC
GG ACCA  CTGATAC  GCTAT TAG      C
|| ||||  |||||||  ||||| |||
CC TGGT  GATTATG  CGGTG ATC      /
  G  AA      ---   G  TCCTATTT
GAM327  GGACCTGTCACCCCACCATGGAGAAAAGAGTCTTTTGGTTCTTTTTAACATAAGTGATTAGTTT 4979
TGTCACCCCACCATGGAGAAAGA 4980
   CT   CCCACC  GA    GT T
GGAC GTCAC    ATG  GAAAAGA C T
|||| |||||    |||  |||||||| |
TTTG TAGTG    TAC  TTTTTCT G T
   AT   AA----  AA    TG T
GAM328  GGAGAAGCGCGAGGGCTACGAGCGTCTCCTGAAGATGCAAAACCAGCGTGGCGGCCGCGCTCTCT
4987 TGCAAAACCAGCGTGGCGGCCGCG 4988
     A   AGG   A-------   CC
GGAGA GCGCG  GCTACG      GCGTCT T
||||| |||||  |||||       |||||
```

TCTCT CGCGC  CGGTGC     CGTAGA /
  -   CGG    GACCAAAA    AG
GAM329
GGAGCCCTTGATGTCCTGCAAATGAAGGAGGAGGATGTCCTTAAGTTCCTTGCAGCAGGAACCCACTTAGGTGG
CACC 5001 GTCCTGCAAATGAAGGAGGAGGAT 5002
  A  -  - ---    AAA -   ---   A
GG GCC CTTGA TG  TCCTGC  TG AAGGAG  GAGG T
II III IIIII II  IIIIII  II IIIIII  IIII
CC CGG GGATT AC  AGGACG  AC TTCCTT  TTCC G
 A  T   C CCA    --- G   GAA   T
GAM330
GGAGCGGATGGGCGGCGCGGGCGGCGAGGGCAGCGACGACGACACCTCGCTCACCTGAGCGCCGCACCGCT
TC 5006 TGGGCGGCGCGGGCGGCGAGGGCA 5007
    ATGG    -- C -   GCAG A
GGAGCGG  GCGGCGC GGG G GCGAGG   CG C
IIIIIII  IIIIIII III I IIIIII   II
CTTCGCC  CGCCGCG TCC C CGCTCC   GC G
   A---    AG  A T   ACA- A
GAM331
GGAGCTGGAGAGGTGCAGGCCCAGGGCGTCGTCCGAGTGAGCAGCGGTGCTGGCCGTGTGGGACCCGGGCC
CGCTTAGCACC 5078 TGGCCGTGTGGGACCCGGGCCCGC 5079
 A   AGAGGT A   A  CG  TC A  G   G
GG GCTGG    GC GGCCC GGG  TCG  CG GT AGCA C
II IIIII    II IIIII III III II II IIII
CC CGATT    CG CCGGG CCC  GGT  GC CG TCGT G
 A  ------ C  - AG GT - G  G
GAM332
GGAGCTGGCCCTGGGCAGCAACAAGCTGGGTGATGTGGGCATGGCGGAGCTGTGCCCAGGGCTGCTCC 5105
TGGCGGAGCTGTGCCCAGGGCTGC 5106
    T     G ACAA  GG G  T
GGAGC GGCCCTGGGCA CA   GCT GT ATG G
IIIII IIIIIIIIIII II   III II III
CCTCG TCGGGACCCGT GT   CGA CG TAC G
    -      - ---- GG G  G
GAM333
GGAGGGCCAGGGTTTCCCCGGGCGCGGGGCTTATCTTCCTTTGCCTGCTATGAAAAACATTCTCACCTTCC 5123
GCCTGCTATGAAAAACATTCTCAC 5124
    CC    ---- CC--    C  CTT
GGAGGG AGGGT  TTC  CGGGCG GGGG  A
IIIIII IIIII  III  IIIIII IIII
CCTTCC TCTTA  AAG  GTCCGT TCCT /
   AC   CAAA TATC    T  TCT
GAM334
GGAGGGCGGGGGAGAGACGAGCGGCTCTGGCCCCTTAATTGTACTTCGGGCTCGTATTGTCTCTCCTTTCGCCA
CCTCC 5135 TATTGTCTCTCCTTTCGCCACCTC 5136
   --  -      - GCTCT   CTTAAT
GGAGG  GCGGG GGAGAGACGA GCG    GGCCC    T
IIIII  IIIII IIIIIIIIII III    IIIII
CCTCC  CGCTT CCTCTCTGTT TGC    TCGGG    G
   AC   T      A ----- CTTCAT

GAM335  GGAGGTGGGAGGGGAGGGCCACACGATGCGTTGCTGCGCCCCCCGCCTTCCTCTCACTCCTCT 5145
TGGGAGGGGAGGGCCACACGATGC 5146
    TGG       CACACGAT   T
GGAGG  GAGGGGAGGGC     GCGT G
|||||  ||||||||||     ||||
TCTCC  CTCTCCTTCCG     CGCG C
    TCA        CCCCC---   T
GAM336
GGAGTCTCCTCTCTACCGCCACTGTCACACCGTAGCCCACATGGATAGCACAGTTGTCAGACAAGATTCC 5161
TAGCACAGTTGTCAGACAAGATTC 5162
      CC  CTACC  C    CACA-  AGC
GGAGTCT TCT   GC ACTGT   CCGT  C
||||||| |||   || |||||   ||||
CCTTAGA AGA   TG TGACA   GGTA  /
     AC  C---- T   CGATA   CAC
GAM337  GGATAACAGCAATGTTCAGGGAACAAAGGAGATAACTTTAAACTCTGACGTGCCGTGAGCC 5176
TAACAGCAATGTTCAGGGAACAAA 5177
 ATA A  A  T   AAC   GAG
GG  AC GCA TGT CAGGG  AAAG  A
||  || ||| ||| |||||  ||||
CC  TG CGT GCA GTCTC  TTTC  /
 GAG  C  -  -   AAA   AAT
GAM338  GGATACAAGTGGGGCCATGCCTCCCTGGCCCTGACTCCAGGCTGGGGTATCCTGAACTGTATCC 5197
TACAAGTGGGGCCATGCCTCCCTG 5198
    A G- CC    --    CCC
GGATACA GT GGG ATGCCTC CCTGG  T
||||||| || ||| ||||||| |||||
CCTATGT CA TCC TATGGGG GGACC  G
   - AG -- TC   TCA
GAM339  GGATATCATCACTCAGATTAAAGCAGCTTCTGGACTTTGTTTTGAAATGTAAAAGTGATGAAAATCC
5213 TATCATCACTCAGATTAAAGCAGC 5214
   A-      ---- GA     CTTC
GGAT TCATCACT   CA TTAAAGCAG  T
|||| ||||||||   || |||||||||
CCTA AGTAGTGA   GT AGTTTTGTT  G
    AA    AAAT AA      TCAG
GAM340  GGATATGGGGTGCAAGTCGAGTTCGGGACCACGCTTGGGGAAGTGCGCCAGAAACTATCC 5220
TATGGGGTGCAAGTCGAGTTCGGG 5221
    TGG---   AG GAG    AC
GGATA    GGTGCA TC  TTCGGG  C
|||||    |||||| ||  ||||||
CCTAT    CCGCGT AG  GGGTTC  A
    CAAAGA    GA ---    GC
GAM341  GGATGAAAACATGGACCTCTTGGAAGGTATAACTGGCTTTGAAGACTCTGTCCGAAAGTTTATCT 5228
TGAAAACATGGACCTCTTGGAAGG 5229
    AACA   C--- G   G T
GGATGAA  TGGAC  TCTT GAAG TA A
|||||||  |||||  |||| |||| ||
TCTATTT  GCCTG  AGAA TTTC GT A
    GAAA    TCTC  G   G C

GAM342
GGATGGGGCAGAGCTGAGAAGCCAAGGGGGGAAGAGTTGGGGCTGACCTCTTCTTCACCTCGGGCCTTAATCA
CTGACCAAGTCC 5248 TGAGAAGCCAAGGGGGGAAGAGTT 5249
   GG - AGC-  AA AA  G    TT GG
GGAT GG CAG   TGAG GCC GGGG GAAGAG GG C
|||| || |||   |||| ||| |||| |||||| ||
CCTG CC GTC   ATTC CGG CTCC CTTCTT CC T
   AA A ACTA  -- G- A    CT AG
GAM343
GGATGTAGTCGTTCAACTAACGGTGACTTTTACAAATGAGACGGAAAATCATGTAAACTGTATCCTTTAGTTTTATC
GCTGTATCT 5284 TGTAAACTGTATCCTTTAGTTTTA 5285
      C TC   C TG T-   AA GACG
GGATGTAGT GT AACTAA GG AC TTTACA TGA   G
||||||||| || |||||| || || |||||| |||
TCTATGTCG TA TTGATT CC TG AAATGT ACT   /
      C TT   T TA TC    -- AAAA
GAM344
GGCAAAGACGGCCATAGGGTGCTCTGAGTTTTGGGATGGTCACATGACACAATCCAGCACTTGAACCTGGGGCC
TCGTGCC 5296 TAGGGTGCTCTGAGTTTTGGGATG 5297
   AA C  ATA  GC T  T  A - A
GGCA GA GGCC  GGGT TC GAGT TTGGG TG GTC C
|||| || ||||  |||| || |||| ||||| || |||
CCGT CT CCGG  TCCA AG TTCA GACCT AC CAG A
   G- - GG-  -- - C   A A T
GAM345
GGCAACTTCAGGATGACAAAAACCAAAGTCTCTTCTGCTGGGAAATCCCAGTACAGATCGTTTCTCATCTCTAAGT
GCC 5306 TGACAAAAACCAAAGTCTCTTCTG 5307
   A CA   CAA  CAAA  CTTC    A
GGCA CTT GGATGA AAAC  GTCT  TGCTGGG A
|||| ||| |||||| |||   |||   |||||||
CCGT GAA TCTACT TTTG  TAGA  ATGACCC A
   - TC   C-- C--- C---    T
GAM346  GGCACTAGGGACTCTTTGCAGGGTTCCTTCCTCGGATCATCCAAGGCTGTCCCTACTGTGCC 5337
TCCAAGGCTGTCCCTACTGTGCC 5338
    --   T-  CAG T TT
GGCAC TAGGGAC CTTTG  GGT CC C
||||| ||||||| |||||  ||| ||
CCGTG ATCCCTG GGAAC  CTA GG C
   TC   TC   CTA - CT
GAM347
GGCAGAGCTGGGCTGACACAGACGGACTGGGATTGGCTAAGGAAGATCACCTGGCCCCTCCAGCCCTAGCCCT
GGCTCTTTTGTC 5348 TGACACAGACGGACTGGGATTGGC 5349
   ---  -  ACACAGAC A  ATT   A AAG
GGCA  GAGCT GGGCTG    GG CTGGG  GGCTA GG  A
||||  ||||| |||||||    || |||||  ||||| ||
CTGT  CTCGG CCCGAT    CC GACCT  CCGGT CC  /
   TTT  T  --------  C  CC-  - ACT
GAM348  GGCATCAGAGTAGGTATATGACTTTTTTTTTTTTTTTTTTTAGGAGAGATGGGTCCCCGCTCTGGTGCC
5360 TCAGAGTAGGTATATGACTTTTTTT 5361
     TA TATAT  TT     TT

```
GGCATCAGAG GG   GACT TTTTTTTT T
||||||||| ||    |||| ||||||||
CCGTGGTCTC CC   CTGG AGAGAGGA T
     GC ----- GT     TT
GAM349
GGCATCGGGAAGAGCCTAAGTCCACATTATAAAATAGGAAGTGGATGCGGGTACAGTTACTCCCGGGACC 5370
TGCGGGTACAGTTACTCCCGGGAC 5371
 CA   AGA----- AA   ATTATAA
GG TCGGGA     GCCT GTCCAC   A
|| ||||||      |||| ||||||
CC GGCCCT      TGGG TAGGTG   /
 AG   CATTGACA CG    AAGGATA
GAM350
GGCCATTGTTCCGCGCCGATGGCGAGATCCTTGTTCCTCAGATAGCGTTCATCGCCCGTCGTGGTCAACGGGCC
 5379 TAGCGTTCATCGCCCGTCGTGGTC 5380
   A- TT  C AT  - TCC   CC
GGCC TTG CCGCG CG GGCGA GA  TTGTT T
|||| ||| ||||| || ||||| ||  |||||
CCGG AAC GGTGC GC CCGCT CT  GATAG /
  GC T-  T --   A TGC   AC
GAM351
GGCCCAGCGGCCTCTTTCCTACGTACCTCGGACTGACGGGGCGGTCTGACAAGTGCCGTGGGTTGGGCTTCGC
CGGGCT 5384 TGACAAGTGCCGTGGGTTGGGCTT 5385
   A -- CTTT   - C--   AC
GGCCC GCG GCCT  CCTACG TAC  TCGGACTG G
||||| ||| ||||   |||||| |||  ||||||||
TCGGG CGC CGGG  GGGTGC GTG  AGTCTGGC G
   C TT TT--   C AAC    GG
GAM352
GGCCGGTGATCCCTCCAAAGAACCAGAAGCGGGTGGGTTCACTATGAGATCTGAGGAGGCTTCGTGGGCT 5401
TGAGATCTGAGGAGGCTTCGTGGG 5402
   G TC  AA AC- GA C T
GGCC GTGA CCTCC AGA  CA AG GGG G
|||| |||| ||||| |||  || || |||
TCGG TGCT GGAGG TCT  GT TC CTT G
   G TC  AG AGA A- A  G
GAM353 GGCCTGGGAGGGCATGGGTCAAGGGCGTCCGGGAAGCTGGAGCTCTTCCTGCTGACCTTCCGGCC
5418 TGGGAGGGCATGGGTCAAGGGCGT 5419
   T  G - TC  G  G
GGCC GGGAGG CA TGGG  AAGGGC TCCGG A
|||| |||||| || ||||  |||||| |||||
CCGG CCTTCC GT GTCC  TTCTCG AGGTC A
   -  A C --   - G
GAM354 GGCGAGCGACAGCCCCTGCTGGGTCCCCCTGAGTCCATGCGGGAACATGTGGTCGCTGCC 5459
TGCGGGAACATGTGGTCGCTGCC 5460
  G   A C----  - TCCC
GGC AGCGAC GC   CCTGC TGGG  C
||| |||||| ||    ||||| ||||
CCG TCGCTG TG   GGGCG ACCT  C
 -   G TACAA  T  GAGT
```

GAM355  GGCGGGGCCGGGGGGCCCGGGGAGCGGCCTGGCTACGCTGCCCGGGCTCCCGCCCTCAGCC 5469
TGCCCGGGCTCCCGCCCTCAGCC 5470
  -  C       G  GCCT
GGC GGGG CGGGGGCCCGGG AGCG   G
||| |||| |||||||||||| ||||
CCG CTCC GCCCTCGGGCCC TCGC   /
  A   C        G  ATCG
GAM356
GGCTCAATGAAATGAAAGTGAAAAGAACCTGACTTTACTTCATCTTTCTTTTGATTAACTTGTGATCTTGAGCC
5507 TGAAATGAAAGTGAAAAGAACCTG 5508
    T A- TG A-- G    CC- CTT
GGCTCAA GA  A  A  AGT AAAAGAA  TGA   T
||||||| || | |  ||| ||||||| |||
CCGAGTT CT  T  T  TTA TTTTCTT  ACT  /
     - AG GT CAA  G     TCT  TCA
GAM357
GGCTCTGCTCCTCACATTGCCAGTTAATCTTCGTGTGACTACAGTACCTGGAAAAACGGGGACAGCAGCC 5514
TACAGTACCTGGAAAAACGGGGAC 5515
   -  C   ACATTG   T ATCT-- G
GGCT CTG TCCTC     CCAG TA    TC T
|||| ||| |||||     |||| ||    ||
CCGA GAC AGGGG     GGTC AT    AG G
   C   -   CAAAAA   C GACATC  T
GAM358  GGCTGACAGGGACCGCCGGCCGCCCCGGCTCCGCTTTGCCGGCAGTGAGTCCGCTGTCTTCC 5522
TGACAGGGACCGCCGGCCGCCCCG 5523
 CT    -  - ---    CGCCC  G
GG  DACAG GGAC C  GCCGGC    CG C
|| ||||| |||| |  |||||||     ||
CC  CTGTC CCTG G  CGGCCG    GC T
  TT   G   A TGA     TTTC- C
GAM359  GGGAACTTAGGAAGTGAGAAGTCAGATTACCCTAGTCCTCTAGGGTGCTTAAAGCTAACTAGTCCC
5541 TAGGAAGTGAGAAGTCAGATTACC 5542
   AC   GA  GAG   CAGATT     T
GGGA  TTAG AGT  AAGT     ACCCTAG C
|||| |||| ||| ||||     |||||||
CCCT GATC TCG  TTCG     TGGGATC C
   --  AA  AAA   ------      T
GAM360
GGGAATGATAGCATTGAAGGACTCGGGGATATCTAACAGCAATACCTGATCACTACTTCGCACTAGTTTCTC 5556
CACTACTTCGCACTAGTTTCTC 5557
   TGA  CAT   GAC---    GATATCTA
GGGAA TAG TGAAG     TCGGG      A
||||| ||| |||||      |||||
CTCTT ATC GCTTC     AGTCC      /
   TG- AC-   ATCACT    ATAACGAC
GAM360
GGGAATGATAGCATTGAAGGACTCGGGGATATCTAACAGCAATACCTGATCACTACTTCGCACTAGTTTCTC 5556
TCACTACTTCGCACTAGTTTCTC 5557
   TGA  CAT   GAC---    GATATCTA
GGGAA TAG TGAAG     TCGGG      A

```
|||||  |||  |||||      |||||
CTCTT  ATC  GCTTC    AGTCC      /
   TG-  AC-   ATCACT    ATAACGAC
GAM361
GGGAGAATCCCCTAAGCTCCAGGGCCCAGGGTCTAACCTGAGAGGTCGGGGCTGCAGGAAGCTGGGGGAGGC
TCCC 5566 TCCCCTAAGCTCCAGGGCCCAGGG 5567
    AA    A - AG-   AG GT AAC
GGGAG  TCCCCTA GCT CC  GGCCC  G  CT  C
|||||  |||||||| ||| ||  ||||| | ||
CCCTC  AGGGGGT CGA GG  TCGGG  C  GA  T
   GG     -  A ACG    G- TG GAG
GAM362  GGGAGGGTCACTTGAGCCCAGGAATTGTGAGATCAACTGGGCATATAGGGAGATCCTGTC 5577
TCAACTGGGCATATAGGGAGATCC 5578
 G   A-  A--    GA-  G
GG AGGGTC CTTG  GCCCAG  ATT T
|| |||||| |||| |||||| |||
CT TCCTAG GGAT CGGGTC  TAG G
  G   AG  ATA    AAC  A
GAM363  GGGAGTGAAATTTTCCTCTCTTCCCCTGCACATTAGGAAGGGTATCAGAGGGGTTGGTGTACATTCCC
5609 ATCAGAGGGGTTGGTGTACATTCC 5610
    AA- TT    TC--  GCACA
GGGAGTG  ATT  CCTCTCT   CCCT    T
|||||||  |||  |||||||   ||||
CCCTTAC  TGG  GGGGAGA   GGGA   /
    ATG  TT    CTAT   AGGAT
GAM364
GGGAGTGGACGCCGCTGGCAGGATGGTGCTGGAGAGCGTGGCCCGTATCGTGAAGGTGCAGCTCCCTGCATAT
CTGAAGCGGCTCCCAGTCCC 5617 TGGCAGGATGGTGCTGGAGAGCGT 5618
   G  AC    GGCA   G  T A  GTG  -  GTAT
GGGA TGG  GCCGCT   GGATG TGC GG GAGC  GC CC   C
|||| |||  ||||||   ||||| ||| || ||||  || ||
CCCT ACC  CGGCGA   TCTAT ACG CC CTCG  CG GG   G
  G  CT    AG--   -  T -  A-- T AAGT
GAM365
GGGATGTCCTGCTCCAATACCCGCACTGCTCTGGAGTATTGCCCTCTTTCCCAAGGAGATGCTGCTGGTGGAGC
TGGTATGGGTGCGGTCTTCCC 5631 TACCCGCACTGCTCTGGAGTATTG 5632
   TGTC  T A  C A TG CT -   GC CTT
GGGA   CTGC CC ATACC GC C  CT GG AGTATT  CCT  T
||||   |||| || ||||| || | || || ||||||  |||
CCCT   GGCG GG TATGG CG G  GG TC TCGTAG  GGA  C
   TCT-  T G  T A GT -- G   A- ACC
GAM366  GGGATTACAGGCGTTGAGTCACCGTGCCCGGCCAGTACCCACTTCTCTTAATGCTCTATGAGTTCC
5639 TTACAGGCGTTGAGTCACCGTGCC 5640
     AC- -     TCACC  CCC CC
GGGATT  AG GCGTTGAG   GTG  GG  A
||||||  || |||||||||    |||  ||
CCTTGA  TC CGTAATTC    CAC  CC  G
   GTA  T      TCTT-  --- AT
GAM367
GGGCAGGTGCCTGGTCAATCAGTCCTCGGGATGGCAGCCATCAACCCGTGGGCCTCCTGGGGTGACCTTACGG
ACCAATCTTGGGGGATGAAAGCTGTTGACCCATGGGCCTCCTGGGCTCTGTGTCC 5660
```

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TGGCAGCCATCAACCCGTGGGCCT 5661
   - T  TG TCAATCA   TC  A      ---  AA  ----  G TCCT  G
GGGCA GG GCC  G    GTCC  GGG TGGCAGC  CATC  CCCG   TGG CC   GGG T
|||||  || |||  |      ||||  ||| ||||||||  |||| ||||   ||| ||   |||
CCTGT TC CGG  C    CGGG  CCC GTTGTCG  GTAG GGGT   ACC GG   TCC G
    G T  GT CTC----  TA  A     AAA  G-  TCTA  A CAT-  A
GAM368  GGGCCAAAGAGCAGCACCAGAACGCTGTGGGGAAGAGCAGCTGGGTGCTCGCCAGGGCCC 5676
GCTGGGTGCTCGCCAGGGCCC 5677
   AAAGA -   AGAAC   GGG
GGGCC  GC AGCACC   GCTGT  G
|||||   || ||||||   |||||
CCCGG   CG TCGTGG   CGACG  A
    GAC-- C   GT---   AGA
GAM369  GGGCCCTGAGATGGGGTCTGACCTCAGTTCCTGCGGGGAACTTCACCAGTGACCCCAGTCAGTGCCC
5703 TGAGATGGGGTCTGACCTCAGTTC 5704
    C  GA    TGACCTC-   TG
GGGC CTGA TGGGGTC    AGTTCC  C
|||| |||| ||||||      ||||||
CCCG GACT ACCCCAG     TCAAGG  /
    T  G-   TGACCACT    GG
GAM370
GGGCGAGCTCGGTGGTGACGCGCGGCCCTCACGTGACCCAGAGCTGCAGAGCGACGCAGCCTTCGGTGCAGT
CGTCACTCGCGTCTGGCTACCAGCTCCCC 5719 CGGTGCAGTCGTCACTCGCGTCTG 5720
   C  C   --    C--  C-  - G CCC A   AGA
GGG GAGCT GGTGGT  GACGCG   GGC CT CAC TGA  AG GCTGC  G
||| ||||| ||||||  ||||||   ||| || ||| |||   || |||||
CCC CTCGA CCATCG  CTGCGC   CTG GA GTG GCT  TC CGACG   C
    -  -   GT    TCA  CT C -  --- -   CAG
GAM371
GGGCGCTAACACACACAACGGCGCTCTGGGGGGGCGCCACAACACCCCCTTGTAGACCGCAATTGGTCGTTTA
GCGCACC 5729 TAACACACACAACGGCGCTCTGGG 5730
   -  C - A CG C  --   CGCC
GG GCGCTAA AC AC CAA  GCG TCTG  GGGGGG   A
|| |||||||| || || |||  ||| ||||  ||||||
CC CGCGATT TG TG GTT  CGC AGAT  TCCCCC   C
   A   - C - AA C  GT   ACAA
GAM372  GGGCGTATGCCTTTCCTGGAGGCGGGGACGATCCGGGTAGGAGACAAAGGGCGAGCTCCC 5747
TCCGGGTAGGAGACAAAGGGCGAG 5748
   C A   ---------   GG  G
GGG GT TGCCTTT     CCTGGA  CG G
||| || |||||||      |||||| ||
CCC CG GCGGGAA     GGGCCT GC G
    T A   ACAGAGGAT    A-  A
GAM373  GGGCTGGCGTCTGGGTGGGGTGGGCGCGGTTGGGCGGCGTCCGCCCATAGTTCCGCGCGTGCCC
5765 TGGCGTCTGGGTGGGGTGGGCGCG 5766
   TG  C  TG---     G TT
GGGC  GCGT TGGG    GGGTGGGCGC G  G
|||| |||| ||||    |||||||||| |
CCCG  TGCG GCCT    CCCGCCTGCG C  /
   --  C  TGATA     G GG
```

GAM374

GGGGAACCGCGGTGGCTTCCGCGGAGGTTTCGGCAGTGGCATCCGGGGCCGGGGTCGCGGCCGTGGACGGG
GCCGGGGCCGAGGCCGCGGAGCTCGCGGAGGCAAGGCCGAGGATAAGGAGTGGATGCCC 5800
TGGCATCCGGGGCCGGGGTCGCGG 5801

```
  GAA   GGTGGCT G AG--   G AGT A  G  GG  G  GTG
GGG  CCGC   TCC CGG  GTTTC GC  GGC TCCG GGCC  GGTC CGGCC  G
III IIII    III III   IIIII II  III IIII IIII  IIII IIIII
CCC GGTG    AGG GCC  CGGAG CG  TCG AGGC CCGG  CCGG GCCGG  A
  GTA  AGGAAT- A GGAA   G C-- -  G  AG  G  GGC
```

GAM375

GGGGAACCGCGGTGGCTTCCGCGGAGGTTTCGGCAGTGGCATTCGGGGCCGGGGTCGCGGCCGTGGACGGG
GCCGGGGCCGAGGCCGCGGAGCTCGCGGAGGCAAGGCCGAGGATAAGGAGTGGATGCCC 5813
TGGCATTCGGGGCCGGGGTCGCGG 5814

```
  GAA   GGTGGCT G AG--   G AGT A  G  GG  G  GTG
GGG  CCGC   TCC CGG  GTTTC GC  GGC TTCG GGCC  GGTC CGGCC  G
III IIII    III III   IIIII II  III IIII IIII  IIII IIIII
CCC GGTG    AGG GCC  CGGAG CG  TCG AGGC CCGG  CCGG GCCGG  A
  GTA  AGGAAT- A GGAA   G C-- -  G  AG  G  GGC
```

GAM376  GGGGAGAATAGAAAGAAAACAATTGACAAAATCCTCAAATGTAAACTCAATTTGCCTCCCT 5837
TGTAAACTCAATTTGCCTCCCT 5838

```
   AA   AA AA-- A  CAA
GGGGAG TAGA GA  ACA TTGA  A
IIIIII IIII II   III IIII
TCCCTC GTTT CT   TGT AACT  A
   C-  AA CAAA  A   CCT
```

GAM377

GGGGATGGAAGGCGATGGCCCCTGCGAGGACGATGGCCCGGCCCGCCTCGCCCCGGCGGCATCCCTGCCGTC
GCC 5849 AAGGCGATGGCCCCTGCGAGGACG 5850

```
 G   A  C  G - T--   A AT C
GG GATGG AGG GATG CC CC  GCGAGG CG GGC C
II IIIII III IIII II II  IIIIII II III
CC CTGCC TCC CTAC GG GG  CGCTCC GC CCG /
 G   G  -  - C CCC   - -- G
```

GAM378

GGGGGACTGAATGGCGCATTCCGGGCGGGAGGGCAAAACAACCCCACTGGTTTTCCCCGCCCCCCCTGGAATC
TGCCCCCCGTGTCCCCC 5853 TGGCGCATTCCGGGCGGGAGGGCA 5854

```
   - AAT  C    C A- C  AACC
GGGGGAC TG  GGCG ATTCCGGG GGG GGG AAAAC   C
IIIIIIII II   IIII IIIIIIIII III III IIIII
CCCCCTG GC  CCGT TAAGGTCC CCC CCC TTTTG  C
    T CCC  C    C CG C   GTCA
```

GAM379

GGGGGAGTTGTGGTGCTTCTGGGTCTCTGGGCCCCGCCTGCTGGCCTGGGATGCCCTCATGTTGGGAAGCATT
CCGTGCCCCC 5875 GGGATGCCCTCATGTTGGGAAGCA 2525

```
   AGT TG    G TCTCT  -- -- T
GGGGG  TG GTGCTTCT GG    GGGC CCC GCC G
IIIII II IIIIIIII II    IIII III III
CCCCC  GC TACGAAGG TT    CCCG GGG CGG C
   GT- CT    G GTACT  TA TC T
```

GAM379

GGGGGAGTTGTGGTGCTTCTGGGTCTCTGGGCCCCGCCTGCTGGCCTGGGATGCCCTCATGTTGGGAAGCATT

CCGTGCCCCC 5876 GGGATGCCCTCATGTTGGGAAGCA 2525
    AGT TG    G TCTCT  -- -- T
GGGGG  TG GTGCTTCT GG   GGGC CCC GCC G
||||| || |||||||| ||   |||| ||| |||
CCCCC  GC TACGAAGG TT   CCCG GGG CGG C
    GT- CT    G GTACT  TA TC  T
GAM379
GGGGGAGTTGTGGTGCTTCTGGGTCTCTGGGCCCCGCCTGCTGGCCTGGGATGCCCTCATGTTGGGAAGCATT
CCGTGCCCCC 5877 GGGATGCCCTCATGTTGGGAAGCA 2525
    AGT TG    G TCTCT  -- -- T
GGGGG  TG GTGCTTCT GG   GGGC CCC GCC G
||||| || |||||||| ||   |||| ||| |||
CCCCC  GC TACGAAGG TT   CCCG GGG CGG C
    GT- CT    G GTACT  TA TC  T
GAM379
GGGGGAGTTGTGGTGCTTCTGGGTCTCTGGGCCCCGCCTGCTGGCCTGGGATGCCCTCATGTTGGGAAGCATT
CCGTGCCCCC 5878 GGGATGCCCTCATGTTGGGAAGCA 2525
    AGT TG    G TCTCT  -- -- T
GGGGG  TG GTGCTTCT GG   GGGC CCC GCC G
||||| || |||||||| ||   |||| ||| |||
CCCCC  GC TACGAAGG TT   CCCG GGG CGG C
    GT- CT    G GTACT  TA TC  T
GAM380
GGGGGGAGGAACCCACCAACAGGGGGGGGTCTCCACAACTCCTCAGTGTCCGCCCCACTTGTGTCGGGAAGCCC
CCCCC 5879 TCCGCCCCACTTGTGTCGGGAAGC 5880
    A AA- AC A  G   CTC AACT
GGGGGG GG  CCC CA CAGG GGGGT  CAC   C
|||||| ||  ||| || |||| |||||  |||
CCCCCC CC  GGG GT GTTC CCCCG  GTG   /
    - GAA CT - A   CCT ACTC
GAM381 GGGGGGCACCAATGACAAGGGAATTGGGATGGGGATGACAGTCCCTATTTCCTTTGCTGTGTTCCCC
5892 TGACAAGGGAATTGGGATGGGGAT 5893
     CAATGA    ATTGG    G
GGGGGGCAC    CAAGGGA   GATGGGGAT A
|||||||||    |||||||   |||||||||
CCCCTTGTG    GTTTCCT   TTATCCCTG C
     TC----    -----    A
GAM382 GGGGGTCGTCCTTGGCACGCGCTGGGGAGTGCTAGTCCTGAGGCGAGCCGGTAGATCTCC 5913
AGGCGAGCCGGTAGATCTCC 5914
    GT TT  A  G  G   GTG
GGGGGTC CC GGC CGC CT GGGA   C
||||||| || ||| ||| || ||||
CCTCTAG GG CCG GCG GA TCCT  /
    AT -- A  - G   GAT
GAM383
GGGGTAGTGGATGGCAACTGATGGAACAGGAGAATGCTCAGCAGCATTTGCTCTTCCAGCCTGTCACGCCTC
5924 TGGCAACTGATGGAACAGGAGAAT 5925
    A  AT AACTGA   C GA    C
GGGGT GTGG GGC    TGGAA AG  GAATGCT A
||||| |||| |||    ||||| ||  ||||||

```
CTCCG CACT CCG    ACCTT TC TTTACGA G
  -  GT  ------  C G-    C
GAM384 GGGTAATCAGGGAAGTGGTATTTCAGCAGGGACCTAAAGGATGAGAAGACACAAACCTGCAAAGACCC
5945 TGAGAAGACACAAACCTGCAAAGA 5946
  AAT--  GAA  GTA    GC----  G
GGGT   CAGG  GTG  TTTCA    AG G
||||   ||||  |||  |||||    ||
CCCA   GTCC  CAC  AGAGT    TC A
  GAAAC  AAA  AGA    AGGAAA  C
GAM385
GGGTCCACTATCATTTAATTTCCCTTGAACCTGCTCTGCTAGTTTAATCTGCTAATATGAAAGTTAATTAAGACCT
5969 TATCATTTAATTTCCCTTGAACCT 5970
   C------  A  TTAATTTCCC    CT T
GGGTC    ACT TCAT      TTGAAC GC C
|||||    ||| ||||      |||||| ||
TCCAG    TGA AGTA      AATTTG CG /
  AATTAAT  A  TAATCGTCT-    AT T
GAM386
GGGTGAAGATGGCGGCAGCCGAGGCCGCGAACTGCATCATGGAGGTGTCCTGTGGCCAGGCGGAAAGCAGTG
AGAAGCCC 5975 TGGCGGCAGCCGAGGCCGCGAACT 5976
   GAAGATG- GGCA- GA    AACT   AT
GGGT   GC  GCC GGCCGCG  GCATC G
||||   ||  ||| |||||||  |||||
CCCG   CG  CGG CCGGTGT  TGTGG /
  AAGAGTGA AAAGG A-    CC--   AG
GAM387 GGGTGAGAGGCTGGTGGTTGCCTCCCGTCCTGGGCAGGCTGCAGCCTCATGCCATGTCTCTCTCCC
5985 TGAGAGGCTGGTGGTTGCCTCCCG 5986
   T    -  ----   CT C CC
GGG GAGAGGC TGGT   GGTTGC CC GT T
||| |||||||| ||||   |||||| || ||
CCC CTCTCTG ACCG   CCGACG GG CG /
   T    T  TACT    TC A GG
GAM388 GGGTGCGGGACTTAAACACAACCTGGACCTCGTGGGGCGGGTGCCCACTAAAGTGCTGGACCC 6007
TGCGGGACTTAAACACAACCTGGA 6008
  G  G  AAACACA-  GA T
GGGT CGG ACTT     ACCTG CC C
|||| ||| ||||      ||||| ||
CCCA GTC TGAA     TGGGC GG G
  G  G  ATCACCCG   GG T
GAM389
GGGTGGCAGCACCAGGGGACACACCTGCCAAACCCACCAGATGGAGGGGCCCTCCCTGGTCTCTGGCCACCC
6019 TGGCAGCACCAGGGGACACACCTG 6020
   - C-   ACACA  G  AACCC
GGGTGGC AG ACCAGGGG   CCT CCA   A
|||||||| || ||||||||   ||| |||
CCCACCG TC TGGTCCCT   GGA GGT   /
   G  TC    CCCGG  -  AGACC
GAM390
GGGTTATCTGCAACTGAGAGGGGCTGGTTAAGGCGTCCCCAAGTTGGAAGGGCGCTTTGCTTCTGTTTTCTGGA
TGCAGAGTCCT 6033 TGAGAGGGGCTGGTTAAGGCGTCC 6034
```

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  TTA    A -  G CT  T      -- AA
GGG  TCTGCA CT GAGAG GG  GGT AAGGCGTCC CC G
III  IIIIII II IIIII II III IIIIIIIII II
TCC  AGACGT GG CTTTT TC  TCG TTTCGCGGG GG /
  TG-    A T  G T- -      AA TT
GAM391
GGGTTCCAATGGGTGCACAGTTCCAAAAATGTGGAGGGACCCTTCTCAGTTTTGAGGCCATGAATCCAAAGCCC
6044 TGGGTGCACAGTTCCAAAAATGTG 6045
   CCAA   G CA TC   A T   G
GGGTT   TGGGT CA GT CAAAA TG GGAGG A
IIIII   IIIII II II IIIII II IIIII
CCCGA   ACCTA GT CG GTTTT AC CTTCC /
   A---   A AC GA   G T   C
GAM392
GGTAGGGAGTGAAAGGCCCGGCCACCTAAAGGCACAGCTGGTGCCTGGGTCAAGCTGAGGCGGCATCTCTCTG
CC 6066 TGAAAGGCCCGGCCACCTAAAGGC 6067
     - AAAG  - C-- AA   AG
GGTAGGGAG TG  GCC CGGC  ACCT AGGCAC C
IIIIIIIII II  III IIII  IIII IIIIII
CCGTCTCTC AC  CGG GTCG  TGGG TCCGTG /
    T GG-- A  AAC  --   GT
GAM393 GGTGAAGGTGCTGAGGAAAGCTCCCAGGATGAGCCTGGGAGTGCTTCAGGTATCAGCTTCCAGCC
6072 TGGGAGTGCTTCAGGTATCAGCTT 6073
  --  G ----   AAA     AT
GGT GAAG TG  CTGAGG  GCTCCCAGG G
III IIII II  IIIIII  IIIIIIIII
CCG CTTC AC  GACTTC  TGAGGGTCC /
  AC  G TATG   G--    GA
GAM394 GGTGACAACATGCTGGAGCCAAGTGCTAACATGGCCTTGGTTCAAGGGATGGAAAGTCACC 6089
TGACAACATGCTGGAGCCAAGTGC 6090
   AA-- G G-   T AA
GGTGAC  CAT CT GAGCCAAG GCT C
IIIIII  III II IIIIIIII III
CCACTG  GTA GG CTTGGTTC CGG /
   AAAG G AA    - TA
GAM395
GGTGCCTGGTCAATCAGTCCTCGGGATGGCAGCCATCAACCCGTGGGCCTCCTGGGGTGACCTTACGGACC
6103 TCAGTCCTCGGGATGGCAGCCATC 6104
  G T---  ATCAGT    T AG  CA
GGT CC  GGTCA    CCTCGGGA GGC CCAT A
III II  IIIII    IIIIIIIII III IIII
CCA GG  CCAGT    GGGGTCCT CCG GGTG C
  - CATT  ------    - -- CC
GAM396 GGTGGGGAAGACTGAAGAAGTGTTAACTGAAAACAGGTGACACAGAGTCACCAGTTTTCCGAGAACC
6117 TGACACAGAGTCACCAGTTTTCCG 6118
   GG--   AA A---   A A
GGT  GGAAGACTG GA  GTGTTA CTG A
III  IIIIIIIII II  IIIIII III
CCA  CCTTTGAC CT  CACAGT GAC A
  AGAG     CA GAGA    G A
```

GAM397

GGTGTGCCCGGAACCGGCCCTTGGTGGGGAAATAATGCCTTTGCTAAGGGGGCCCCGGATTCCGGGTCGCC

6135 TAAGGGGGCCCCGGATTCCGGGTC 6136

    T    -   ----     TG  AAAT

GGTG GCCCGGAA CCGG   CCCTTGG GGG   A

|||| |||||||| ||||    ||||||| |||

CCGC TGGGCCTT GGCC   GGGAATC TTC   /

  -     A  CCGG     GT  CGTA

GAM398

GGTTTTCAAGGTGTCATGAAAAGATGGGGATTTAAAGGCCAGCCTGCTACGCATGGTCAAACGAAAACCCACAG

GAGACCTGGAGCT 6161 TGAAAAGATGGGGATTTAAAGGCC 6162

    CA   G A AAAAGA   GA  AAA-   - CTG

GGTTTT AGGT TC TG    TGGG TTT   GGCCA GC  C

|||||| |||| || ||    |||| |||   |||||| ||

TCGAGG TCCA AG AC   ACCC AAG  CTGGT CG  /

   --   G G ------  AA  CAAA   A CAT

GAM399  GGTTTTTCTATGAGATGAGAATTATGAACACTTCATATAGGTAAATTCCATAGGTTGAGCT 6189

TATAGGTAAATTCCATAGGTTGAG 6190

    T-   AG  GAGAAT-    C

GGTTT TCTATG AT     TATGAA A

||||| |||||| ||     ||||||

TCGAG GGATAC TA     ATACTT /

   TT    CT AATGGAT    C

GAM400  GTACAGATTTTTATAAAATCATCTATACAGATGAAGTACAAATTTTTATAAAATAATCTATAC 6197

TGAAGTACAAATTTTTATAAAATA 6198

   C   --    ---------    A

GTA AGATT TTTATAAAA     TCATCT T

||| ||||| |||||||||     ||||||

CAT TCTAA AAATATTTT     AGTAGA A

  A   TA       TAAACATGA    C

GAM401

GTACCAGGCCAGTTATAACCAGAGCTTTTCTAGTCAGCCTCACCAAGTAGAACAAACAGAGCTTCAGCAAGAACA

GCTTCAAACAGTGGTTGGCACTTAC 6201 TAACCAGAGCTTTTCTAGTCAGCC 6202

   CC  -   TT AACCA-   T  A C--  C ACCAAGTA

GTA AG GCCAG AT    GAGCT TTCT GT  AGC TC     G

||| || ||||| ||    ||||| |||| ||  ||| ||

CAT TC CGGTT TG    TTCGA AAGA CG  TCG AG     /

  -- A   GG ACAAAC   C  A ACT  - ACAAACAA

GAM402

GTACGGCGTGTCCTCCCTGCAGCGCGGCGTGGCCGACTACATGCGCGCGCACCTGGCGGGAGGCGCGGGCCC

GGC 6210 TGCGCGCGCACCTGGCGGGAGGCG 6211

 AC  G  -   T A----   -  GCC

GT GGC TGT CCTCCC GC   GCGCG GCGTG  G

|| ||| ||| |||||| ||    ||||| |||||

CG CCG GCG GGAGGG CG   CGCGC CGTAC  A

 GC  G  C   - GTCCA   G   ATC

GAM403  GTAGAGCTTTATGCTGAAAAGGTGGCCACTAGAGGTCTGTGTGCCATTGCCCAGGCAGAGTCTCTGC

6262 GTGTGCCATTGCCCAGGCAGAGTC 6263

   - TA  GAAAA   - T A

GTAGAG CTT TGCT   GGTGGC CAC AG G

```
||||||| ||| ||||    |||||| ||| ||
CGTCTC GAG  ACGG    TTACCG GTG TC G
   T  --   ACCCG    T  - T
GAM404
GTAGAGGAAGATGAGCTTGGCGTACAACTCCTCCTCCAGCTCCAGCTCCCGAGTCTCCCGCACCAGGAAGATGT
CCTGGCAGAGCTTGAGGATGCGGTCCACGCACGGCAGCTCCTCGAAC 6289
TGTCCTGGCAGAGCTTGAGGATGC 6290
 A-   A ATGA  TG  ACA  CC-   C   CA  CCCGA  C GC
GT GAGGA G  GCT GCGT  ACT  TCCTC AGCTC GCT   GTCT CC  A
|| ||||| |  ||| ||||  |||  ||||| ||||| |||   |||| ||
CA CTCCT C  CGG CGCA  TGG  AGGAG TCGAG CGG   TAGA GG  C
 AG   - GA--  CA  CC-  CGT   T   A- TCCTG  A AC
GAM405
GTATACTGTTATCTCCCAGGGCACCCAGTGCAAGGCTCTTTATCTCATCCCGCTTGGGTGTACCTGGTTACCCTC
AGTGAC 6304 TCCCAGGGCACCCAGTGCAAGGCT 6305
 A   TTATCTC   -      T AA CTCTTT
GT TACTG     CCAGG GCACCCAG GC GG    A
|| |||||     ||||| ||||||||| || ||
CA GTGAC     GGTCC TGTGGGTT CG CC    /
 -   TCCCATT   A     - C- TACTCT
GAM406
GTATCGACGGAGCATGTACAGGGAGGCATGCACCGCAGTGGTGAATACACGTCGAGCTGCAAGCATTCACTGCA
TGCTCTGGTAC 6311 TGTACAGGGAGGCATGCACCGCAG 6312
   GAC      CAG  G A  C-- CA  GTG
GTATC  GGAGCATGTA  GGA GC TGCA  CG GTG  A
|||||  ||||||||||  ||| || ||||  || |||
CATGG  TCTCGTACGT  CTT CG ACGT  GC CAC  /
   ---       CA-  A A  CGA TG  ATA
GAM407  GTATGAAAGGGGGAAACAAAGAACAGCCTTTTAGGTAAGGCTTTTCAGTACCTGCCTCGTGC 6329
TGAAAGGGGGAAACAAAGAACAGC 6330
   AA  G  AA  AAA   C    TT
GTATGA GG GG  AC  GAA AGCCTT  A
|||||| || || ||  ||| |||||||
CGTGCT CC TC TG  CTT TCGGAA  G
   --  G  CA  A--  T    TG
GAM408
GTCAAGAGAATCAAATTTGCTCTTTACAGGTGCTGGGTCAAAGTCTTCCCGGTTGGAGTCAAGATCAGAATAGCT
CCTCTTGC 6357 TCAAATTTGCTCTTTACAGGTGCT 6358
 T   AATCAAA   C  T AGGT   TCAA
G CAAGAG     TTTG TCTT AC  GCTGGG   A
| |||||||    |||| |||| ||   ||||||
C GTTCTC     AGAC AGAA TG  TGGCCC   G
 -   CTCGATA  T   C AGGT    TTCT
GAM409
GTCATGTGATGCTCAATCAGCAAACCAGGGATTGGCTTCATCCTGGGAAAAAGCTATCTGGGTGCAACAAGAC
6372 TGTGATGCTCAATCAGCAAACCAG 6373
 A GA    ATC  AAA---    ATTG
GTC TGT TGCTCA AGC    CCAGGG  G
||| ||| |||||| |||    ||||||
CAG ACA GTGGGT TCG    GGTCCT   C
```

```
   A  AC    CTA  AAAAG    ACTT
GAM410
GTCCCTCCCTCCCCTGCTGTGACCTTGTGGGGGGTTGAGAAACCTAGGCACTCATGGCCCCCTGGAGGGGCAGG
GCAGGCAGGGCTGGGGC 6380 TGGCCCCCTGGAGGGGCAGGGCAG 6381
    T-  CC    G A-  GT    --  AAACC
GTCCC CCCT CCTGCT TG CCTT GGGGGT TGAG   T
|||||  ||||  |||||| ||  ||||  ||||||  ||||
CGGGG GGGA GGACGG AC GGAG CCCCCG ACTC   /
    TC  C-   G GG  GT    GT  ACGGA
GAM411  GTCCTTTCTTTCGCCAGGCTGGGGACCCGCTTCGCGTTATCATCCTGGTCGCAGGGAAGGC 6419
TATCATCCTGGTCGCAGGGAAGGC 6420
 T    T -   C GG  C C
G CCTTTCTT CG CCAGG TG  GAC CG T
| |||||||| || ||||| || ||| ||
C GGAAGGGA GC GGTCC AC  TTG GC /
  -      C T   T TA  C T
GAM412
GTCTCACACATGACATGTGAAAATCTGACTCAAAGTTCTTTATCTTGAAGCTGTGTTTATATGTTCCGTGTGCAC
6436 TGACATGTGAAAATCTGACTCAAA 6437
 CT   AT       AATCTGAC  AG TC
GT CACAC GACATGTGAA     TCAA T T
|| |||||  ||||||||||      |||| |
CA GTGTG TTGTATATTT     AGTT A /
 C-  CC       GTGTCGA-  CT TT
GAM413  GTGACATTAAAACAAGGGGATATTACCCAAAAGGGGTGGGTGAAGTGATGGTTCGAATGTCAC 6452
TGACATTAAAACAAGGGGATATTA 6453
    AA  AAGGGG  A    AAA
GTGACATT AAC    AT TTACCCA  G
||||||||  |||     || ||||||||
CACTGTAA TTG    TG AGTGGGT  /
   GC  GTAG-- A     GGG
GAM414
GTGAGGATGGCAGTGCAGGATGCAGTAGATGCCCTGATGCAGAAGTGCTTTCAACTCCTCGTCCTTCAACTCCAA
CACCTTCCTCAC 6474 TGGCAGTGCAGGATGCAGTAGATG 6475
    ------  C  GC-    C--  A T-  C GAT
GTGAGGA    TGG AGT  AGGATG  AGT GA GC CT  G
|||||||     ||| |||  ||||||  ||| || || ||
CACTCCT    ACC TCA  TCCTGC  TCA CT CG GA  C
    TCCACA  -  ACT    TCC  A TT  T AGA
GAM415
GTGATGAGCACGACGGGACGGGCAGATCCATTCATGCAACCGGTATGAGATCTCCTTACCCTCTGTTGCATCAT
6489 GAGATCTCCTTACCCTCTGTTGCA 6490
   -  C C  AC  C   CAT    AA
GTGATG AGCA GA GGG  GGG AGATC  TCATGC  C
||||||  |||| || |||  ||| |||||  ||||||
TACTAC TTGT CT CCC  TCC TCTAG  AGTATG  /
   G  - -  AT  -  ---    GC
GAM416
GTGATGTCCGGAGATTCGGAGCGGCGATATCTGGATCTAAGTCTCCGCTCCGATGTGAAGTCTATCTCTGTGACA
CCAT 6500 TGTCCGGAGATTCGGAGCGGCGAT 6501
```

```
  A  -    ----------        C  ATCTG
GTG TGTC CGGAGAT        TCGGAGCGG GAT    G
||| |||| |||||||        |||||||||| |||
TAC ACAG GTCTCTA        AGCCTCGCC CTG    A
  C  T    TCTGAAGTGT        T  AATCT
GAM417
GTGCCAGCGATGATGAGATAGCCAGGCTGAAGAAGCCAGACCAAGGCATCAAGGGGCGATCAGCCTGGTCTCT
ATGAAGACTGGCGC 6514 TGAGATAGCCAGGCTGAAGAAGCC 6515
     CGATGAT- ATA       AGAA  AGA  AAGG
GTGCCAG      GAG GCCAGGCTGA  GCC  CC   C
|||||||      ||| ||||||||||  |||  ||
CGCGGTC      CTC TGGTCCGACT  CGG  GG   A
     AGAAGTAT ---       AG-- --- AACT
GAM418
GTGCTCCTTTTTGATATAGATAAAATATTTAATGCTTCTATTTACATCTGCTCATGTAGGTTTTACAATATTCCATGT
ATATCCAATGTGGATGGTAC 6529 TAAAATATTTAATGCTTCTATTTA 6530
   --  TT- T    G AA    -  T  TCTATT    CT
GTGC TCC  TT GATATA AT  AATATT TAA GCT    TACAT  G
|||| |||  || |||||| ||  |||||| ||| |||    |||||
CATG AGG  AA CTATAT TA  TTATAA ATT TGG    ATGTA  C
   GT  TGT C    G CC    C  T  ------    CT
GAM419
GTGGAGCAGATAACCATTGTTTCTCGGCCGCTATCTGGTCAGAGGGGAGCTGGGCCGGGAAATTCTGCCTAC
6547 TAACCATTGTTTCTCGGCCGCTAT 6548
     A   TAACCATT        -- A- GG
GTGG GCAGA       GTTTCTCGGCC GCT TCT T
|||| |||||       |||||||||||| ||| |||
CATC CGTCT       TAAAGGGCCGG CGA GGA C
    -  --------        GT GG GA
GAM420
GTGGCACAGCTGGAGAGTGGGGAGCTGGGACTTGAGCCCAGGTAGTGTGTCCCCAGCACCTTCAACTAAACTC
CATTCTGTGCTGC 6550 CCCCAGCACCTTCAACTAAACTCC 6551
  TG   C-  ---  --  A    -  TTGA-  C
G GCACAG TGGAG  AGT  GGGG GCTGGG AC    GC  C
| |||||| |||||  |||  |||| |||||| ||    ||
C CGTGTC ACCTC  TCA  TTCC CGACCC TG    TG A
  GT    TT  AAA  AC   A    C TGTGA  G
GAM421
GTGGCAGAAGATCCCAGCTGACCACGGCCCCTTTCTCTGGGGTCAGAGGGAGAAGACAGGCGCAGTCAGCAGG
GGCAGCTGTTGC 6561 TCCCAGCTGACCACGGCCCCTTTC 6562
  TG   AAGA  A    CA G C----- TT   G
G GCAG   TCCC GCTGAC CG CC    CT CTCTG G
| ||||   |||| |||||| || ||    || |||||
C TGTC   GGGG CGACTG GC GG    GA GAGAC G
  GT   GAC-  A    AC - ACAGAA GG    T
GAM422 GTGGCCCACGTGGGCAGGACGGCCGCAGGATGGGGTGGCTGTGCTGGTCCGACACCTGGGCTAC
6593 GTGCTGGTCCGACACCTGGGCTAC 6594
      C  -- -- G      AGG
GTGGCCCA GTG GG CAG ACGGCCGC  A
|||||||| ||| || ||| ||||||||
```

CATCGGGT CAC CC GTC TGTCGGTG  T
     C  AG TG  G     GGG
GAM423
GTGGGGGCGCTCAATAACTTGGATACCGGTCGGCATGGTCACAACACCCGACAGTGCTCTTCGCCAGAAGTTGG
CGGCCCTAC 6611 TAACTTGGATACCGGTCGGCATGG 6612
     G  T  AAC  ATAC  TC   G  ACAA
GTGGGG CGC CAAT  TTGG   CGG GGCAT GTC   C
||||| ||| |||| |||| ||| ||||| |||
CATCCC GCG GTTG  GACC   GCT TCGTG CAG   /
     G  -  AA-  ----  TC   A  CCCA
GAM424
GTGTGAGTGGCTTTGCAGGCCTGGTGGTGGGAGAGCCTCAGGCTCCCTCCTTCTTCGTTCCTGACCATGCCCTT
GGGC 6623 TTGCAGGCCTGGTGGTGGGAGAGC 6624
  G  T  TTTG-  CCT-- T  TG  A    T
GT TGAG GGC   CAGG   GG GG  GG GAGCC C
|| |||| |||   ||||    || || || |||||
CG GTTC CCG   GTCC    TC TC  CC CTCGG /
  G  -  TACCA  TTGCT T  CT  -    A
GAM425
GTGTGCGCTGCCTCTGGCATCCTAGAGACCCGGATTTACTCAGCTAGGAGAGAGGATGGATCACAGGGTCTAAG
GGTGGCCATTC 6673 TGGCATCCTAGAGACCCGGATTTA 6674
  T  C  TG  TC  C    AGA  C  GA  A  AG
G GTG GC CC  TGG ATCCT  GA CCG  TTT CTC  C
| ||| || || ||| |||||  || ||| ||| |||
C TAC CG GG  ATC TGGGA  CT GGT  GAG GAG  T
  T  -  GT  GA  -    CA-  A  AG  A  GA
GAM426
GTTGTGGGGCTGGTTGCTGTCTTTACGTTTCACAACCATGGAAGGACTGCCAACCTCTACTCCCTTCACAGC
6679 GAAGGACTGCCAACCTCTACTCCC 6680
     --  CT----   -T    A  TTCA
GTTGTG GGG    GGTTG C GTCTTT CGT   C
|||||| |||    ||||| | |||||| |||
CGACAC CCC    CCAAC G CAGGAA GTA   /
     TT  TCATCT    C T    G  CCAA
GAM427
GTTGTTCTCAGATATCAGTTCTTCCCAGGTGAACAGCAGTGAATCTGTGACTTCACCAAATGGATTAAAGTCAATG
AGCCAC 6693 TATCAGTTCTTCCCAGGTGAACAG 6694
  T  TCA  ATC   TTCCCA    CA-  TG
GT GTTC  GAT  AGTTC    GGTGAA  GCAG  A
|| |||| ||| |||||    |||||| ||||
CA CGAG  CTG  TTAGG    CCACTT  TGTC  /
  C  TAA  AAA    TAAA--    CAG  TA
GAM428
GTTTCATTCCAATGAGAGTTGCACACTGTCAGCTTGGTTTTGTGGCTGCTGATAGTCGTACTTTCTTGAAATGGAA
T 6716 TGAGAGTTGCACACTGTCAGCTTG 6717
     C  T  T AC     TT  T
GTTTCATT CAA GAGAGT GC ACTGTCAGC GGTT T
|||||||| ||| ||||| || ||||||||| ||||
TAAGGTAA GTT CTTTCA TG TGATAGTCG TCGG G
     A  -  - C-     --  T

GAM429 TAAGATTTTAGCAATACTTCCAATATTGATTTCCTTACCAAATGGAATCTAGAAGCTAAATTTTTA 6729
TGGAATCTAGAAGCTAAATTTTTA 6730
     T   AA- C-   ATA  ATTT
TAAGA TTTAGC  TA TTCCA  TTG   C
||||| ||||||  || |||||  |||
ATTTT AAATCG  AT AAGGT  AAC   C
     T   AAG CT   A--  CATT
GAM430
TAGAGATGGGGTTTCAACTTGTTGGCCAGGCTGGTCTTGAACTCCTGGCCCCAGGTGATCCACCCACTTTA 6752
TGGGGTTTCAACTTGTTGGCCAGG 6753
     A   GTT- A  TT    CT  CT
TAGAG TGGG   TCA CTTG  GGCCAGG  GGT  T
||||| ||||   ||| ||||  ||||||| |||
ATTTC ACCC   AGT GGAC  CCGGTCC  TCA  /
     -   ACCT -  C-       --  AG
GAM431
TAGCCGTGATGTCCGGGGGCCGTGTACATCATGTTACCGTGGGGGTGGGGTCTGCATTGGCTGCTGGGCATATG
GCTG 6759 TGTCCGGGGGCCGTGTACATCATG 6760
        A   G   -  C ATG   G
TAGCCGTG TGTCCGG GGCCG TGTA ATC   TTACC T
|||||||| ||||||| ||||| |||| |||   |||||
GTCGGTAT ACGGGTC TCGGT ACGT TGG   GGTGG G
        -   G   T  C --- G
GAM432
TAGGGAAAGCTGGTACGCCTGCAGGTACCGGTCCGGAATTCCCGGGTCGACCCACGCGTCCGGTCCGTGTGCT
GTGCCAGGGCCTGAAGGACTCCCCCTG 6766 CTGCAGGTACCGGTCCGGAATTCC 6767
    AA - GG C -- - - T  ATTCCC  T
TAGGG AG CT TA GCCT GCA GGTAC CGG CCGGA    GGG C
||||| || || || |||| ||| ||||| ||| |||||    |||
GTCCC TC GG GT CGGG CGT TCGTG GCC GGCCT    CCC G
    CC A AA C  AC G  T T  GCGCA- A
GAM433
TAGGGCGCCTGGCAGTGGTCAAGCCTGAAACCAAGCAATACCCGTCTGTTTTCACCCAAGCCCCAGAGCCCTA
6788 TGGCAGTGGTCAAGCCTGAAACCA 6789
    GC  CAGT  CAAGCC   C AG AAT
TAGGGC CTGG  GGT    TGAAA CA C  A
|||||| ||||  |||     ||||| || |
ATCCCG GACC  CCG     ACTTT GT G  /
     A-  ----  AACCC-   T CT CCC
GAM434
TAGGGGTCTGTACCGGGCTGGCCTGTGCCTATCACCTCTTATGCAAACCTTCCCACCCCTGTATTCCCACCCCTG
 6806 TGCAAACCTTCCCACCCCTGTATT 6807
     CT--  C  C  CCTG--- C  TCA
TAGGGGT  GTAC GGG TGG      TGC TA   C
|||||||  |||| ||| |||      ||| ||
GTCCCCA  TATG CCC ACC      ACG AT   C
     CCCT   T  C  CTTCCAA  T  TCT
GAM435 TAGTATATGAATATGCGGGATATAAGTCTTATGAATAGACACCACGTATAACTCTTACTG 6817
TATGAATATGCGGGATATAAGTCT 6818
     TATGAA    - ATATAA  TAT

```
TAGTA    TATGCG GG    GTCT  G
|||||    |||||| ||    ||||
GTCAT    ATATGC CC    CAGA  /
   TCTCA-   A  A-----  TAA
GAM436  TATAAGAATATGCTGCCAATTTCTGTCATTGTCTTTGACCTATCTGTTTGTGTATCCTAATA 6826
TAAGAATATGCTGCCAATTTCTGT 6827
  A  A    T- CA  TTCT   TTG
TAT AG ATATGC  GC  AT   GTCA  T
||| || |||||| || ||    ||||
ATA TC TATGTG  TG  TA   CAGT  /
   A  C    TT TC TC--   TTC
GAM437  TATAAGATGTATAAGAAGTCTTAACGGTTGCAGGGTAACCGATGAAATTTTACATCTAGTA 6856
TAAGATGTATAAGAAGTCTTAACG 6857
   A    TAAG   C  A     A
TAT AGATGTA   AAGT TTA CGGTTGC G
||| |||||||   |||| ||| |||||||
ATG TCTACAT   TTTA AGT GCCAATG /
   A    ----   A  A     G
GAM438
TATACAGGTAGAGATGTATGCAGATGTGTCCATATATGTTCCATATTTACATTTTGATAGCATGGATGTATGCATCT
CTTGGTGTA 6869 ATAGCATGGATGTATGCATCTCTT 6870
    AGGT        GA   C-- TAT  TCCA
TATAC  AGAGATGTATGCA TGTGT  CA  ATGT   T
|||||  ||||||||||||| |||||  ||  ||||
ATGTG  TCTCTACGTATGT GTACG  GT  TACA   /
   GT--       AG   ATA TT-   TTTA
GAM439  TATAGAATTATCTAAATGTTTCTTGAGGGAGAAAAAGCCAGCCGATCAAGACATTCGGATAATTTTTTA
6887 TAGAATTATCTAAATGTTTCTTGA 6888
  T    TA  TT    G- AGAAA
TA AGAATTATC AATG TCTTGA GG   A
|| |||||||| |||| |||||| ||
AT TTTTAATAG TTAC AGAACT CC   A
  T    GC   --    AG GACCG
GAM440
TATGAAAGGTGTGAACTTGCAATGTCCTCCTGTCTTAAACCCAAGTTGACAGTGCCCTCTCAAAACTTTTCATA
6903 TGAAAGGTGTGAACTTGCAATGTC 6904
     G- ACTT  A  CTC  GTCTT
TATGAAAGGT TGA   GCA TGTC  CT    A
|||||||||| |||   ||| ||||  ||
ATACTTTTCA ACT   CGT ACAG  GA    A
     AA  CTCC  G   TT- ACCCA
GAM441  TATGAGAATGATCCAGAATTAGGATCCGAAGAGAGAGGAACTACTCCTGGATGGACATCATA 6916
TGAGAATGATCCAGAATTAGGATC 6917
   GAATG   AAT  GA  GAAG
TATGA   ATCCAG  TAG TCC   A
|||||   ||||||  ||| |||
ATACT   TAGGTC  ATC AGG   /
   ACAGG   CTC  A- AGAG
GAM442  TATGGCCGTGGGCCTCAACAAGGGCCACAAAGTGACCAAGAACGTGAGCAAGCCCAGGCACATG
6920 TGGCCGTGGGCCTCAACAAGGGCC 6921
```

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     -  G    ---   ACAAG-- C  A
  TATG GCC TGGGC  CTCA     GG CAC A
  |||| ||| |||||  ||||      || |||
  GTAC CGG ACCCG  GAGT     CC GTG /
    A  -   AAC   GCAAGAA A  A
  GAM443
  TATGGGGTTCAATAAGGTTGCACCTAAAAGTGCTCTTCCTTAGGAAGGATTATCGGGGGCATCTACTCATGAAAA
  CCATG 6933 TAAGGTTGCACCTAAAAGTGCTCT 6934
      GG   ATAA- T  A  AAAAGTG T    T
  TATGG TTCA   GG TGC CCT     C CTTCC T
  ||||| ||||   || ||| |||      | |||||
  GTACC AAGT   TC ACG GGG     G GAAGG /
    AA   ACTCA T  -  GCTATTA -   A
  GAM444
  TATTCCCGCTGGCAGCAGGCACCGCTGGCCCCCTTCGTTCCCGGCACGCTGGCTGATGGCGTGGTGTA 6946
  TTCCCGCTGGCAGCAGGCACCGCT 6947
    T  -  GG   A  ACC    CCCCC
  TAT CC CGCT CAGC GGC  GCTGG    T
  ||| || |||| |||| |||  |||||
  ATG GG GCGG GTCG TCG  CGGCC    T
    T  T   TA  G  CA-    CTTGC
  GAM445
  TCAATGGAAGCGGTACTTTCTGGCTGGCTTGAGGTTGATGTATGTGGCCTTCATCTCCTCGGCCTCAGGGTTCCG
  CACATCTTTGA 6957 TCTCCTCGGCCTCAGGGTTCCGCA 6958
     T  A--  T  TT   CT  T  TT   TATGT
  TCAA GGA  GCGG ACT CTGG  GGCT GAGG GATG    G
  |||| |||  |||| ||| ||||  |||| |||| ||||
  AGTT TCT  CGCC TGG DACT CCGG CTCC CTAC   /
    -  ACA  T  --  --  -  T-  TTCCG
  GAM446  TCACAGAGATATCAAACCTTCCAATATTCTTCTGGACAGAAGTGGAAATATTAAGCTCTGTGA 6982
  TATCAAACCTTCCAATATTCTTCT 6983
        ATATCAAACC   ATATT    G
  TCACAGAG       TTCCA    CTTCT G
  ||||||||       |||||    |||||
  AGTGTCTC       AAGGT    GAAGA A
      GAATTATA--   -----    C
  GAM447
  TCACCATCTGCAGCCTTGAAGGAGCTTGGTTCGGAGACAGGCAAAGGAGCCATGTGTGGAGAGCCTGGTTTCTC
  AGTACTTCCAGACCGTGA 7008 GTGTGGAGAGCCTGGTTTCTCAGT 7009
    CA   C- CC  A   T  GGAG- - AA
  TCAC TCTG AG TTGA GGAGCT GGTTC   ACA GGC A
  |||| |||| || |||| |||||| |||||   ||| |||
  AGTG AGAC TC GACT CTTTGG CCGAG   TGT CCG G
    CC   CT AT  -   T  AGGTG  A AG
  GAM448
  TCACCATCTGCAGCCTTGAAGGAGCTTTGGTTCGGAGACAGGCAAAGGAGCCATGTGTGGAGAGCCTGGTTTCT
  CAGTACTTCCAGACCGTGA 7028 GTGTGGAGAGCCTGGTTTCTCAGT 7009
    CA   C- CC  A   TT  GGAG- - AA
  TCAC TCTG AG TTGA GGAGCT GGTTC   ACA GGC A
  |||| |||| || |||| |||||| |||||   ||| |||
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AGTG AGAC TC GACT CTTTGG CCGAG   TGT CCG G
   CC  CT AT  -   T-   AGGTG  A  AG
GAM448
TCACCATCTGCAGCCTTGAAGGAGCTTTGGTTCGGAGACAGGCAAAGGAGCCATGTGTGGAGAGCCTGGTTTCT
CAGTACTTCCAGACCGTGA 7029 GTGTGGAGAGCCTGGTTTCTCAGT 7009
   CA  C- CC  A    TT   GGAG-  - AA
TCAC TCTG AG TTGA GGAGCT GGTTC   ACA GGC A
|||| |||| || |||| ||||||| |||||    ||| |||
AGTG AGAC TC GACT CTTTGG CCGAG   TGT CCG G
   CC  CT AT  -   T-   AGGTG  A  AG
GAM448
TCACCATCTGCAGCCTTGAAGGAGCTTTGGTTCGGAGACAGGCAAAGGAGCCATGTGTGGAGAGCCTGGTTTCT
CAGTACTTCCAGACCGTGA 7030 GTGTGGAGAGCCTGGTTTCTCAGT 7009
   CA  C- CC  A    TT   GGAG-  - AA
TCAC TCTG AG TTGA GGAGCT GGTTC   ACA GGC A
|||| |||| || |||| ||||||| |||||    ||| |||
AGTG AGAC TC GACT CTTTGG CCGAG   TGT CCG G
   CC  CT AT  -   T-   AGGTG  A  AG
GAM448
TCACCATCTGCAGCCTTGAAGGAGCTTTGGTTCGGAGACAGGCAAAGGAGCCATGTGTGGAGAGCCTGGTTTCT
CAGTACTTCCAGACCGTGA 7031 GTGTGGAGAGCCTGGTTTCTCAGT 7009
   CA  C- CC  A    TT   GGAG-  - AA
TCAC TCTG AG TTGA GGAGCT GGTTC   ACA GGC A
|||| |||| || |||| ||||||| |||||    ||| |||
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   CC  CT AT  -   T-   AGGTG  A  AG
GAM448
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CAGTACTTCCAGACCGTGA 7032 GTGTGGAGAGCCTGGTTTCTCAGT 7009
   CA  C- CC  A    TT   GGAG-  - AA
TCAC TCTG AG TTGA GGAGCT GGTTC   ACA GGC A
|||| |||| || |||| ||||||| |||||    ||| |||
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   CC  CT AT  -   T-   AGGTG  A  AG
GAM448
TCACCATCTGCAGCCTTGAAGGAGCTTTGGTTCGGAGACAGGCAAAGGAGCCATGTGTGGAGAGCCTGGTTTCT
CAGTACTTCCAGACCGTGA 7033 GTGTGGAGAGCCTGGTTTCTCAGT 7009
   CA  C- CC  A    TT   GGAG-  - AA
TCAC TCTG AG TTGA GGAGCT GGTTC   ACA GGC A
|||| |||| || |||| ||||||| |||||    ||| |||
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   CC  CT AT  -   T-   AGGTG  A  AG
GAM448
TCACCATCTGCAGCCTTGAAGGAGCTTTGGTTCGGAGACAGGCAAAGGAGCCATGTGTGGAGAGCCTGGTTTCT
CAGTACTTCCAGACCGTGA 7034 GTGTGGAGAGCCTGGTTTCTCAGT 7009
   CA  C- CC  A    TT   GGAG-  - AA
TCAC TCTG AG TTGA GGAGCT GGTTC   ACA GGC A
|||| |||| || |||| ||||||| |||||    ||| |||
AGTG AGAC TC GACT CTTTGG CCGAG   TGT CCG G
   CC  CT AT  -   T-   AGGTG  A  AG
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GAM448
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CAGTACTTCCAGACCGTGA 7035 GTGTGGAGAGCCTGGTTTCTCAGT 7009
   CA  C- CC  A    TT   GGAG-  - AA
TCAC TCTG AG TTGA GGAGCT GGTTC    ACA GGC A
|||| |||| || |||| |||||| |||||    ||| |||
AGTG AGAC TC GACT CTTTGG CCGAG    TGT CCG G
   CC  CT AT  -    T-   AGGTG  A  AG
GAM448
TCACCATCTGCAGCCTTGAAGGAGCTTTGGTTCGGAGACAGGCAAAGGAGCCATGTGTGGAGAGCCTGGTTTCT
CAGTACTTCCAGACCGTGA 7036 GTGTGGAGAGCCTGGTTTCTCAGT 7009
   CA  C- CC  A    TT   GGAG-  - AA
TCAC TCTG AG TTGA GGAGCT GGTTC    ACA GGC A
|||| |||| || |||| |||||| |||||    ||| |||
AGTG AGAC TC GACT CTTTGG CCGAG    TGT CCG G
   CC  CT AT  -    T-   AGGTG  A  AG
GAM448
TCACCATCTGCAGCCTTGAAGGAGCTTTGGTTCGGAGACAGGCAAAGGAGCCATGTGTGGAGAGCCTGGTTTCT
CAGTACTTCCAGACCGTGA 7037 GTGTGGAGAGCCTGGTTTCTCAGT 7009
   CA  C- CC  A    TT   GGAG-  - AA
TCAC TCTG AG TTGA GGAGCT GGTTC    ACA GGC A
|||| |||| || |||| |||||| |||||    ||| |||
AGTG AGAC TC GACT CTTTGG CCGAG    TGT CCG G
   CC  CT AT  -    T-   AGGTG  A  AG
GAM448
TCACCATCTGCAGCCTTGAAGGAGCTTTGGTTCGGAGACAGGCAAAGGAGCCATGTGTGGAGAGCCTGGTTTCT
CAGTACTTCCAGACCGTGA 7038 GTGTGGAGAGCCTGGTTTCTCAGT 7009
   CA  C- CC  A    TT   GGAG-  - AA
TCAC TCTG AG TTGA GGAGCT GGTTC    ACA GGC A
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   CC  CT AT  -    T-   AGGTG  A  AG
GAM448
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CAGTACTTCCAGACCGTGA 7039 GTGTGGAGAGCCTGGTTTCTCAGT 7009
  CA   C- CC  A    TT   GGAG-  - AA
TCAC TCTG AG TTGA GGAGCT GGTTC    ACA GGC A
|||| |||| || |||| |||||| |||||    ||| |||
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   CC  CT AT  -    T-   AGGTG  A  AG
GAM448
TCACCATCTGCAGCCTTGAAGGAGCTTTGGTTCGGAGACAGGCAAAGGAGCCATGTGTGGAGAGCCTGGTTTCT
CAGTACTTCCAGACCGTGA 7040 GTGTGGAGAGCCTGGTTTCTCAGT 7009
  CA   C- CC  A    TT   GGAG-  - AA
TCAC TCTG AG TTGA GGAGCT GGTTC    ACA GGC A
|||| |||| || |||| |||||| |||||    ||| |||
AGTG AGAC TC GACT CTTTGG CCGAG    TGT CCG G
   CC  CT AT  -    T-   AGGTG  A  AG
GAM448
TCACCATCTGCAGCCTTGAAGGAGCTTTGGTTCGGAGACAGGCAAAGGAGCCATGTGTGGAGAGCCTGGTTTCT
CAGTACTTCCAGACCGTGA 7041 GTGTGGAGAGCCTGGTTTCTCAGT 7009

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    CA   C- CC  A    TT   GGAG-  - AA
TCAC TCTG AG TTGA GGAGCT GGTTC   ACA GGC A
|||| |||| || |||| |||||| |||||    ||| |||
AGTG AGAC TC GACT CTTTGG CCGAG   TGT CCG G
   CC  CT AT  -   T-   AGGTG  A  AG
GAM448
TCACCATCTGCAGCCTTGAAGGAGCTTTGGTTCGGAGACAGGCAAAGGAGCCATGTGTGGAGAGCCTGGTTTCT
CAGTACTTCCAGACCGTGA 7042 GTGTGGAGAGCCTGGTTTCTCAGT 7009
    CA   C- CC  A    TT   GGAG-  - AA
TCAC TCTG AG TTGA GGAGCT GGTTC   ACA GGC A
|||| |||| || |||| |||||| |||||    ||| |||
AGTG AGAC TC GACT CTTTGG CCGAG   TGT CCG G
   CC  CT AT  -   T-   AGGTG  A  AG
GAM448
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CAGTACTTCCAGACCGTGA 7043 GTGTGGAGAGCCTGGTTTCTCAGT 7009
    CA   C- CC  A    TT   GGAG-  - AA
TCAC TCTG AG TTGA GGAGCT GGTTC   ACA GGC A
|||| |||| || |||| |||||| |||||    ||| |||
AGTG AGAC TC GACT CTTTGG CCGAG   TGT CCG G
   CC  CT AT  -   T-   AGGTG  A  AG
GAM448
TCACCATCTGCAGCCTTGAAGGAGCTTTGGTTCGGAGACAGGCAAAGGAGCCATGTGTGGAGAGCCTGGTTTCT
CAGTACTTCCAGACCGTGA 7044 GTGTGGAGAGCCTGGTTTCTCAGT 7009
    CA   C- CC  A    TT   GGAG-  - AA
TCAC TCTG AG TTGA GGAGCT GGTTC   ACA GGC A
|||| |||| || |||| |||||| |||||    ||| |||
AGTG AGAC TC GACT CTTTGG CCGAG   TGT CCG G
   CC  CT AT  -   T-   AGGTG  A  AG
GAM448
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CAGTACTTCCAGACCGTGA 7045 GTGTGGAGAGCCTGGTTTCTCAGT 7009
    CA   C- CC  A    TT   GGAG-  - AA
TCAC TCTG AG TTGA GGAGCT GGTTC   ACA GGC A
|||| |||| || |||| |||||| |||||    ||| |||
AGTG AGAC TC GACT CTTTGG CCGAG   TGT CCG G
   CC  CT AT  -   T-   AGGTG  A  AG
GAM448
TCACCATCTGCAGCCTTGAAGGAGCTTTGGTTCGGAGACAGGCAAAGGAGCCATGTGTGGAGAGCCTGGTTTCT
CAGTACTTCCAGACCGTGA 7046 GTGTGGAGAGCCTGGTTTCTCAGT 7009
    CA   C- CC  A    TT   GGAG-  - AA
TCAC TCTG AG TTGA GGAGCT GGTTC   ACA GGC A
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AGTG AGAC TC GACT CTTTGG CCGAG   TGT CCG G
   CC  CT AT  -   T-   AGGTG  A  AG
GAM448
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CAGTACTTCCAGACCGTGA 7047 GTGTGGAGAGCCTGGTTTCTCAGT 7009
    CA   C- CC  A    TT   GGAG-  - AA
TCAC TCTG AG TTGA GGAGCT GGTTC   ACA GGC A
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AGTG AGAC TC GACT CTTTGG CCGAG    TGT CCG G
  CC   CT AT   -    T-   AGGTG  A  AG
GAM448
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CAGTACTTCCAGACCGTGA 7048 GTGTGGAGAGCCTGGTTTCTCAGT 7009
  CA   C- CC  A    TT   GGAG-  -  AA
TCAC TCTG AG TTGA GGAGCT GGTTC   ACA GGC A
||||  ||||  ||  ||||  ||||||  |||||     |||  |||
AGTG AGAC TC GACT CTTTGG CCGAG    TGT CCG G
  CC   CT AT   -    T-   AGGTG  A  AG
GAM448
TCACCATCTGCAGCCTTGAAGGAGCTTTGGTTCGGAGACAGGCAAAGGAGCCATGTGTGGAGAGCCTGGTTTCT
CAGTACTTCCAGACCGTGA 7049 GTGTGGAGAGCCTGGTTTCTCAGT 7009
  CA   C- CC  A    TT   GGAG-  -  AA
TCAC TCTG AG TTGA GGAGCT GGTTC   ACA GGC A
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  CC   CT AT   -    T-   AGGTG  A  AG
GAM448
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CAGTACTTCCAGACCGTGA 7050 GTGTGGAGAGCCTGGTTTCTCAGT 7009
  CA   C- CC  A    TT   GGAG-  -  AA
TCAC TCTG AG TTGA GGAGCT GGTTC   ACA GGC A
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AGTG AGAC TC GACT CTTTGG CCGAG    TGT CCG G
  CC   CT AT   -    T-   AGGTG  A  AG
GAM448
TCACCATCTGCAGCCTTGAAGGAGCTTTGGTTCGGAGACAGGCAAAGGAGCCATGTGTGGAGAGCCTGGTTTCT
CAGTACTTCCAGACCGTGA 7051 GTGTGGAGAGCCTGGTTTCTCAGT 7009
  CA   C- CC  A    TT   GGAG-  -  AA
TCAC TCTG AG TTGA GGAGCT GGTTC   ACA GGC A
||||  ||||  ||  ||||  ||||||  |||||     |||  |||
AGTG AGAC TC GACT CTTTGG CCGAG    TGT CCG G
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GAM448
TCACCATCTGCAGCCTTGAAGGAGCTTTGGTTCGGAGACAGGCAAAGGAGCCATGTGTGGAGAGCCTGGTTTCT
CAGTACTTCCAGACCGTGA 7052 GTGTGGAGAGCCTGGTTTCTCAGT 7009
  CA   C- CC  A    TT   GGAG-  -  AA
TCAC TCTG AG TTGA GGAGCT GGTTC   ACA GGC A
||||  ||||  ||  ||||  ||||||  |||||     |||  |||
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  CC   CT AT   -    T-   AGGTG  A  AG
GAM448
TCACCATCTGCAGCCTTGAAGGAGCTTTGGTTCGGAGACAGGCAAAGGAGCCATGTGTGGAGAGCCTGGTTTCT
CAGTACTTCCAGACCGTGA 7053 GTGTGGAGAGCCTGGTTTCTCAGT 7009
  CA   C- CC  A    TT   GGAG-  -  AA
TCAC TCTG AG TTGA GGAGCT GGTTC   ACA GGC A
||||  ||||  ||  ||||  ||||||  |||||     |||  |||
AGTG AGAC TC GACT CTTTGG CCGAG    TGT CCG G
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GAM448
TCACCATCTGCAGCCTTGAAGGAGCTTTGGTTCGGAGACAGGCAAAGGAGCCATGTGTGGAGAGCCTGGTTTCT
CAGTACTTCCAGACCGTGA 7054 GTGTGGAGAGCCTGGTTTCTCAGT 7009
    CA   C- CC  A    TT   GGAG- -  AA
TCAC TCTG AG TTGA GGAGCT GGTTC    ACA GGC A
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GAM448
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CAGTACTTCCAGACCGTGA 7055 GTGTGGAGAGCCTGGTTTCTCAGT 7009
    CA   C- CC  A    TT   GGAG- -  AA
TCAC TCTG AG TTGA GGAGCT GGTTC    ACA GGC A
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    CC   CT AT   -    T-   AGGTG  A  AG
GAM448
TCACCATCTGCAGCCTTGAAGGAGCTTTGGTTCGGAGACAGGCAAAGGAGCCATGTGTGGAGAGCCTGGTTTCT
CAGTACTTCCAGACCGTGA 7056 GTGTGGAGAGCCTGGTTTCTCAGT 7009
    CA   C- CC  A    TT   GGAG- -  AA
TCAC TCTG AG TTGA GGAGCT GGTTC    ACA GGC A
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    CC   CT AT   -    T-   AGGTG  A  AG
GAM448
TCACCATCTGCAGCCTTGAAGGAGCTTTGGTTCGGAGACAGGCAAAGGAGCCATGTGTGGAGAGCCTGGTTTCT
CAGTACTTCCAGACCGTGA 7057 GTGTGGAGAGCCTGGTTTCTCAGT 7009
    CA   C- CC  A    TT   GGAG- -  AA
TCAC TCTG AG TTGA GGAGCT GGTTC    ACA GGC A
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    CC   CT AT   -    T-   AGGTG  A  AG
GAM448
TCACCATCTGCAGCCTTGAAGGAGCTTTGGTTCGGAGACAGGCAAAGGAGCCATGTGTGGAGAGCCTGGTTTCT
CAGTACTTCCAGACCGTGA 7058 GTGTGGAGAGCCTGGTTTCTCAGT 7009
    CA   C- CC  A    TT   GGAG- -  AA
TCAC TCTG AG TTGA GGAGCT GGTTC    ACA GGC A
|||| |||| || |||| |||||| |||||    ||| |||
AGTG AGAC TC GACT CTTTGG CCGAG    TGT CCG G
    CC   CT AT   -    T-   AGGTG  A  AG
GAM448
TCACCATCTGCAGCCTTGAAGGAGCTTTGGTTCGGAGACAGGCAAAGGAGCCATGTGTGGAGAGCCTGGTTTCT
CAGTACTTCCAGACCGTGA 7059 GTGTGGAGAGCCTGGTTTCTCAGT 7009
    CA   C- CC  A    TT   GGAG- -  AA
TCAC TCTG AG TTGA GGAGCT GGTTC    ACA GGC A
|||| |||| || |||| |||||| |||||    ||| |||
AGTG AGAC TC GACT CTTTGG CCGAG    TGT CCG G
    CC   CT AT   -    T-   AGGTG  A  AG
GAM448
TCACCATCTGCAGCCTTGAAGGAGCTTTGGTTCGGAGACAGGCAAAGGAGCCATGTGTGGAGAGCCTGGTTTCT
```

CAGTACTTCCAGACCGTGA 7060 GTGTGGAGAGCCTGGTTTCTCAGT 7009
  CA  C- CC  A    TT   GGAG- - AA
TCAC TCTG AG TTGA GGAGCT GGTTC   ACA GGC A
|||| |||| || |||| |||||| |||||    ||| |||
AGTG AGAC TC GACT CTTTGG CCGAG    TGT CCG G
  CC  CT AT  -   T-   AGGTG A  AG
GAM449  TCACCCTGTCGCACTTCACCGTGGGGATAACGGGGTCTACCATGGTCTAGAAGTGCACTGGTGA 7061
ACCATGGTCTAGAAGTGCACTGGT 7062
   CT C    ---    -  AA
TCACC GT GCACTTC  ACCGTGG GGAT C
||||| || ||||||| ||||||| ||||
AGTGG CA CGTGAAG TGGTACC TCTG G
   T- -    ATC    A  GG
GAM450
TCAGGAACATGGTTACCCCACGATCAACTTGGGTATTGTAGGAGACAACCCAGATGACTTACTCAATGCCTTGAA
TTGAGGGGTATTCAGTCGTGCTTGA 7075 TGACTTACTCAATGCCTTGAATTG 7076
   AACA-- GT   A - ACTT    TAG A ACC
TCAGG   TG TACCCC CGAT CA  GGGTATTG GAG CA  C
|||||    || |||||| |||| ||  |||||||| ||| ||
AGTTC   AC ATGGGG GTTA GT  TCCGTAAC TTC GT  /
   GTGCTG TT   A  A ----    TCA A AGA
GAM451
TCAGTGCCCCAGCTGCAATGGCCCCATCTTCCCCCCAACCAACTGGCTGGCCCGTGGCCTCCGCACTGA 7091
TGGCCCGTGGCCTCCGCACTGA 7092
    CCCA TG AAT  -- TCTTCCCC
TCAGTGC  GC C  GGCC CCA    C
||||||||  || |  |||| |||
AGTCACG  CG G  CCGG GGT    /
    CCTC GT C--  TC  CAACCAAC
GAM452
TCAGTTATTCAGGAGTTTCTGTATGGGGCACAAATTAGCTCTTCTTAGCAGCAGACTAATCTGAAGAAATGA 7099
CTTAGCAGCAGACTAATCTGAAGA 7100
  GTTA    --  - AT---  ACA
TCA  TTCAGG AGTTT CTGT   GGGGC A
|||  |||||| ||||| ||||    |||||
AGT  AAGTCT TCAGA GACG   TCTCG A
   AAAG   AA  C  ATTCT  ATT
GAM453  TCATACCAGTTTCCATCAGGATTTATCAGATCTGAAACATCCTGCAGATAAGCTGGTTGA 7115
TACCAGTTTCCATCAGGATTTATC 3102
  T    CCAT-   TTA  G
TCA ACCAGTTT   CAGGAT TCA A
||| |||||||||   |||||| |||
AGT TGGTCGAA   GTCCTA AGT T
   -    TAGAC    CAA  C
GAM453  TCATACCAGTTTCCATCAGGATTTATCAGATCTGAAACATCCTGCAGATAAGCTGGTTGA 7116
TACCAGTTTCCATCAGGATTTATC 3102
  T    CCAT-   TTA  G
TCA ACCAGTTT   CAGGAT TCA A
||| |||||||||   |||||| |||
AGT TGGTCGAA   GTCCTA AGT T

```
      -      TAGAC      CAA  C
GAM453  TCATACCAGTTTCCATCAGGATTTATCAGATCTGAAACATCCTGCAGATAAGCTGGTTGA 7117
TACCAGTTTCCATCAGGATTTATC 3102
    T       CCAT-      TTA  G
TCA ACCAGTTT    CAGGAT  TCA A
||| |||||||     |||||| |||
AGT TGGTCGAA    GTCCTA  AGT T
      -      TAGAC      CAA  C
GAM453  TCATACCAGTTTCCATCAGGATTTATCAGATCTGAAACATCCTGCAGATAAGCTGGTTGA 7118
TACCAGTTTCCATCAGGATTTATC 3102
    T       CCAT-      TTA  G
TCA ACCAGTTT    CAGGAT  TCA A
||| |||||||     |||||| |||
AGT TGGTCGAA    GTCCTA  AGT T
      -      TAGAC      CAA  C
GAM453  TCATACCAGTTTCCATCAGGATTTATCAGATCTGAAACATCCTGCAGATAAGCTGGTTGA 7119
TACCAGTTTCCATCAGGATTTATC 3102
    T       CCAT-      TTA  G
TCA ACCAGTTT    CAGGAT  TCA A
||| |||||||     |||||| |||
AGT TGGTCGAA    GTCCTA  AGT T
      -      TAGAC      CAA  C
GAM453  TCATACCAGTTTCCATCAGGATTTATCAGATCTGAAACATCCTGCAGATAAGCTGGTTGA 7120
TACCAGTTTCCATCAGGATTTATC 3102
    T       CCAT-      TTA  G
TCA ACCAGTTT    CAGGAT  TCA A
||| |||||||     |||||| |||
AGT TGGTCGAA    GTCCTA  AGT T
      -      TAGAC      CAA  C
GAM453  TCATACCAGTTTCCATCAGGATTTATCAGATCTGAAACATCCTGCAGATAAGCTGGTTGA 7121
TACCAGTTTCCATCAGGATTTATC 3102
    T       CCAT-      TTA  G
TCA ACCAGTTT    CAGGAT  TCA A
||| |||||||     |||||| |||
AGT TGGTCGAA    GTCCTA  AGT T
      -      TAGAC      CAA  C
GAM453  TCATACCAGTTTCCATCAGGATTTATCAGATCTGAAACATCCTGCAGATAAGCTGGTTGA 7122
TACCAGTTTCCATCAGGATTTATC 3102
    T       CCAT-      TTA  G
TCA ACCAGTTT    CAGGAT  TCA A
||| |||||||     |||||| |||
AGT TGGTCGAA    GTCCTA  AGT T
      -      TAGAC      CAA  C
GAM453  TCATACCAGTTTCCATCAGGATTTATCAGATCTGAAACATCCTGCAGATAAGCTGGTTGA 7123
TACCAGTTTCCATCAGGATTTATC 3102
    T       CCAT-      TTA  G
TCA ACCAGTTT    CAGGAT  TCA A
||| |||||||     |||||| |||
AGT TGGTCGAA    GTCCTA  AGT T
      -      TAGAC      CAA  C
```

GAM453 TCATACCAGTTTCCATCAGGATTTATCAGATCTGAAACATCCTGCAGATAAGCTGGTTGA 7124
TACCAGTTTCCATCAGGATTTATC 3102
  T    CCAT-    TTA  G
TCA ACCAGTTT    CAGGAT  TCA A
||| ||||||||    |||||| |||
AGT TGGTCGAA    GTCCTA  AGT T
   -     TAGAC     CAA   C
GAM453 TCATACCAGTTTCCATCAGGATTTATCAGATCTGAAACATCCTGCAGATAAGCTGGTTGA 7125
TACCAGTTTCCATCAGGATTTATC 3102
  T    CCAT-    TTA  G
TCA ACCAGTTT    CAGGAT  TCA A
||| ||||||||    |||||| |||
AGT TGGTCGAA    GTCCTA  AGT T
   -     TAGAC     CAA   C
GAM453 TCATACCAGTTTCCATCAGGATTTATCAGATCTGAAACATCCTGCAGATAAGCTGGTTGA 7126
TACCAGTTTCCATCAGGATTTATC 3102
  T    CCAT-    TTA  G
TCA ACCAGTTT    CAGGAT  TCA A
||| ||||||||    |||||| |||
AGT TGGTCGAA    GTCCTA  AGT T
   -     TAGAC     CAA   C
GAM454
TCATCGATGGCAAGGGTGTCCTTCGCCAGATCACTGTTAATGATTTGCCTGTGGGACGCTCCGTGGATGA 7127
TGGCAAGGGTGTCCTTCGCCAGAT 7128
    G  CAAG     TCGC-     CTG
TCATC ATGG  GGTGTCCT    CAGATCA  T
||||| ||||  ||||||||    |||||||
AGTAG TGCC  TCGCAGGG   GTTTAGT  /
    G  ----     TGTCC     AAT
GAM455 TCATTTTGTTTTCTTTCTCTTAATTCTGTTAATTTATTTAATCTCATGGGAGAGAAACATGA 7145
TCTCATGGGAGAGAAACATGA 7146
  TTT      TTAATTCT   TT
TCA TGTTTTCTTTCTC     GTTAA T
||| |||||||||||||     |||||
AGT ACAAAAGAGAGGG     TAATT /
   ---       TACTC---   TA
GAM456 TCCAGGGTTAGTTTTTGTAGCCTCGGTGGCCCGTCGGCTCATGGACGCTCGAACTTCCGGCCCTTGGA
7191 TGGACGCTCGAACTTCCGGCCCTT 7192
   -  AGTT-  T  C  G  -  C
TCCA GGGTT    TTTG AGC TC GTG GCC G
|||| |||||    |||| ||| || || ||| |||
AGGT CCCGG    AAGC TCG AG TAC CGG T
    T  CCTTC  -  C  G  T  C
GAM457
TCCCCCTACCCCACTTTTGCCTTCTAACTTTGGTGCCCAGCTCAGGGTGAGGCAGTTAAGGGTCCAGGGA 7205
TCAGGGTGAGGCAGTTAAGGGTCC 7206
  CCT  CACTT    CTA     T C
TCCC ACCC   TTGCCTT  ACTTTGG GC C
|||| ||||   |||||||  |||||||| ||
AGGG TGGG   GACGGAG  TGGGACT CG /

```
      ACC   AATT-    ---    - A
GAM458  TCCCGGGCCAAGGGGGTGGCCTGCACAGGCCCGATGTCTACTTGCTTGCACCAGCCCGGGA 7226
TGTCTACTTGCTTGCACCAGCCCG 7227
      -----  G  --------  G
TCCCGGGC   CAAG GGGT    GGCCT C
|||||||    |||| ||||    |||||
AGGGCCCG   GTTC TTCA    CCGGA A
      ACCAC  G  TCTGTAGC   C
GAM459  TCCCTTTCCTGACCTTTAGTCTTTCACTTCCAATTTGTGGAATGATATTTTAGGAATAACGGA 7262
GAATGATATTTTAGGAATAACGGA 7263
  CT--    CCTTTA  -  TTCC
TCC  TTCCTGA    GTC TTTCAC  A
|||  |||||||    ||| ||||||
AGG  AAGGATT    TAG AAGGTG  /
  CAAT    TTA--- T   TTTA
GAM460
TCCGAGGGCGAGCTCCAGAAAAGTTTTGCAATCTGGAGATAAGGAGCTTGATGGGCAGCTAGACTTGGA 7273
TAAGGAGCTTGATGGGCAGCTAGA 7274
    ---  GA T GAA    GCA  T
TCCGAG  GGC GC CCA  AAGTTTT  ATC G
||||||  ||| || |||  |||||||  |||
AGGTTC  TCG CG GGT  TTCGAGG  TAG G
    AGA  A- -  AG-    AA- A
GAM461
TCCGCGGAGGTTTCGGCAGTGGCATCCGGGGCCGGGGTCGCGGCCGTGGACGGGGCCGGGGCCGAGGCCGC
GGAGCTCGCGGAGGCAAGGCCGAGGA 7290 TGGCATCCGGGGCCGGGGTCGCGG 5801
  G  AG--   G AGT A  G  GG  G  GTG
TCC CGG   GTTTC GC  GGC TCCG GGCC  GGTC CGGCC  G
||| |||   ||||| ||  ||| |||| ||||  |||| |||||
AGG GCC   CGGAG CG  TCG AGGC CCGG  CCGG GCCGG  A
  A GGAA   G C-- -  G  AG  G  GGC
GAM461
TCCGCGGAGGTTTCGGCAGTGGCATCCGGGGCCGGGGTCGCGGCCGTGGACGGGGCCGGGGCCGAGGCCGC
GGAGCTCGCGGAGGCAAGGCCGAGGA 7291 TGGCATCCGGGGCCGGGGTCGCGG 5801
  G  AG--   G AGT A  G  GG  G  GTG
TCC CGG   GTTTC GC  GGC TCCG GGCC  GGTC CGGCC  G
||| |||   ||||| ||  ||| |||| ||||  |||| |||||
AGG GCC   CGGAG CG  TCG AGGC CCGG  CCGG GCCGG  A
  A GGAA   G C-- -  G  AG  G  GGC
GAM461
TCCGCGGAGGTTTCGGCAGTGGCATCCGGGGCCGGGGTCGCGGCCGTGGACGGGGCCGGGGCCGAGGCCGC
GGAGCTCGCGGAGGCAAGGCCGAGGA 7292 TGGCATCCGGGGCCGGGGTCGCGG 5801
  G  AG--   G AGT A  G  GG  G  GTG
TCC CGG   GTTTC GC  GGC TCCG GGCC  GGTC CGGCC  G
||| |||   ||||| ||  ||| |||| ||||  |||| |||||
AGG GCC   CGGAG CG  TCG AGGC CCGG  CCGG GCCGG  A
  A GGAA   G C-- -  G  AG  G  GGC
GAM461
TCCGCGGAGGTTTCGGCAGTGGCATCCGGGGCCGGGGTCGCGGCCGTGGACGGGGCCGGGGCCGAGGCCGC
GGAGCTCGCGGAGGCAAGGCCGAGGA 7293 TGGCATCCGGGGCCGGGGTCGCGG 5801
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  G  AG--     G  AGT  A   G  GG  G   GTG
TCC CGG     GTTTC GC   GGC TCCG GGCC  GGTC CGGCC  G
||| |||     ||||| ||   ||| |||| ||||  |||| |||||
AGG GCC     CGGAG CG   TCG AGGC CCGG  CCGG GCCGG  A
  A  GGAA     G  C--  -   G  AG  G   GGC
GAM461
TCCGCGGAGGTTTCGGCAGTGGCATCCGGGGCCGGGGTCGCGGCCGTGGACGGGGCCGGGGCCGAGGCCGC
GGAGCTCGCGGAGGCAAGGCCGAGGA 7294 TGGCATCCGGGGCCGGGGTCGCGG 5801
  G  AG--     G  AGT  A   G  GG  G   GTG
TCC CGG     GTTTC GC   GGC TCCG GGCC  GGTC CGGCC  G
||| |||     ||||| ||   ||| |||| ||||  |||| |||||
AGG GCC     CGGAG CG   TCG AGGC CCGG  CCGG GCCGG  A
  A  GGAA     G  C--  -   G  AG  G   GGC
GAM461
TCCGCGGAGGTTTCGGCAGTGGCATCCGGGGCCGGGGTCGCGGCCGTGGACGGGGCCGGGGCCGAGGCCGC
GGAGCTCGCGGAGGCAAGGCCGAGGA 7295 TGGCATCCGGGGCCGGGGTCGCGG 5801
  G  AG--     G  AGT  A   G  GG  G   GTG
TCC CGG     GTTTC GC   GGC TCCG GGCC  GGTC CGGCC  G
||| |||     ||||| ||   ||| |||| ||||  |||| |||||
AGG GCC     CGGAG CG   TCG AGGC CCGG  CCGG GCCGG  A
  A  GGAA     G  C--  -   G  AG  G   GGC
GAM461
TCCGCGGAGGTTTCGGCAGTGGCATCCGGGGCCGGGGTCGCGGCCGTGGACGGGGCCGGGGCCGAGGCCGC
GGAGCTCGCGGAGGCAAGGCCGAGGA 7296 TGGCATCCGGGGCCGGGGTCGCGG 5801
  G  AG--     G  AGT  A   G  GG  G   GTG
TCC CGG     GTTTC GC   GGC TCCG GGCC  GGTC CGGCC  G
||| |||     ||||| ||   ||| |||| ||||  |||| |||||
AGG GCC     CGGAG CG   TCG AGGC CCGG  CCGG GCCGG  A
  A  GGAA     G  C--  -   G  AG  G   GGC
GAM461
TCCGCGGAGGTTTCGGCAGTGGCATCCGGGGCCGGGGTCGCGGCCGTGGACGGGGCCGGGGCCGAGGCCGC
GGAGCTCGCGGAGGCAAGGCCGAGGA 7297 TGGCATCCGGGGCCGGGGTCGCGG 5801
  G  AG--     G  AGT  A   G  GG  G   GTG
TCC CGG     GTTTC GC   GGC TCCG GGCC  GGTC CGGCC  G
||| |||     ||||| ||   ||| |||| ||||  |||| |||||
AGG GCC     CGGAG CG   TCG AGGC CCGG  CCGG GCCGG  A
  A  GGAA     G  C--  -   G  AG  G   GGC
GAM461
TCCGCGGAGGTTTCGGCAGTGGCATCCGGGGCCGGGGTCGCGGCCGTGGACGGGGCCGGGGCCGAGGCCGC
GGAGCTCGCGGAGGCAAGGCCGAGGA 7298 TGGCATCCGGGGCCGGGGTCGCGG 5801
  G  AG--     G  AGT  A   G  GG  G   GTG
TCC CGG     GTTTC GC   GGC TCCG GGCC  GGTC CGGCC  G
||| |||     ||||| ||   ||| |||| ||||  |||| |||||
AGG GCC     CGGAG CG   TCG AGGC CCGG  CCGG GCCGG  A
  A  GGAA     G  C--  -   G  AG  G   GGC
GAM461
TCCGCGGAGGTTTCGGCAGTGGCATCCGGGGCCGGGGTCGCGGCCGTGGACGGGGCCGGGGCCGAGGCCGC
GGAGCTCGCGGAGGCAAGGCCGAGGA 7299 TGGCATCCGGGGCCGGGGTCGCGG 5801
  G  AG--     G  AGT  A   G  GG  G   GTG
TCC CGG     GTTTC GC   GGC TCCG GGCC  GGTC CGGCC  G
```

```
III III   IIII II  III IIII IIII  IIII IIIII
AGG GCC   CGGAG CG  TCG AGGC CCGG  CCGG GCCGG  A
  A GGAA   G C-- -  G AG  G  GGC
GAM461
TCCGCGGAGGTTTCGGCAGTGGCATCCGGGGCCGGGGTCGCGGCCGTGGACGGGGCCGGGGCCGAGGCCGC
GGAGCTCGCGGAGGCAAGGCCGAGGA 7300 TGGCATCCGGGGCCGGGGTCGCGG 5801
  G AG--   G AGT A  G  GG  G  GTG
TCC CGG   GTTTC GC  GGC TCCG GGCC  GGTC CGGCC  G
III III   IIII II  III IIII IIII  IIII IIIII
AGG GCC   CGGAG CG  TCG AGGC CCGG  CCGG GCCGG  A
  A GGAA   G C-- -  G AG  G  GGC
GAM462
TCCGGAGTAAACGGCTCTTCATTAGCTTGGAGTGGCCGCAGGTCCCGTGACCAGCACCCGCGAGACCCTGTGC
GACAGCTGGGCTGATGCTCCGTTTCTCTGGG 7301 TAGCTTGGAGTGGCCGCAGGTCCC 7302
     T  CTCTT    TG A- G C   - C  ACCA
TCCGGAG AAACGG   CATTAGCT G GT GC GCAGG TC CGTG   G
IIIIIIII IIIIII    IIIIIIIII I II II IIIII II IIII
GGGTCTC TTTGCC   GTAGTCGG C CA CG TGTCC AG GCGC   /
    -   TC---    GT GA G - C A  CCAC
GAM463
TCCGTTACTGAGATTGGAGTGACTTAGAAGAGGGTGACCTCCATGAAAGCAGGTAGGATCACAGATGCGGA 7309
TGAAAGCAGGTAGGATCACAGATG 7310
    TA  A   GGAG- A  AGAA-  G
TCCGT CTG GATT   TG CTT   GAGG T
IIIII III IIII    II III    IIII
AGGCG GAC CTAG   AC GAA   CTCC G
   TA  A  GATGG - AGTAC   A
GAM464
TCCTCCATCCCAGCATAGAGAATGGGGACTCCCTGAGTAATGGGAGTTCTTTCATGTCCTCTGCTTGGGGTGGG
GGA 7323 TCCCAGCATAGAGAATGGGGACTC 7324
      - T A AT---    TGA
TCCTCCATCCCA GCA AG GA   GGGGACTCCC  G
IIIIIIIIIIII III II II    IIIIIIIIII
AGGGGGTGGGGT CGT TC CT    TTCTTGAGGG  T
     T  C - GTACT      TAA
GAM465
TCGTCAATGGAAGAACCGCCTTTCGGGGCGTTGGACCTTCCAATTCCCGGTCAGATGGAGAACCAGCGCAGTAC
CCGAGAAAAGGGTCGCCCGTTGACGA 7338 TGGAGAACCAGCGCAGTACCCGAG 7339
     AA A GCC    ----    ACC   AT CCG
TCGTCAATGG GA CC TTTCGGG  GCGTTGG TTCCA TC  G
IIIIIIIIII II II IIIIIII   IIIIIII IIIII II
AGCAGTTGCC CT GG AGAGCCC  CGCGACC GAGGT AG /
     CG G AAA   ATGA   AA- -- ACT
GAM466 TCTATCATAAGAAGTGGACAGCACGAAACTTGTGAAACCAATGTGCCTTTAAACTTCTAATATGCTTAGA
7348 TAAGAAGTGGACAGCACGAAACTT 7349
  T- --  GGACA-  AAAC TG
TCTA CATA AGAAGT   GCACG  TTG A
IIII IIII IIIIII    IIIII  III
AGAT GTAT TCTTCA   CGTGT  AAC A
  TC  AA   AATTTC  ---- CA
```

GAM467
TCTCCCTCAGGACCAGCTGTCAGTCCCCAGGCCCTGAGGTGGTGCCTGCATCCTAGGTCTGTGGGGCATTACTG
GTGTCACTCTGAGGGAGA 7361 TGTCAGTCCCCAGGCCCTGAGGTG 7362
        -----   C TCA   -    CTGA T  C
TCTCCCTCAGG   ACCAG TG  GTCCC CAGGCC   GG GGTG C
IIIIIIIIIII    IIIII II IIIII IIIII   II IIII
AGAGGGAGTCT   TGGTC AT  CGGGG GTCTGG   TC CTAC T
      CACTG   - TA-  T  A--- -  G
GAM468  TCTGACAGCAGCCATTATCCTGCTCCATACCTTTTGGGGAGTTGTGTTCTTTGATGCCTGTGAGA 7380
TGACAGCAGCCATTATCCTGCTCC 7381
  G  - GC TTATCCT--   ATA T
TCT ACAG CA CA      GCTCC  CC T
III IIII II II      IIIII  II
AGA TGTC GT GT      TGAGG  GG T
  G  C A- TTCTTGTGT   --- T
GAM469  TCTGACAGGGCCCATGTCCCACAAGGCTGCTTGGCCTCAGTGGGTGCTTGGCTGTGCTGGA 7395
TGACAGGGCCCATGTCCCACAAGG 7396
  GA G  CAT -  A-   G
TCT CA GGCC  GT CCCAC AGGCT C
III II IIII  II IIIII IIIII
AGG GT TCGG  CG GGGTG TCCGG T
  TC G  TT- T   AC   T
GAM470
TCTGGCTGCAGATCTGGAGGTGGAGGCAGTACCCTGGACTCTATTCTGCTGCCCCTTCAGGGTTTGGAGGAGCC
GGA 7429 CTGCAGATCTGGAGGTGGAGGCAG 7430
     G---   -   T A  TACCCTG
TCTGGCT   CAGATC TGGAGG GG GGCAG    G
IIIIIII   IIIIII IIIIII II IIIII
AGGCCGA   GTTTGG ACTTCC CC TCGTC    A
   GGAG    G   - G   TTATCTC
GAM471
TCTGTTATAACATCTCAACTTACCTGTTGCCACTTGGAATATATATCGATACATTATGGTGCCGAGTGGTAACATG
GGAGTGTTTGATCCAACAGA 7457 TCTCAACTTACCTGTTGCCACTTG 7458
    ATAAC  TCA-  A -      AA-  TATCG
TCTGTT   ATC  ACTT CC TGTTGCCACTTGG  TATA   A
IIIIII    III    IIII II IIIIIIIIIII   IIII
AGACAA    TAG  TGAG GG ACAATGGTGAGCC  GTAT   /
   CC--- TTTG  - T      GTG  TACAT
GAM472
TCTTGGCGCGCGGCACTGGGAGCCGCGGGCCGAGCCTGTCAAGCCCCGCAGCAGCAGCGCGTCAGGA 7463
TGTCAAGCCCCGCAGCAGCAGCGC 7464
     G A- - A C--   C
TCTTGGCGCGC GC  CTG GG GC  GCGGGC G
IIIIIIIIIII II III II II  IIIIII
AGGACTGCGCG CG  GAC CC CG  TGTCCG /
    A AC  G C AAC   A
GAM473
TCTTGGGAACTGGAGTAAAGGTCACTCTTGCTACGCTTTAGCAGAGACTGGTGGCATTTTGCCCCTGCCCTGAGA
7481 AGCAGAGACTGGTGGCATTTTGCC 7482
  TG AACT A   -  --- -  CG

```
TCT GG   GG GTAAAG GTCAC  TCT TGCTA C
||| ||   || |||||| |||||  ||| |||||
AGA CC   CC CGTTTT CGGTG  AGA ACGAT /
  GT CGT- C    A   GTC  G   TT
GAM474  TCTTGGTGACAAAATATGTTGTGTAGAGTTCAGGGGAGAGTGCGTCATATGTTGTTCCTAGGA 7493
TGACAAAATATGTTGTGTAGAGTT 7494
    TG   A   T TG AGAG  A
TCTTGG ACAA ATATG TG  T   TTC G
|||||| |||| |||||| || |   |||
AGGATC TGTT TATAC GC  G   GAG G
   CT  G   T GT A---  G
GAM475
TCTTGTGTTGAGACTTCGTGGTGGTGCTAAGAAAAGGAAGAAGAAGTCTTACACCACTCCCAAGAAGAATAAGCA
CAAGA 7511 TACACCACTCCCAAGAAGAATAAG 7512
      GAGA   GT---    C   AAAGGA
TCTTGTGTT  CTTC   GGTGGTG TAAGA    A
|||||||||  ||||   ||||||| |||||
AGAACACGA  GAAG   TCACCAC ATTCT    G
      ATAA  AACCC    -   GAAGAA
GAM476
TCTTGTTCAACATAGGGTAGGTGGCAGCCACGGGTCCAACTCGCTTGAGGCTGGGCCCTGGGCGCTCCATTTTG
TGTTCCAGGA 7541 TAGGGTAGGTGGCAGCCACGGGTC 7542
    TTC     A T A AC    A- G
TCTTG  AACATAGGGT GG GGC GCC  GGGTCCA CTC C
|||||  ||||||||| || ||| ||| ||||||| |||
AGGAC  TTGTGTTTTA CC TCG CGG  CCCGGGT GAG T
   C--     - - - GT    CG  T
GAM477
TCTTTATAGCAGTATGAGAATGAACTAACACAGTAAATTGGTACTGCGGAGAGTAGAGTATTGCTATAAAGA 7561
TAGCAGTATGAGAATGAACTAACA 7562
        GAGAA AA AACA   AA
TCTTTATAGCAGTAT   TG CT  CAGTA T
||||||||||||||   || ||   |||||
AGAAATATCGTTATG   AT GA  GTCAT T
        AG--- GA GGC-   GG
GAM478
TGAACTGAATGAGAGAGAAAAAGAGGTCCAGAGTAGTTTGTGGAGCGATGTTTCCATCTCTAATGCCACTCAGCT
CA 7578 TGAGAGAGAAAAAGAGGTCCAGAG 7579
  A  A -----  --  AAGAGG  G T
TGA CTGA TG   AGAGA GAAA    TCCA AG A
||| |||| ||   ||||| ||||    |||| ||
ACT GACT AC   TCTCT CTTT    AGGT TT G
  C  C CGTAA   AC  GTAGCG  G T
GAM479
TGAATGGCCGCTCGCCGAGTGCTGTTTGCAAACTTAGGAACCCCCTCGCGCGGGGCCTAGCGGGGGGTACGTGG
CGCATGCGGTAACACTCA 7602 TAGCGGGGGGTACGTGGCGCATGCG 7603
  A -- T--  A  G  AAACT  AAC  TC
TGA TG GCCGC  CGCCG GTGCT TTTGC   TAGG  CCCC G
||| || ||||| ||||| |||||    |||| ||||
ACT AC TGGCG  GCGGT CATGG GGGCG   ATCC  GGGG C
```

```
   C AA  TAC  G  -  -----  ---  CG
GAM480  TGAGCTGACTGTGTCCTGCCAAGGCAGTGGCTGCCCAAGGAAGCCTGCATAGGAGATCTCA 7622
GGCTGCCCAAGGAAGCCTGCATAG 7623
   CTGA-    C------------------  C
TGAG   CTGTGT          CTGC A
||||   ||||||          ||||
ACTC   GATACG          GACG A
   TAGAG    TCCGAAGGAACCCGTCGGT  G
GAM481  TGAGTATAGCAAAGGACTAAGATATTTTCTTCTTGAAGAGACTTTTCGATTAGTCCTCATATATTTA 7628
TAGCAAAGGACTAAGATATTTTCT 7629
     GCAA        -- TAT-    C
TGAGTATA  AGGACTAA GA   TTTCTT T
||||||||  |||||||| ||   ||||||
ATTTATAT  TCCTGATT CT   AGAGAA T
      AC--       AG TTTC    G
GAM482  TGATAGAATAGGAAAATTTTAACATTTTTGTTTCTAAGGATAGTTTTAATTTTCTTATTTTTTTCA 7634
TAGAATAGGAAAATTTTAACATTT 7635
   T-          TT   -    T
TGA  AGAATAGGAAAATT  AAC  ATTTTTG T
|||  ||||||||||||||  |||  |||||||
ACT  TTTTATTCTTTTAA  TTG  TAGGAAT T
   TT          TT  A      C
GAM483  TGATCTCCTGTGGGTCTGGTGCTATATTCTAGAGAAGTTTGCACCTGGACAATAGGAATTCG 7637
TCTCCTGTGGGTCTGGTGCTATAT 7638
   TC   GG   -   TATA   T
TGA  TCCTGT  GTCT GGTGC   TTC A
|||  ||||||  |||| |||||   |||
GCT  AGGATA  CAGG CCACG   AAG G
   TA   A-   T   TTTG   A
GAM484  TGATCTGGAAGCCAACCTGGCTGTCCTGAAGCTGTACCAGTTCAACCCAGCCTTCTTTCAGACCA 7649
TGGAAGCCAACCTGGCTGTCCTGA 7650
   A      CCAACCT   TCC   G  T
TG TCTGGAAG       GGCTG  TGAA CTG A
|| ||||||||       |||||  |||| ||
AC AGACTTTC       CCGAC  ACTT GAC /
   C     TT-----   CCA   -   C
GAM485
TGATGAAATGCACTTTCCCGTGCAGCAGTGTTCTTTTGCCTGTCAACTGCTGGGTGGTTTTTGCATTCATCA 7667
TGAAATGCACTTTCCCGTGCAGCA 7668
     A  CTTTC  G     GTTCTTT
TGATGAA TGCA    CCGT CAGCAGT    T
|||||||  ||||    |||| |||||||
ACTACTT ACGT    GGTG GTCGTCA    G
    -  TTTT-  G    ACTGTCC
GAM486  TGATGAGAACACCGTGTACAGCATCGGCGAGGACGGGAAGGTAGGCGGCTGCAGGATTCA 7677
TGAGAACACCGTGTACAGCATCGG 7678
   TGAGAA  -  G  AGCA  GCG
TGA    CA CCGT TAC   TCG  A
|||    || |||||| |||   |||
ACT    GT GGCG ATG   GGC  /
```

```
   TAGGAC  C   G  GAAG  AGG
GAM487  TGATGGTGCTTGTGCCGCTCCTTGTGGCCCTTATGCTTGGGCCCGGCCGCGCTCACCGTCA 7689
TGGTGCTTGTGCCGCTCCTTGTGG 7690
     CTT   C  CCTT T   TTA
TGATGGTG  GTGC GCT  G GGCCC  T
||||||||  |||| |||   | |||||
ACTGCCAC  CGCG CGG   C CCGGG  G
     T--   C  ---- -   TTC
GAM488
TGCACTGGCACCTAGACATGTACAACAGGAACCGTGTGGATACATCCCCCACACCTGTTTCTGTGGCATGGTCAT
GTGTATGCA 7704 AGACATGTACAACAGGAACCGTGT 7705
   CTG  CTAGA  A A   C-   ATAC
TGCA  GCAC   CATGT CA CAGGAAC  GTGTGG   A
||||  ||||    |||||| || |||||||  ||||||
ACGT  TGTG   GTACG GT GTCTTTG  CACACC   /
   A--  TACTG   - -   TC    CCCT
GAM489  TGCAGATGACACCAGGTTCAGGAAAGAGGATGTCTACAGTTGCTTTCGCTTCCTACGTGGTGTTTTGCA
7719 TGACACCAGGTTCAGGAAAGAGGA 7720
    TG   G TC   A A  T CTA
TGCAGA  ACACCA GT  AGGAA G GGA GT   C
||||||  |||||| ||  ||||| | ||| ||
ACGTTT  TGTGGT CA  TCCTT C CTT CG   A
    --    G  --   - G  T TTG
GAM490
TGCATGAGGTTTGGTAACAGGCAAAGTCATCTGGTTAACGTGACTGATGCAAAAAGTCCAGGCCTGGGCA 7736
TGAGGTTTGGTAACAGGCAAAGTC 7737
   ATG     TAACAG- A-   CTGG
TGC  AGGTTTGG   GCA  AGTCAT   T
|||  ||||||||     ||| ||||||
ACG  TCCGGACC   CGT  TCAGTG   /
   GG-     TGAAAAA  AG    CAAT
GAM491
TGCCAGGCATAATCAACATTCCTCATTACTTCTTCAACATCCTCTTGAAAGCTGTGCTCATTTTACAAATGAGAAAA
CAGATTTAGAGAAATATAATGACTTGTATGAGGTCACATAGCTTATGAGTGGCA 7753
TGAGAAAACAGATTTAGAGAAATA 7754
   GG   TCAACATT-   T TTCT  ACATCC-  G  G  G--    T
TGCCA  CATAA      CCTCAT AC  TCA     TCTT AAA CTGT  CTCATTT A
||||| |||||        |||||| ||   |||      |||| ||| ||||  |||||||
ACGGT  GTATT      GGAGTA TG   AGT      AGAG TTT GACA  GAGTAAA /
   GA    CGATACACT   - TTC-  AATATAA  A  A  AAA     C
GAM492
TGCCCCTTCCATGACCAGCCACATCTGAAAAGGAAAGCATTCTGCTCTTTCCAGATCTACGCTGTGCCTTGGCAG
GGCA 7778 TGACCAGCCACATCTGAAAAGGAA 7779
   CTT  TGAC-  CAC-   A  GAA  AT
TGCCC  CCA   CAGC   ATCTG AAAG  AGC  T
|||||  |||    ||||   |||||  ||||   |||
ACGGG  GGT   GTCG   TAGAC TTTC  TCG  /
   AC-  TCCGT   CATC    C   ---  TC
GAM493
TGCCCGCGTACATGGGCTGAGGAATGTTCAAGCAGAAGAAATGGTAGAGTTTTCTTCAGGCTTAAAGGGTA 7803
AATGGTAGAGTTTTCTTCAGGCTT 7804
```

```
   GCGTACAT G    TG  AAG  GAA
TGCCC     GG CTGAGGAA TTC  CA  G
|||||      || ||||||||  |||  ||
ATGGG     TC GACTTCTT GAG  GT  /
   AAAT---- G     TT  ATG  AAA
GAM494  TGCCGACTCTATCGATCCCTTACCTTCAATGAGACCTACCAGGACATCAGTGAGTTGGTA 7821
TACCAGGACATCAGTGAGTTGGTA 7822
       T  C  C-  TACCT- AA
TGCCGACTC AT GAT  CCT    TC  T
||||||||| || |||  |||      ||
ATGGTTGAG TG CTA  GGA    AG  /
      -  A  CA  CCATCC  AG
GAM495  TGCCTCTGCTTTCATTTCTATGGTTATTCGTGGAATGACTCATTGACCACGCGGAGAAGGCA 7835
GACTCATTGACCACGCGGAGAAGG 7836
   ---   TTTCATT T  -     G
TGCC  TCTGC    TC ATG GTTATTC T
||||  |||||     || ||| |||||||
ACGG  AGGCG    AG TAC CAGTAAG /
    AAG   CACC--- T  T     G
GAM496  TGCCTGGAATGGCAGCATCTACATGTTCAACTGGCACCCAGTGCTTATGGTTGCTGGCATGGTGGTA
7839 TGGCAGCATCTACATGTTCAACTG 7840
    TGGA  G   TCTA  TTCA    C
TGCC  ATG CAGCA  CATG  ACTGG A
||||  ||| |||||  ||||  ||||| 
ATGG  TAC GTCGT  GTAT  TGACC /
   TGG- G  TG-- TCG-   C
GAM497
TGCGGCCGATGGCGGGCTGCGGGCAAGCGTCACCCTGCTGGGTGCCGGGCTGCTGCTGAGCCTGCTGCCGGC
CCTGCTGCG 7858 TGGCGGGCTGCGGGCAAGCGTCAC 7859
    CGAT  G  T    A-  T  -  T  TG
TGCGGC  GGC GGC GCGGGC  AGCG CA CCC GC  G
||||||   ||| ||| ||||||  |||| || ||| || 
GCGTCG   CCG CCG CGTCCG  TCGT GT GGG CG  /
    TC--  G  T    AG  C  C  C TG
GAM498  TGCTCACAGGGTGTGACTGGCCCACTATCTAGGGTAGTGAGCCTATTTTGTGGCCCCTGTGTGCA
7876 TCACAGGGTGTGACTGGCCCACTA 7877
    T    T G  T----- C    CT
TGC CACAGGG GT AC    GGC CACTAT  A
||| |||||||| || ||     ||| ||||||
ACG GTGTCCC CG TG    CCG GTGATG  /
   T    - G TTTTAT  A     GG
GAM499
TGCTCCCGACCATCACCTGTGGGCACACCATCGAGATCCTCCGGGAGAAGGGCTTCGACCAGGCGCCCGTGGT
GGATGAGGCGGGGGGTA 7890 TCACCTGTGGGCACACCATCGAGA 7891
     AC-  AC TG   ACA  A--   AT  CCG
TGCTCCCG  CATC  C  TGGGC  CC  TCGAG  CCT  G
|||||||||  ||||  |  ||||| ||  |||||  |||
ATGGGGGC  GTAG  G  GCCCG  GG  AGCTT  GGA  G
     GGA   GT GT   C-- ACC    CG  AGA
GAM500  TGCTGGCATGCTAGGTTTCTGGGTTCTCTCTCCCTGAGCGGTCCTGGTGACCCTGCTTGAAGCA 7896
TGGCATGCTAGGTTTCTGGGTTCT 7897
```

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    GG  T  TA    T TG  TT T   TC
TGCT  CA GC  GGTT C  GG  C CTC  C
||||  ||  ||  ||||  |  ||  |  | |||
ACGA  GT CG  CCAG G  CC  G GAG  /
    A-  T  TC    T GT  TG C    TC
GAM501  TGCTGGGAATACCATAGCCACCTTTTAGGGAAACTTAAATTATGTTTTTGGATACCCTGTA 7909
TGGGAATACCATAGCCACCTTTTA 7910
    T   A   A   T-  CACCT     G
TGC GGG AT CCA  AGC     TTTAGG  A
||| ||| || |||  |||     ||||||
ATG CCC TA GGT  TTG     AAATTC  A
    T   A  -  TT  TATT-     A
GAM502
TGGAGTACCTTCTACTGCCTCAGTGGGCAAATCCAAAACCCCATTAGTGGCAAGGAAGAAAGTGTTCCG 7918
TTAGTGGCAAGGAAGAAAGTGTTC 7919
       C   A- -  TC-     CAAAT
TGGAGTAC TTCT  CT GCC  AGTGGG    C
|||||||| ||||  || |||   ||||||
GCCTTGTG AAGA  GA CGG   TTACCC    C
       A   AG A  TGA     CAAAA
GAM503  TGGATAACAGTATAATAGCATTTACAATATTTCACTCTTTGTTCTCTTAATGTCTTATATAGTTATTTA
7924 TAACAGTATAATAGCATTTACAAT 7925
       A    TA   TAC--   TTTC
TGGATAAC GTATAA GCATT    AATA   A
|||||||| |||||| |||||    ||||
ATTTATTG TATATT TGTAA    TTGT   C
       A    C-   TTCTC   TTCT
GAM504
TGGATTCCGGATGACACACACAGTCACCACCATCAGTTACCTGAACCTGGCCGTGGCTGACTTCTGTTTCACCTC
CA 7952 TGACACACACAGTCACCACCATCA 7953
    TTCC  A  C  CA---     CA  ---   T
TGGA   GG TGA ACA   CAGTCAC CCA  TCAG T
||||   || ||| |||   ||||||| |||  ||||
ACCT   CC ACT TGT   GTCGGTG GGT  AGTC A
    ----  -  T  CTTCA     CC  CCA   C
GAM505  TGGCAGGTGGTATTGGGGTCCCTCAGCCCACCTGGGCCGTGACCTCAAGTGTCCACTGCTG 7992
TGACCTCAAGTGTCCACTGCTG 7993
    G  TA--     CCTCA   A
TGGCAG TGG   TTGGGGTC   GCCC C
|||||| |||   |||||||||   ||||
GTCGTC ACC   AACTCCAG   CGGG C
    -  TGTG     TGC--   T
GAM506
TGGCCAAGGGCCGCGGCCGCGGAGGCCTGCAGCAGCAGAAGCAGCAGAAAGGCCGCGGCATGGGCGGCGCT
GGCCG 8026 GCAGAAAGGCCGCGGCATGGGCGG 8027
     A G   G---     AGGC-  A AGC
TGGCCA G GCCGC   GCCGCGG   CTGC GC  A
|||||| | |||||   |||||||   |||| ||
GCCGGT C CGGCG   CGGCGCC   GACG CG  /
     - G   GGTA     GGAAA  A AAG
```

GAM507
TGGGATGGCAAAGTTTGTTGGCTCAGACTGTTGCTAACAGGAACTCTGAAGCCCGGGCTTTCAAGCCAGAAACAA
TCTCA 8051 TGGCAAAGTTTGTTGGCTCAGACT 8052
      ------- ---    TT  -  ----    G
TGGGA    TGGC  AAAGTTTG  GGCT CAGA   CTGTT C
|||||    ||||  ||||||||| |||| ||||   |||||
ACTCT    ACCG  TTTCGGGC  CCGA GTCT   GACAA /
   AACAAAG  AAC    --  A  CAAG    T
GAM508 TGGGCAGGGTCCGCTGATCGTGGGCATCTTGCTGGTGTTGATGGCTGTGGTCTATGCATCTCTGAATA
8071 TGGCTGTGGTCTATGCATCTCTGA 8072
 GG   TCC  T--   TG G  TT  T
TG CAGGG  GC  GATCG  G CATC  GC G
|| |||||  ||  |||||  | ||||  ||
AT GTCTC  CG  CTGGT  C GTAG  TG G
 AA   TA-  TAT   GT G   T-  T
GAM509
TGGGGCTGAGAGGCGAGACACTGATGGCACTCTTACTTCTGTCAGCTGCCGCAAAGTCTCGTCCACTTGCTGCA
8091 TGAGAGGCGAGACACTGATGGCAC 8092
  G  T  A  -   AC A   CT T  T
TG GGC GAG GG CGAGAC  TG TGGCA  CT AC T
|| ||| ||| || |||||| || ||||| || ||
AC TCG TTC CC GCTCTG  AC GCCGT GA TG C
  G  -  A T   AA  -   C- C T
GAM510
TGGGTCTGTTTACAGAGTGTGGTAATTTCGTTCTTTAGATTTGCAGAATTTATAAAGAAAGAAAATTACAGCCTGCA
CACCCA 8109 TATAAAGAAAGAAAATTACAGCCT 8110
   C TTTA AG   AA  G    --   G
TGGGT TG   CAG TGTGGT TTTC TTCTTTA GATTT C
||||| ||   ||| |||||| |||| ||||||| |||||
ACCCA AC   GTC ACATTA AAAG AAGAAAT TTAAG /
   C ---- CG    --  A   AT  A
GAM511  TGGTGAGGTATAGGAGTTGGAGTTTCGCAAATAGCCTGAGACCTTGAGAACATTTCCTTCCTCACCA
8136 TGAGACCTTGAGAACATTTCCTTC 8137
      TAT   ------ TG A    -- AA
TGGTGAGG AGGAG   T G GTTTC GC A
|||||||| |||||    | | ||||| ||
ACCACTCC TCCTT    A T CAGAG CG /
     T-- TACAAG GT C   TC AT
GAM512 TGGTGGGCCCCAGGCCCTCGTGCAGATCATGCGTAACTACAGTTATGAAAAGCTGCTCTGGACCACCA
8149 TGAAAAGCTGCTCTGGACCACCA 8150
   GCC   CCCTCGT  ATCATG    T
TGGTGG  CCAGG    GCAG   CGTAAC A
||||||  |||||    ||||    ||||||
ACCACC  GGTCT    CGTC    GTATTG C
   A--  -------  GAAAA-   A
GAM513
TGGTTCATAGAAGCAGCCACCAGCAGATGACAAAGAAGCTTCAGTTCTCCTTAAAGAAGTTAGGGGTAGGACAAG
TATCTCGTGGTATTGAAGAGGTGAATATGTTTACAAACCA 8162 TGACAAAGAAGCTTCAGTTCTCCT 8163
   CATAG  GC--  AG--  - G AA A  CA   --   AG
TGGTT  AAGCA  CACC   CAG AT AC AGA GCTT  GTTCT CCTTAA A

```
||||||    |||||    ||||    ||| || ||  ||| ||||  |||||  |||||
ACCAA    TTTGT    GTGG    GTT TG TG  TCT TGAA  CAGGA  GGGATT /
  ACA--    ATAA    AGAA   A G C- A  --   TG     GA
GAM514
TGGTTTTGGTGGCCCAGGCTGGGAGTGCAAGGGCGCAATCTCAGCTCAGTGAAACCTCGGCCTCCCGTGTCCA
8187 TCTCAGCTCAGTGAAACCTCGGCC 8188
  TTT  T-  C ----------    G  AA
TGG  TGG  GGCC AG       GCTGGGA TGC  G
|||  |||  |||| ||         ||||||| |||
ACC  GCC  CCGG TC        CGACTCT ACG  G
  TGT  CT   C CAAAGTGACT    A  CG
GAM515
TGTCCCATAGAGCTTTTGCATCCTCTGGATGTATTGCGAAAGAAATGTCCAGACTTTGAGGGCTACAGGGTACA
8210 GTCCAGACTTTGAGGGCTACAGGG 8211
  -  ATAG    GCATCC     A GC
TGT CCC   AGCTTTT    TCTGGATGT TT  G
||| |||   |||||||      ||||||||| ||
ACA GGG   TCGGGAG    AGACCTGTA AG  A
  T  ACA-    TTTC--    A AA
GAM516
TGTCTATGGAAATGTGAATAAAGGCAATCCATGAATAGGTCAACTTCTTCCTGGGTAACCTCCCCAGGTGTTTTGT
GGACA 8218 TGTGAATAAAGGCAATCCATGAAT 8219
    TG  - G AATAA  CA   T  T  T
TGTCTA GAA AT TG    AGG  ATCCA GAA AGG  C
|||||| ||| || ||     ||| ||||| ||| |||
ACAGGT TTT TG AC    TCC  TGGGT CTT TTC  A
    GT  G  G CCC--  AA    C  C  A
GAM517  TGTGAATCACCGGCAGAGCCTGGTGGAGCTGGAGGACCGGTTCCTGGGCCTGACAGACACA 8236
TCACCGGCAGAGCCTGGTGGAGCT 8237
   AA ACCGG  A  GGT      A
TGTG  TC   CAG GCCT   GGAGCTGG  G
|||| ||   ||| ||||   ||||||||
ACAC  AG    GTC CGGG   CCTTGGCC  G
   -- ACA-- - T--     A
GAM518
TGTGCATCCCAGCAGTAAGCAACAATGGCTGATCCAGAAGGTACAGACGGGGAGGGCACGGGTTGTAACGGCT
GGTTTTATGTACA 8254 TCCCAGCAGTAAGCAACAATGGCT 8255
    C---    A AA   AA- G GA  AGAAGG
TGTGCAT   CCAGC GT  GCAAC   TG CT  TCC     T
||||||||   ||||| ||  |||||   || || |||
ACATGTA   GGTCG CA  TGTTG   AC GG  GGG     /
    TTTT    G A-   GGC  G  AG   CAGACA
GAM519  TGTGTGGTGATCGAGTGGTCTGTGTTCCTATTGCTGGTGGGGTGATAGGGTGGGCTAAAAACCATGCA
8272 TAGGGTGGGCTAAAAACCATGCA 8273
    GATCGAG   TG GTT   TG  GG
TGTGTGGT    TGGTC  T  CCTAT CT  T
||||||||     |||||  |  ||||| ||
ACGTACCA     ATCGG  G  GGATA GG  /
    AAA----   GT ---   GT GG
GAM520
TGTTCTTGGTGAGAAGGGCCGGCGGATTCGGGAACTGACTGCTGTAGTTCAGAAGAGGTTTGGCTTTCCAGAGG
```

GCA 8283 TGAGAAGGGCCGGCGGATTCGGGA 8284
  - T  AA   GGCGGA  GG   A T
TGTTCT TGG GAG  GGGCC    TTC  GAACTG C G
||||||| ||| ||| |||||    ||| ||||||| |
ACGGGA ACC TTC TTTGG    AAG  CTTGAT G C
   G T  GG   AG----  A-    - T
GAM521
TGTTGAGATGAGGGTTTCAGGGAAGCAGAAAAACCAAGTGCTGGATCATTTCTCCTTTGAGGGGCCTTTGTCCAA
TTCAGCA 8300 TGAGGGTTTCAGGGAAGCAGAAAA 8301
   ---- TG   TT AGG  C   AA-- AG
TGTTGA  GA AGGGT C  GAAG AGAAA   CCA T
||||||  || |||||  |  |||| |||||   |||
ACGACT   CT TTCCG G  TTTC TCTTT  GGT /
    TAAC GT    GG AG-  C   ACTA  CG
GAM522
TGTTGAGTGCAGATGAAGGGTTGTATGAGGCCCCATCCTGGGAGGGCTGTACACCTTCTTGGCACAGCAGCA
8319 TGAAGGGTTGTATGAGGCCCCATC 8320
   A- AGAT   GT   GA   CA C
TGTTG GTGC   GAAGG TGTAT GGCCC TC T
||||| ||||   ||||| ||||| ||||| ||
ACGAC CACG   CTTCC ACATG TCGGG AG G
    GA  GTT-  --  --  -- G
GAM523 TGTTTCATGACTGGTAACAGAGTAGTCTCGAGGGGATCCTTGGAGAACCTGTTCTGACTTTAGAAGCA
8335 TGACTGGTAACAGAGTAGTCTCGA 8336
    A  CT AA     -- G  G
TGTTTC TGA GGT CAGAGTAG TCTC AGGG A
|||||| ||| ||| |||||||| |||| ||||
ACGAAG ATT TCA GTCTTGTC AGAG TTCC /
    - -- --    CA  G   T
GAM524
TTAAACATGTCACCTAAATGCACTTGATGGTGTTGAAATGTGCACCTTCTTAAATTTTAAGATGACTTAGTTTAA
8344 TGTCACCTAAATGCACTTGATGGT 8345
    AT-  C  A  TGCACTT  T    TGA
TTAAAC  GTCA CT AA     GA GGTGT  A
|||||| |||| || ||       || |||||
AATTTG  CAGT GA TT     CT CCACG  A
    ATT  A  A  TTAAATT  T    TGT
GAM525
TTACTGTTTATGGAAGGGGAGACTTAGTATCATAATGATGTCAATCTTCTGCATACTGATCACTAATTCAATCAACA
ATAG 8355 TGGAAGGGGAGACTTAGTATCATA 8356
  C  T G  GG  A  C    - T T  G
TTA TGTT AT GAA  GG GA TTAGTAT CA AA GAT T
||| |||| || |||  || || |||||||| || || |||
GAT ACAA TA CTT  TC CT AGTCATA GT TT CTA C
  A  C  A  AA A -    C  C - A
GAM526
TTATGAAAGGTGTGAACTTGCAATGTCCTCCTGTCTTAAACCCAAGTTGACAGTGCCCTCTCAAAACTTTTCATAA
8366 TGAAAGGTGTGAACTTGCAATGTC 6904
     G- ACTT  A  CTC  GTCTT
TTATGAAAGGT TGA   GCA TGTC  CT   A

```
||||||||||| |||  ||| |||| ||
AATACTTTTCA ACT  CGT ACAG  GA   A
       AA  CTCC  G   TT- ACCCA
GAM526
TTATGAAAGGTGTGAACTTGCAATGTCCTCCTGTCTTAAACCCAAGTTGACAGTGCCCTCTCAAAACTTTTCATAA
8367 TGAAAGGTGTGAACTTGCAATGTC 6904
       G- ACTT  A   CTC GTCTT
TTATGAAAGGT TGA   GCA TGTC  CT   A
||||||||||| |||  ||| |||| ||
AATACTTTTCA ACT  CGT ACAG  GA   A
       AA  CTCC  G   TT- ACCCA
GAM526
TTATGAAAGGTGTGAACTTGCAATGTCCTCCTGTCTTAAACCCAAGTTGACAGTGCCCTCTCAAAACTTTTCATAA
8368 TGAAAGGTGTGAACTTGCAATGTC 6904
       G- ACTT  A   CTC GTCTT
TTATGAAAGGT TGA   GCA TGTC  CT   A
||||||||||| |||  ||| |||| ||
AATACTTTTCA ACT  CGT ACAG  GA   A
       AA  CTCC  G   TT- ACCCA
GAM526
TTATGAAAGGTGTGAACTTGCAATGTCCTCCTGTCTTAAACCCAAGTTGACAGTGCCCTCTCAAAACTTTTCATAA
8369 TGAAAGGTGTGAACTTGCAATGTC 6904
       G- ACTT  A   CTC GTCTT
TTATGAAAGGT TGA   GCA TGTC  CT   A
||||||||||| |||  ||| |||| ||
AATACTTTTCA ACT  CGT ACAG  GA   A
       AA  CTCC  G   TT- ACCCA
GAM526
TTATGAAAGGTGTGAACTTGCAATGTCCTCCTGTCTTAAACCCAAGTTGACAGTGCCCTCTCAAAACTTTTCATAA
8370 TGAAAGGTGTGAACTTGCAATGTC 6904
       G- ACTT  A   CTC GTCTT
TTATGAAAGGT TGA   GCA TGTC  CT   A
||||||||||| |||  ||| |||| ||
AATACTTTTCA ACT  CGT ACAG  GA   A
       AA  CTCC  G   TT- ACCCA
GAM526
TTATGAAAGGTGTGAACTTGCAATGTCCTCCTGTCTTAAACCCAAGTTGACAGTGCCCTCTCAAAACTTTTCATAA
8371 TGAAAGGTGTGAACTTGCAATGTC 6904
       G- ACTT  A   CTC GTCTT
TTATGAAAGGT TGA   GCA TGTC  CT   A
||||||||||| |||  ||| |||| ||
AATACTTTTCA ACT  CGT ACAG  GA   A
       AA  CTCC  G   TT- ACCCA
GAM526
TTATGAAAGGTGTGAACTTGCAATGTCCTCCTGTCTTAAACCCAAGTTGACAGTGCCCTCTCAAAACTTTTCATAA
8372 TGAAAGGTGTGAACTTGCAATGTC 6904
       G- ACTT  A   CTC GTCTT
TTATGAAAGGT TGA   GCA TGTC  CT   A
||||||||||| |||  ||| |||| ||
AATACTTTTCA ACT  CGT ACAG  GA   A
```

```
          AA  CTCC  G   TT- ACCCA
GAM526
TTATGAAAGGTGTGAACTTGCAATGTCCTCCTGTCTTAAACCCAAGTTGACAGTGCCCTCTCAAAACTTTTCATAA
8373 TGAAAGGTGTGAACTTGCAATGTC 6904
      G- ACTT  A   CTC GTCTT
TTATGAAAGGT TGA   GCA TGTC  CT   A
||||||||||| |||   ||| ||||  ||
AATACTTTTCA ACT   CGT ACAG  GA   A
         AA  CTCC  G   TT- ACCCA
GAM526
TTATGAAAGGTGTGAACTTGCAATGTCCTCCTGTCTTAAACCCAAGTTGACAGTGCCCTCTCAAAACTTTTCATAA
8374 TGAAAGGTGTGAACTTGCAATGTC 6904
      G- ACTT  A   CTC GTCTT
TTATGAAAGGT TGA   GCA TGTC  CT   A
||||||||||| |||   ||| ||||  ||
AATACTTTTCA ACT   CGT ACAG  GA   A
         AA  CTCC  G   TT- ACCCA
GAM526
TTATGAAAGGTGTGAACTTGCAATGTCCTCCTGTCTTAAACCCAAGTTGACAGTGCCCTCTCAAAACTTTTCATAA
8375 TGAAAGGTGTGAACTTGCAATGTC 6904
      G- ACTT  A   CTC GTCTT
TTATGAAAGGT TGA   GCA TGTC  CT   A
||||||||||| |||   ||| ||||  ||
AATACTTTTCA ACT   CGT ACAG  GA   A
         AA  CTCC  G   TT- ACCCA
GAM526
TTATGAAAGGTGTGAACTTGCAATGTCCTCCTGTCTTAAACCCAAGTTGACAGTGCCCTCTCAAAACTTTTCATAA
8376 TGAAAGGTGTGAACTTGCAATGTC 6904
      G- ACTT  A   CTC GTCTT
TTATGAAAGGT TGA   GCA TGTC  CT   A
||||||||||| |||   ||| ||||  ||
AATACTTTTCA ACT   CGT ACAG  GA   A
         AA  CTCC  G   TT- ACCCA
GAM526
TTATGAAAGGTGTGAACTTGCAATGTCCTCCTGTCTTAAACCCAAGTTGACAGTGCCCTCTCAAAACTTTTCATAA
8377 TGAAAGGTGTGAACTTGCAATGTC 6904
      G- ACTT  A   CTC GTCTT
TTATGAAAGGT TGA   GCA TGTC  CT   A
||||||||||| |||   ||| ||||  ||
AATACTTTTCA ACT   CGT ACAG  GA   A
         AA  CTCC  G   TT- ACCCA
GAM526
TTATGAAAGGTGTGAACTTGCAATGTCCTCCTGTCTTAAACCCAAGTTGACAGTGCCCTCTCAAAACTTTTCATAA
8378 TGAAAGGTGTGAACTTGCAATGTC 6904
      G- ACTT  A   CTC GTCTT
TTATGAAAGGT TGA   GCA TGTC  CT   A
||||||||||| |||   ||| ||||  ||
AATACTTTTCA ACT   CGT ACAG  GA   A
         AA  CTCC  G   TT- ACCCA
GAM526
TTATGAAAGGTGTGAACTTGCAATGTCCTCCTGTCTTAAACCCAAGTTGACAGTGCCCTCTCAAAACTTTTCATAA
```

```
8380 TGAAAGGTGTGAACTTGCAATGTC 6904
      G- ACTT A   CTC GTCTT
TTATGAAAGGT TGA   GCA TGTC  CT    A
||||||||||| |||   ||| ||||  ||
AATACTTTTCA ACT   CGT ACAG  GA    A
         AA CTCC G   TT- ACCCA
GAM526
TTATGAAAGGTGTGAACTTGCAATGTCCTCCTGTCTTAAACCCAAGTTGACAGTGCCCTCTCAAAACTTTTCATAA
8381 TGAAAGGTGTGAACTTGCAATGTC 6904
      G- ACTT A   CTC GTCTT
TTATGAAAGGT TGA   GCA TGTC  CT    A
||||||||||| |||   ||| ||||  ||
AATACTTTTCA ACT   CGT ACAG  GA    A
         AA CTCC G   TT- ACCCA
GAM526
TTATGAAAGGTGTGAACTTGCAATGTCCTCCTGTCTTAAACCCAAGTTGACAGTGCCCTCTCAAAACTTTTCATAA
8382 TGAAAGGTGTGAACTTGCAATGTC 6904
      G- ACTT A   CTC GTCTT
TTATGAAAGGT TGA   GCA TGTC  CT    A
||||||||||| |||   ||| ||||  ||
AATACTTTTCA ACT   CGT ACAG  GA    A
         AA CTCC G   TT- ACCCA
GAM526
TTATGAAAGGTGTGAACTTGCAATGTCCTCCTGTCTTAAACCCAAGTTGACAGTGCCCTCTCAAAACTTTTCATAA
8383 TGAAAGGTGTGAACTTGCAATGTC 6904
      G- ACTT A   CTC GTCTT
TTATGAAAGGT TGA   GCA TGTC  CT    A
||||||||||| |||   ||| ||||  ||
AATACTTTTCA ACT   CGT ACAG  GA    A
         AA CTCC G   TT- ACCCA
GAM526
TTATGAAAGGTGTGAACTTGCAATGTCCTCCTGTCTTAAACCCAAGTTGACAGTGCCCTCTCAAAACTTTTCATAA
8384 TGAAAGGTGTGAACTTGCAATGTC 6904
      G- ACTT A   CTC GTCTT
TTATGAAAGGT TGA   GCA TGTC  CT    A
||||||||||| |||   ||| ||||  ||
AATACTTTTCA ACT   CGT ACAG  GA    A
         AA CTCC G   TT- ACCCA
GAM526
TTATGAAAGGTGTGAACTTGCAATGTCCTCCTGTCTTAAACCCAAGTTGACAGTGCCCTCTCAAAACTTTTCATAA
8385 TGAAAGGTGTGAACTTGCAATGTC 6904
      G- ACTT A   CTC GTCTT
TTATGAAAGGT TGA   GCA TGTC  CT    A
||||||||||| |||   ||| ||||  ||
AATACTTTTCA ACT   CGT ACAG  GA    A
         AA CTCC G   TT- ACCCA
GAM526
TTATGAAAGGTGTGAACTTGCAATGTCCTCCTGTCTTAAACCCAAGTTGACAGTGCCCTCTCAAAACTTTTCATAA
8386 TGAAAGGTGTGAACTTGCAATGTC 6904
      G- ACTT A   CTC GTCTT
```

```
TTATGAAAGGT TGA  GCA TGTC  CT    A
||||||||||| |||   ||| |||| ||
AATACTTTTCA ACT   CGT ACAG  GA    A
         AA  CTCC  G   TT- ACCCA
GAM526
TTATGAAAGGTGTGAACTTGCAATGTCCTCCTGTCTTAAACCCAAGTTGACAGTGCCCTCTCAAAACTTTTCATAA
8387 TGAAAGGTGTGAACTTGCAATGTC 6904
      G- ACTT  A  CTC GTCTT
TTATGAAAGGT TGA  GCA TGTC  CT    A
||||||||||| |||   ||| |||| ||
AATACTTTTCA ACT   CGT ACAG  GA    A
         AA  CTCC  G   TT- ACCCA
GAM526
TTATGAAAGGTGTGAACTTGCAATGTCCTCCTGTCTTAAACCCAAGTTGACAGTGCCCTCTCAAAACTTTTCATAA
8388 TGAAAGGTGTGAACTTGCAATGTC 6904
      G- ACTT  A  CTC GTCTT
TTATGAAAGGT TGA  GCA TGTC  CT    A
||||||||||| |||   ||| |||| ||
AATACTTTTCA ACT   CGT ACAG  GA    A
         AA  CTCC  G   TT- ACCCA
GAM526
TTATGAAAGGTGTGAACTTGCAATGTCCTCCTGTCTTAAACCCAAGTTGACAGTGCCCTCTCAAAACTTTTCATAA
8389 TGAAAGGTGTGAACTTGCAATGTC 6904
      G- ACTT  A  CTC GTCTT
TTATGAAAGGT TGA  GCA TGTC  CT    A
||||||||||| |||   ||| |||| ||
AATACTTTTCA ACT   CGT ACAG  GA    A
         AA  CTCC  G   TT- ACCCA
GAM527
TTATGAAGACATACTGGATGGCAGTGGGTACTTCGATGTGAGGGACAAGGAGGACCAGTGGATCCGGATCTTCA
TGG 8390 ATACTGGATGGCAGTGGGTACTTC 8391
      CATA   GG G  GTA  GA GA
TTATGAAGA  CTGGAT CA TGG  CTTC TGT  G
|||||||||   ||||| || |||   |||| |||
GGTACTTCT  GGCCTA GT ACC   GAGG ACA  /
      A---   G- G AG-  A-  GG
GAM528 TTCGGGCTGTGCAAGGAGGGGATCAAGGACGGTGCCACCATGAAGACCTTTTGCGGCACACCTGAG
8394 TGAAGACCTTTTGCGGCACACCTG 8395
    C  AA-   GA- A ACGG
TTCGGG TGTGC  GGAGGG  TCA GG   T
|||||| |||||   |||||| ||| ||
GAGTCC ACACG  TTTTCC  AGT CC   /
    -  GCG    AGA  A ACCG
GAM529 TTCTGTGGAGAGAGGTCTAATATAATATGTAGTATTTTATGTAAGGCACTGTTATACAGAA 8403
TGTAAGGCACTGTTATACAGAA 8404
   GA G - A   TATGT
TTCTGTG GA AG GTCT ATATAA   A
||||||| || || |||| ||||||
AAGACAT TT TC CGGA TGTATT   /
   A- G A  A    TTATG
```

```
GAM530 TTCTTTGGCATTTATTCACTAGATCTCTAAACAGGAGATCACTGTTTCGTATGCTCTAGAG 8432
TCACTGTTTCGTATGCTCTAGAG 8433
    TT   TTATTC TA-    AA
TTCT GGCAT    AC  GATCTCT A
IIII IIIII    II  IIIIIII
GAGA TCGTA    TG  CTAGAGG /
    TC   TGCTT- TCA    AC
GAM531 TTGACATTGTAGGCTGGCGCTGGCATCAGGTTCACACTCATGTTCATGCCCTCTTGCATCGTTAA 8440
CATTGTAGGCTGGCGCTGGCATCA 8441
     AT   CT CT   C GTT
TTGAC TGTAGG GGCG GGCAT AG  C
IIIII IIIIII IIII IIIII II
AATTG ACGTTC CCGT TTGTA TC  /
     CT   TC AC   C ACA
GAM532 TTGACATTGTAGGCTGGCGCTGGCATCAGGTTCACACTCATGTTCATGCCTCTTTGCATCGTTAA 8449
CATTGTAGGCTGGCGCTGGCATCA 8441
     AT   CT CT   C GTT
TTGAC TGTAGG GGCG GGCAT AG  C
IIIII IIIIII IIII IIIII II
AATTG ACGTTT CCGT TTGTA TC  /
     CT   CT AC   C ACA
GAM532 TTGACATTGTAGGCTGGCGCTGGCATCAGGTTCACACTCATGTTCATGCCTCTTTGCATCGTTAA 8451
CATTGTAGGCTGGCGCTGGCATCA 8441
     AT   CT CT   C GTT
TTGAC TGTAGG GGCG GGCAT AG  C
IIIII IIIIII IIII IIIII II
AATTG ACGTTT CCGT TTGTA TC  /
     CT   CT AC   C ACA
GAM532 TTGACATTGTAGGCTGGCGCTGGCATCAGGTTCACACTCATGTTCATGCCTCTTTGCATCGTTAA 8452
CATTGTAGGCTGGCGCTGGCATCA 8441
     AT   CT CT   C GTT
TTGAC TGTAGG GGCG GGCAT AG  C
IIIII IIIIII IIII IIIII II
AATTG ACGTTT CCGT TTGTA TC  /
     CT   CT AC   C ACA
GAM532 TTGACATTGTAGGCTGGCGCTGGCATCAGGTTCACACTCATGTTCATGCCTCTTTGCATCGTTAA 8453
CATTGTAGGCTGGCGCTGGCATCA 8441
     AT   CT CT   C GTT
TTGAC TGTAGG GGCG GGCAT AG  C
IIIII IIIIII IIII IIIII II
AATTG ACGTTT CCGT TTGTA TC  /
     CT   CT AC   C ACA
GAM532 TTGACATTGTAGGCTGGCGCTGGCATCAGGTTCACACTCATGTTCATGCCTCTTTGCATCGTTAA 8454
CATTGTAGGCTGGCGCTGGCATCA 8441
     AT   CT CT   C GTT
TTGAC TGTAGG GGCG GGCAT AG  C
IIIII IIIIII IIII IIIII II
AATTG ACGTTT CCGT TTGTA TC  /
     CT   CT AC   C ACA
GAM532 TTGACATTGTAGGCTGGCGCTGGCATCAGGTTCACACTCATGTTCATGCCTCTTTGCATCGTTAA 8455
CATTGTAGGCTGGCGCTGGCATCA 8441
```

```
    AT    CT   CT    C GTT
TTGAC TGTAGG GGCG GGCAT AG  C
||||| |||||| |||| |||||| ||
AATTG ACGTTT CCGT TTGTA TC  /
    CT    CT  AC    C ACA
GAM532 TTGACATTGTAGGCTGGCGCTGGCATCAGGTTCACACTCATGTTCATGCCTCTTTGCATCGTTAA 8456
CATTGTAGGCTGGCGCTGGCATCA 8441
    AT    CT   CT    C GTT
TTGAC TGTAGG GGCG GGCAT AG  C
||||| |||||| |||| |||||| ||
AATTG ACGTTT CCGT TTGTA TC  /
    CT    CT  AC    C ACA
GAM532 TTGACATTGTAGGCTGGCGCTGGCATCAGGTTCACACTCATGTTCATGCCTCTTTGCATCGTTAA 8457
CATTGTAGGCTGGCGCTGGCATCA 8441
    AT    CT   CT    C GTT
TTGAC TGTAGG GGCG GGCAT AG  C
||||| |||||| |||| |||||| ||
AATTG ACGTTT CCGT TTGTA TC  /
    CT    CT  AC    C ACA
GAM532 TTGACATTGTAGGCTGGCGCTGGCATCAGGTTCACACTCATGTTCATGCCTCTTTGCATCGTTAA 8458
CATTGTAGGCTGGCGCTGGCATCA 8441
    AT    CT   CT    C GTT
TTGAC TGTAGG GGCG GGCAT AG  C
||||| |||||| |||| |||||| ||
AATTG ACGTTT CCGT TTGTA TC  /
    CT    CT  AC    C ACA
GAM532 TTGACATTGTAGGCTGGCGCTGGCATCAGGTTCACACTCATGTTCATGCCTCTTTGCATCGTTAA 8459
CATTGTAGGCTGGCGCTGGCATCA 8441
    AT    CT   CT    C GTT
TTGAC TGTAGG GGCG GGCAT AG  C
||||| |||||| |||| |||||| ||
AATTG ACGTTT CCGT TTGTA TC  /
    CT    CT  AC    C ACA
GAM532 TTGACATTGTAGGCTGGCGCTGGCATCAGGTTCACACTCATGTTCATGCCTCTTTGCATCGTTAA 8460
CATTGTAGGCTGGCGCTGGCATCA 8441
    AT    CT   CT    C GTT
TTGAC TGTAGG GGCG GGCAT AG  C
||||| |||||| |||| |||||| ||
AATTG ACGTTT CCGT TTGTA TC  /
    CT    CT  AC    C ACA
GAM532 TTGACATTGTAGGCTGGCGCTGGCATCAGGTTCACACTCATGTTCATGCCTCTTTGCATCGTTAA 8461
CATTGTAGGCTGGCGCTGGCATCA 8441
    AT    CT   CT    C GTT
TTGAC TGTAGG GGCG GGCAT AG  C
||||| |||||| |||| |||||| ||
AATTG ACGTTT CCGT TTGTA TC  /
    CT    CT  AC    C ACA
GAM532 TTGACATTGTAGGCTGGCGCTGGCATCAGGTTCACACTCATGTTCATGCCTCTTTGCATCGTTAA 8462
CATTGTAGGCTGGCGCTGGCATCA 8441
    AT    CT   CT    C GTT
```

```
TTGAC TGTAGG GGCG GGCAT AG  C
||||| |||||| |||| ||||| ||
AATTG ACGTTT CCGT TTGTA TC  /
    CT    CT  AC   C ACA
GAM532 TTGACATTGTAGGCTGGCGCTGGCATCAGGTTCACACTCATGTTCATGCCTCTTTGCATCGTTAA 8463
CATTGTAGGCTGGCGCTGGCATCA 8441
      AT    CT  CT   C GTT
TTGAC TGTAGG GGCG GGCAT AG  C
||||| |||||| |||| ||||| ||
AATTG ACGTTT CCGT TTGTA TC  /
    CT    CT  AC   C ACA
GAM532 TTGACATTGTAGGCTGGCGCTGGCATCAGGTTCACACTCATGTTCATGCCTCTTTGCATCGTTAA 8465
CATTGTAGGCTGGCGCTGGCATCA 8441
      AT    CT  CT   C GTT
TTGAC TGTAGG GGCG GGCAT AG  C
||||| |||||| |||| ||||| ||
AATTG ACGTTT CCGT TTGTA TC  /
    CT    CT  AC   C ACA
GAM532 TTGACATTGTAGGCTGGCGCTGGCATCAGGTTCACACTCATGTTCATGCCTCTTTGCATCGTTAA 8467
CATTGTAGGCTGGCGCTGGCATCA 8441
      AT    CT  CT   C GTT
TTGAC TGTAGG GGCG GGCAT AG  C
||||| |||||| |||| ||||| ||
AATTG ACGTTT CCGT TTGTA TC  /
    CT    CT  AC   C ACA
GAM532 TTGACATTGTAGGCTGGCGCTGGCATCAGGTTCACACTCATGTTCATGCCTCTTTGCATCGTTAA 8468
CATTGTAGGCTGGCGCTGGCATCA 8441
      AT    CT  CT   C GTT
TTGAC TGTAGG GGCG GGCAT AG  C
||||| |||||| |||| ||||| ||
AATTG ACGTTT CCGT TTGTA TC  /
    CT    CT  AC   C ACA
GAM533 TTGAGATGGGCACGTGGAAGTCAAAGGGTTTCTCTTTTTTTTTTTTTTTTTCCCCTTTTAG 8469
TGAGATGGGCACGTGGAAGTCAAA 8470
     T CACGT   TC   T
TTGAGA GGG   GGAAG AAAGGG T
|||||| |||    |||||  ||||||
GATTTT CCC   TTTTT TTTTCT T
     C TTTTT    TT    C
GAM534
TTGAGTGTTTGATAAGAGTAGCATTAGGTATTAGTGGGAAATGATTGGATTTTTCATTTAAGCATTGTTGGGACAA
CTTGTTAACCATTTGG 8493 TAAGAGTAGCATTAGGTATTAGTG 8494
  TG  T    A- AG T - ATT  GG  GA
T AGTG TTGATAAG GT CA TAG GT  AGTG AAAT T
| |||| |||||||| || || ||| ||  |||| ||||
G TTAC AATTGTTC CA GT GTT CG  TTAC TTTA T
 GT  C    AA GG T  A AAT  TT  GG
GAM535 TTGATGTCATGTGTCAAGTGCTTACTGATTTGATTGATGAAGAAGTAAAAAGTGGCATCAA 8508
TGTCATGTGTCAAGTGCTTACTGA 8509
     GTGTCAAG   A G- TG
```

```
TTGATGTCAT     TGCTT CT ATT  A
|||||||||      ||||| || |||
AACTACGGTG     ATGAA GA  TAG  /
     AAAA----   - AG  TT
GAM536  TTGGATGAGGCCCGCACACATTATGGAGGGCAATTTTCTCTACTGATTAAAAGGTTAATTTCATCCAA
8519 TGAGGCCCGCACACATTATGGAGG 8520
      C--- GCACAC   -     CA
TTGGATGAGG  CC    ATTA TGGAGGG  A
||||||||||  ||    |||| ||||||||
AACCTACTTT  GG    TAGT ATCTCTT  /
      AATT AAAAT-  C    TT
GAM537  TTGTACAGACCTTAGTAAAGTCTTCAATTTAATAAAAATCAAAAAGCCAAAACTAAAAGGTCAAGCAA
8528 TCAAAAAGCCAAAACTAAAAGGTC 8529
   ACA    --  AAAGT  CA--  AA
TTGT GACCT TAGT   CTT  ATTT  T
|||| ||||| ||||   |||  ||||
AACG CTGGA ATCA   GAA  TAAA  /
   AA-   AA  AAACC  AAAC  AA
GAM538
TTGTGTCTTACTAAAGCAGCTTATTGTAGGTGTGGCGTTCTAAAACGTTTCCTGCCTGCGATGGTTCACAAAATAA
ACACAA 8549 AAGCAGCTTATTGTAGGTGTGGCG 8550
     C CTAAAGC  T    GT--   C
TTGTGT TTA    AGCT ATTGTAGGT   GGCGTT T
|||||| |||    |||| |||||||||   ||||||
AACACA AAT    TTGG TAGCGTCCG   TTGCAA A
    - AAAACAC  -     TCCT    A
GAM539  TTGTTTTTTCGGTTGGGCATGCTGCTTACCGCAGGATGATGGAAGCGACGGCCCGTACAAAGACAG
8564 TGGAAGCGACGGCCCGTACAAAGA 8565
     TCG  -  A C   A  - AG
TTGTTTTT  GT TGGGC TG TGCTT CCG C  G
||||||||  || |||| || ||||| ||| |
GACAGAAA  CA GCCCG GC GCGAA GGT G  /
     --- T   - A    - A TA
GAM540
TTTCAATTTGACAATGTCCGGCCCTTGAAATTTCATACCCGGTGGGAAAATTTTAAATGGCCGGGACCTTGGTTGG
TTTGAGA 8567 TGTCCGGCCCTTGAAATTTCATAC 8568
      T TG AATG--    C-     CATA  G
TTTCAA T AC    TCCGGCC TTGAAATTT  CCC G
|||||| | ||    ||||||| |||||||||  |||
AGAGTT G TG    GGGCCGG AATTTTAAA  GGG /
    T GT GTTCCA    TA    A--- T
GAM541  TTTCATTTAAAAAATGGTTTCAGCAAATATGAAAATAGAAAGTCCGTTATTTGTCCATTTGTAATATGAGA
8573 TCATTTAAAAAATGGTTTCAGCAA 8574
     TTAAA    TTTCA    TGAAAATA
TTTCAT  AAATGG   GCAAATA     G
||||||  ||||||   |||||||
AGAGTA  TTTACC   TGTTTAT     A
    TAATG   -----    TGCCTGAA
GAM542
TTTCGGATACTTACATAGTTTTGCGGGAAGCCAGATCGAAGATGTATCCCAGCAAGCACACTAGGCAGGTGGCTG
AGA 8579 CAGCAAGCACACTAGGCAGGTGGC 8580
```

```
   A    ACA   ---    -    A  CAGAT
TTTCGG TACTT  TAGT   TTTGC GGGA GC    C
||||| ||||  ||||  ||||| |||| ||
AGAGTC GTGGA  ATCA  GAACG CCCT TG    G
   G    CGG   CAC    A   A  TAGAA
GAM543 TTTCGGCGCTGGGTCGCCCAAAGCAAAATGGAAACGGATAGAGTGGTGGCTCCCAGAATCCCGAAG
8608 TAGAGTGGTGGCTCCCAGAATCCC 8609
   CG--    TC  C AA  AAAA-- G
TTTCGG   CTGGG GCC A GC    TG A
||||||   ||||| ||| | ||    ||
GAAGCC   GACCC CGG T TG    GC A
   CTAA   T-  -GG AGATAG A
GAM544 TTTCGGCGCTGGGTCGCCCAAAGCAAAATGGAGACGGATAGAGTGGTGGCTCCCAAAATCCCGAAA
8621 TAGAGTGGTGGCTCCCAAAATCCC 8622
   CGC--   TC  C AA  AAAA-- G
TTTCGG    TGGG GCC A GC    TG A
||||||    |||| ||| | ||    ||
AAAGCC    ACCC CGG T TG    GC G
   CTAAA   T-  -GG AGATAG A
GAM545 TTTCGGCGCTGGGTCGCCCAAAGCAGAATGGAGACGGATAGAGTGGTGGCTCCCAAAATCCCGAAG
8639 TAGAGTGGTGGCTCCCAAAATCCC 8622
   CGC--   TC  C AA  AGAA-- G
TTTCGG    TGGG GCC A GC    TG A
||||||    |||| ||| | ||    ||
GAAGCC    ACCC CGG T TG    GC G
   CTAAA   T-  -GG AGATAG A
GAM545 TTTCGGCGCTGGGTCGCCCAAAGCAGAATGGAGACGGATAGAGTGGTGGCTCCCAAAATCCCGAAG
8640 TAGAGTGGTGGCTCCCAAAATCCC 8622
   CGC--   TC  C AA  AGAA-- G
TTTCGG    TGGG GCC A GC    TG A
||||||    |||| ||| | ||    ||
GAAGCC    ACCC CGG T TG    GC G
   CTAAA   T-  -GG AGATAG A
GAM545 TTTCGGCGCTGGGTCGCCCAAAGCAGAATGGAGACGGATAGAGTGGTGGCTCCCAAAATCCCGAAG
8641 TAGAGTGGTGGCTCCCAAAATCCC 8622
   CGC--   TC  C AA  AGAA-- G
TTTCGG    TGGG GCC A GC    TG A
||||||    |||| ||| | ||    ||
GAAGCC    ACCC CGG T TG    GC G
   CTAAA   T-  -GG AGATAG A
GAM545 TTTCGGCGCTGGGTCGCCCAAAGCAGAATGGAGACGGATAGAGTGGTGGCTCCCAAAATCCCGAAG
8642 TAGAGTGGTGGCTCCCAAAATCCC 8622
   CGC--   TC  C AA  AGAA-- G
TTTCGG    TGGG GCC A GC    TG A
||||||    |||| ||| | ||    ||
GAAGCC    ACCC CGG T TG    GC G
   CTAAA   T-  -GG AGATAG A
GAM545 TTTCGGCGCTGGGTCGCCCAAAGCAGAATGGAGACGGATAGAGTGGTGGCTCCCAAAATCCCGAAG
8643 TAGAGTGGTGGCTCCCAAAATCCC 8622
   CGC--   TC  C AA  AGAA-- G
```

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TTTCGG   TGGG GCC A GC    TG A
||||||   |||| ||| | ||     ||
GAAGCC   ACCC CGG T TG    GC G
    CTAAA  T-  - GG AGATAG A
GAM545 TTTCGGCGCTGGGTCGCCCAAAGCAGAATGGAGACGGATAGAGTGGTGGCTCCCAAAATCCCGAAG
8644 TAGAGTGGTGGCTCCCAAAATCCC 8622
    CGC--  TC  C AA AGAA-- G
TTTCGG   TGGG GCC A GC    TG A
||||||   |||| ||| | ||     ||
GAAGCC   ACCC CGG T TG    GC G
    CTAAA  T-  - GG AGATAG A
GAM545 TTTCGGCGCTGGGTCGCCCAAAGCAGAATGGAGACGGATAGAGTGGTGGCTCCCAAAATCCCGAAG
8645 TAGAGTGGTGGCTCCCAAAATCCC 8622
    CGC--  TC  C AA AGAA-- G
TTTCGG   TGGG GCC A GC    TG A
||||||   |||| ||| | ||     ||
GAAGCC   ACCC CGG T TG    GC G
    CTAAA  T-  - GG AGATAG A
GAM545 TTTCGGCGCTGGGTCGCCCAAAGCAGAATGGAGACGGATAGAGTGGTGGCTCCCAAAATCCCGAAG
8646 TAGAGTGGTGGCTCCCAAAATCCC 8622
    CGC--  TC  C AA AGAA-- G
TTTCGG   TGGG GCC A GC    TG A
||||||   |||| ||| | ||     ||
GAAGCC   ACCC CGG T TG    GC G
    CTAAA  T-  - GG AGATAG A
GAM545 TTTCGGCGCTGGGTCGCCCAAAGCAGAATGGAGACGGATAGAGTGGTGGCTCCCAAAATCCCGAAG
8647 TAGAGTGGTGGCTCCCAAAATCCC 8622
    CGC--  TC  C AA AGAA-- G
TTTCGG   TGGG GCC A GC    TG A
||||||   |||| ||| | ||     ||
GAAGCC   ACCC CGG T TG    GC G
    CTAAA  T-  - GG AGATAG A
GAM545 TTTCGGCGCTGGGTCGCCCAAAGCAGAATGGAGACGGATAGAGTGGTGGCTCCCAAAATCCCGAAG
8648 TAGAGTGGTGGCTCCCAAAATCCC 8622
    CGC--  TC  C AA AGAA-- G
TTTCGG   TGGG GCC A GC    TG A
||||||   |||| ||| | ||     ||
GAAGCC   ACCC CGG T TG    GC G
    CTAAA  T-  - GG AGATAG A
GAM545 TTTCGGCGCTGGGTCGCCCAAAGCAGAATGGAGACGGATAGAGTGGTGGCTCCCAAAATCCCGAAG
8649 TAGAGTGGTGGCTCCCAAAATCCC 8622
    CGC--  TC  C AA AGAA-- G
TTTCGG   TGGG GCC A GC    TG A
||||||   |||| ||| | ||     ||
GAAGCC   ACCC CGG T TG    GC G
    CTAAA  T-  - GG AGATAG A
GAM545 TTTCGGCGCTGGGTCGCCCAAAGCAGAATGGAGACGGATAGAGTGGTGGCTCCCAAAATCCCGAAG
8650 TAGAGTGGTGGCTCCCAAAATCCC 8622
    CGC--  TC  C AA AGAA-- G
TTTCGG   TGGG GCC A GC    TG A
```

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||||||   |||| |||| || |   ||
GAAGCC   ACCC CGG T TG    GC G
   CTAAA  T-  - GG  AGATAG  A
GAM545 TTTCGGCGCTGGGTCGCCCAAAGCAGAATGGAGACGGATAGAGTGGTGGCTCCCAAAATCCCGAAG
8651 TAGAGTGGTGGCTCCCAAAATCCC 8622
   CGC--  TC  C AA  AGAA-- G
TTTCGG    TGGG GCC A GC    TG A
||||||   |||| |||| || |   ||
GAAGCC   ACCC CGG T TG    GC G
   CTAAA  T-  - GG  AGATAG  A
GAM545 TTTCGGCGCTGGGTCGCCCAAAGCAGAATGGAGACGGATAGAGTGGTGGCTCCCAAAATCCCGAAG
8652 TAGAGTGGTGGCTCCCAAAATCCC 8622
   CGC--  TC  C AA  AGAA-- G
TTTCGG    TGGG GCC A GC    TG A
||||||   |||| |||| || |   ||
GAAGCC   ACCC CGG T TG    GC G
   CTAAA  T-  - GG  AGATAG  A
GAM545 TTTCGGCGCTGGGTCGCCCAAAGCAGAATGGAGACGGATAGAGTGGTGGCTCCCAAAATCCCGAAG
8653 TAGAGTGGTGGCTCCCAAAATCCC 8622
   CGC--  TC  C AA  AGAA-- G
TTTCGG    TGGG GCC A GC    TG A
||||||   |||| |||| || |   ||
GAAGCC   ACCC CGG T TG    GC G
   CTAAA  T-  - GG  AGATAG  A
GAM545 TTTCGGCGCTGGGTCGCCCAAAGCAGAATGGAGACGGATAGAGTGGTGGCTCCCAAAATCCCGAAG
8654 TAGAGTGGTGGCTCCCAAAATCCC 8622
   CGC--  TC  C AA  AGAA-- G
TTTCGG    TGGG GCC A GC    TG A
||||||   |||| |||| || |   ||
GAAGCC   ACCC CGG T TG    GC G
   CTAAA  T-  - GG  AGATAG  A
GAM545 TTTCGGCGCTGGGTCGCCCAAAGCAGAATGGAGACGGATAGAGTGGTGGCTCCCAAAATCCCGAAG
8655 TAGAGTGGTGGCTCCCAAAATCCC 8622
   CGC--  TC  C AA  AGAA-- G
TTTCGG    TGGG GCC A GC    TG A
||||||   |||| |||| || |   ||
GAAGCC   ACCC CGG T TG    GC G
   CTAAA  T-  - GG  AGATAG  A
GAM545 TTTCGGCGCTGGGTCGCCCAAAGCAGAATGGAGACGGATAGAGTGGTGGCTCCCAAAATCCCGAAG
8656 TAGAGTGGTGGCTCCCAAAATCCC 8622
   CGC--  TC  C AA  AGAA-- G
TTTCGG    TGGG GCC A GC    TG A
||||||   |||| |||| || |   ||
GAAGCC   ACCC CGG T TG    GC G
   CTAAA  T-  - GG  AGATAG  A
GAM545 TTTCGGCGCTGGGTCGCCCAAAGCAGAATGGAGACGGATAGAGTGGTGGCTCCCAAAATCCCGAAG
8657 TAGAGTGGTGGCTCCCAAAATCCC 8622
   CGC--  TC  C AA  AGAA-- G
TTTCGG    TGGG GCC A GC    TG A
||||||   |||| |||| || |   ||
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GAAGCC   ACCC CGG T TG    GC G
   CTAAA   T- -GG AGATAG A
GAM545 TTTCGGCGCTGGGTCGCCCAAAGCAGAATGGAGACGGATAGAGTGGTGGCTCCCAAAATCCCGAAG
8658 TAGAGTGGTGGCTCCCAAAATCCC 8622
   CGC-- TC  C AA AGAA-- G
TTTCGG   TGGG GCC A GC    TG A
||||||   |||| |||| || |   ||
GAAGCC   ACCC CGG T TG    GC G
   CTAAA   T- -GG AGATAG A
GAM545 TTTCGGCGCTGGGTCGCCCAAAGCAGAATGGAGACGGATAGAGTGGTGGCTCCCAAAATCCCGAAG
8659 TAGAGTGGTGGCTCCCAAAATCCC 8622
   CGC-- TC  C AA AGAA-- G
TTTCGG   TGGG GCC A GC    TG A
||||||   |||| |||| || |   ||
GAAGCC   ACCC CGG T TG    GC G
   CTAAA   T- -GG AGATAG A
GAM545 TTTCGGCGCTGGGTCGCCCAAAGCAGAATGGAGACGGATAGAGTGGTGGCTCCCAAAATCCCGAAG
8660 TAGAGTGGTGGCTCCCAAAATCCC 8622
   CGC-- TC  C AA AGAA-- G
TTTCGG   TGGG GCC A GC    TG A
||||||   |||| |||| || |   ||
GAAGCC   ACCC CGG T TG    GC G
   CTAAA   T- -GG AGATAG A
GAM545 TTTCGGCGCTGGGTCGCCCAAAGCAGAATGGAGACGGATAGAGTGGTGGCTCCCAAAATCCCGAAG
8661 TAGAGTGGTGGCTCCCAAAATCCC 8622
   CGC-- TC  C AA AGAA-- G
TTTCGG   TGGG GCC A GC    TG A
||||||   |||| |||| || |   ||
GAAGCC   ACCC CGG T TG    GC G
   CTAAA   T- -GG AGATAG A
GAM545 TTTCGGCGCTGGGTCGCCCAAAGCAGAATGGAGACGGATAGAGTGGTGGCTCCCAAAATCCCGAAG
8662 TAGAGTGGTGGCTCCCAAAATCCC 8622
   CGC-- TC  C AA AGAA-- G
TTTCGG   TGGG GCC A GC    TG A
||||||   |||| |||| || |   ||
GAAGCC   ACCC CGG T TG    GC G
   CTAAA   T- -GG AGATAG A
GAM545 TTTCGGCGCTGGGTCGCCCAAAGCAGAATGGAGACGGATAGAGTGGTGGCTCCCAAAATCCCGAAG
8663 TAGAGTGGTGGCTCCCAAAATCCC 8622
   CGC-- TC  C AA AGAA-- G
TTTCGG   TGGG GCC A GC    TG A
||||||   |||| |||| || |   ||
GAAGCC   ACCC CGG T TG    GC G
   CTAAA   T- -GG AGATAG A
GAM545 TTTCGGCGCTGGGTCGCCCAAAGCAGAATGGAGACGGATAGAGTGGTGGCTCCCAAAATCCCGAAG
8664 TAGAGTGGTGGCTCCCAAAATCCC 8622
   CGC-- TC  C AA AGAA-- G
TTTCGG   TGGG GCC A GC    TG A
||||||   |||| |||| || |   ||
GAAGCC   ACCC CGG T TG    GC G
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   CTAAA   T-  -GG AGATAG  A
GAM545 TTTCGGCGCTGGGTCGCCCAAAGCAGAATGGAGACGGATAGAGTGGTGGCTCCCAAAATCCCGAAG
8665 TAGAGTGGTGGCTCCCAAAATCCC 8622
   CGC--  TC  C AA AGAA-- G
TTTCGG   TGGG GCC A GC   TG A
||||||   |||| |||| || ||   ||
GAAGCC   ACCC CGG T TG   GC G
   CTAAA   T-  -GG AGATAG  A
GAM545 TTTCGGCGCTGGGTCGCCCAAAGCAGAATGGAGACGGATAGAGTGGTGGCTCCCAAAATCCCGAAG
8666 TAGAGTGGTGGCTCCCAAAATCCC 8622
   CGC--  TC  C AA AGAA-- G
TTTCGG   TGGG GCC A GC   TG A
||||||   |||| |||| || ||   ||
GAAGCC   ACCC CGG T TG   GC G
   CTAAA   T-  -GG AGATAG  A
GAM545 TTTCGGCGCTGGGTCGCCCAAAGCAGAATGGAGACGGATAGAGTGGTGGCTCCCAAAATCCCGAAG
8667 TAGAGTGGTGGCTCCCAAAATCCC 8622
   CGC--  TC  C AA AGAA-- G
TTTCGG   TGGG GCC A GC   TG A
||||||   |||| |||| || ||   ||
GAAGCC   ACCC CGG T TG   GC G
   CTAAA   T-  -GG AGATAG  A
GAM545 TTTCGGCGCTGGGTCGCCCAAAGCAGAATGGAGACGGATAGAGTGGTGGCTCCCAAAATCCCGAAG
8668 TAGAGTGGTGGCTCCCAAAATCCC 8622
   CGC--  TC  C AA AGAA-- G
TTTCGG   TGGG GCC A GC   TG A
||||||   |||| |||| || ||   ||
GAAGCC   ACCC CGG T TG   GC G
   CTAAA   T-  -GG AGATAG  A
GAM545 TTTCGGCGCTGGGTCGCCCAAAGCAGAATGGAGACGGATAGAGTGGTGGCTCCCAAAATCCCGAAG
8669 TAGAGTGGTGGCTCCCAAAATCCC 8622
   CGC--  TC  C AA AGAA-- G
TTTCGG   TGGG GCC A GC   TG A
||||||   |||| |||| || ||   ||
GAAGCC   ACCC CGG T TG   GC G
   CTAAA   T-  -GG AGATAG  A
GAM546 TTTCGGCGCTGGGTCGCCCAAAGCAGAATGGAGACGGATAGAGTGGTGGCTCCCAGAATCCCGAAG
8670 TAGAGTGGTGGCTCCCAGAATCCC 8609
   CG--   TC  C AA AGAA-- G
TTTCGG  CTGGG GCC A GC   TG A
||||||  ||||| |||| || ||   ||
GAAGCC  GACCC CGG T TG   GC G
   CTAA   T-  -GG AGATAG  A
GAM546 TTTCGGCGCTGGGTCGCCCAAAGCAGAATGGAGACGGATAGAGTGGTGGCTCCCAGAATCCCGAAG
8671 TAGAGTGGTGGCTCCCAGAATCCC 8609
   CG--   TC  C AA AGAA-- G
TTTCGG  CTGGG GCC A GC   TG A
||||||  ||||| |||| || ||   ||
GAAGCC  GACCC CGG T TG   GC G
   CTAA   T-  -GG AGATAG  A
```

```
GAM546 TTTCGGCGCTGGGTCGCCCAAAGCAGAATGGAGACGGATAGAGTGGTGGCTCCCAGAATCCCGAAG
8672 TAGAGTGGTGGCTCCCAGAATCCC 8609
     CG--    TC  C AA AGAA-- G
TTTCGG   CTGGG GCC A GC    TG A
||||||   ||||| ||| | ||    ||
GAAGCC   GACCC CGG T TG    GC G
    CTAA   T-  -GG AGATAG A
GAM546 TTTCGGCGCTGGGTCGCCCAAAGCAGAATGGAGACGGATAGAGTGGTGGCTCCCAGAATCCCGAAG
8673 TAGAGTGGTGGCTCCCAGAATCCC 8609
     CG--    TC  C AA AGAA-- G
TTTCGG   CTGGG GCC A GC    TG A
||||||   ||||| ||| | ||    ||
GAAGCC   GACCC CGG T TG    GC G
    CTAA   T-  -GG AGATAG A
GAM546 TTTCGGCGCTGGGTCGCCCAAAGCAGAATGGAGACGGATAGAGTGGTGGCTCCCAGAATCCCGAAG
8674 TAGAGTGGTGGCTCCCAGAATCCC 8609
     CG--    TC  C AA AGAA-- G
TTTCGG   CTGGG GCC A GC    TG A
||||||   ||||| ||| | ||    ||
GAAGCC   GACCC CGG T TG    GC G
    CTAA   T-  -GG AGATAG A
GAM546 TTTCGGCGCTGGGTCGCCCAAAGCAGAATGGAGACGGATAGAGTGGTGGCTCCCAGAATCCCGAAG
8676 TAGAGTGGTGGCTCCCAGAATCCC 8609
     CG--    TC  C AA AGAA-- G
TTTCGG   CTGGG GCC A GC    TG A
||||||   ||||| ||| | ||    ||
GAAGCC   GACCC CGG T TG    GC G
    CTAA   T-  -GG AGATAG A
GAM546 TTTCGGCGCTGGGTCGCCCAAAGCAGAATGGAGACGGATAGAGTGGTGGCTCCCAGAATCCCGAAG
8677 TAGAGTGGTGGCTCCCAGAATCCC 8609
     CG--    TC  C AA AGAA-- G
TTTCGG   CTGGG GCC A GC    TG A
||||||   ||||| ||| | ||    ||
GAAGCC   GACCC CGG T TG    GC G
    CTAA   T-  -GG AGATAG A
GAM546 TTTCGGCGCTGGGTCGCCCAAAGCAGAATGGAGACGGATAGAGTGGTGGCTCCCAGAATCCCGAAG
8678 TAGAGTGGTGGCTCCCAGAATCCC 8609
     CG--    TC  C AA AGAA-- G
TTTCGG   CTGGG GCC A GC    TG A
||||||   ||||| ||| | ||    ||
GAAGCC   GACCC CGG T TG    GC G
    CTAA   T-  -GG AGATAG A
GAM546 TTTCGGCGCTGGGTCGCCCAAAGCAGAATGGAGACGGATAGAGTGGTGGCTCCCAGAATCCCGAAG
8679 TAGAGTGGTGGCTCCCAGAATCCC 8609
     CG--    TC  C AA AGAA-- G
TTTCGG   CTGGG GCC A GC    TG A
||||||   ||||| ||| | ||    ||
GAAGCC   GACCC CGG T TG    GC G
    CTAA   T-  -GG AGATAG A
GAM546 TTTCGGCGCTGGGTCGCCCAAAGCAGAATGGAGACGGATAGAGTGGTGGCTCCCAGAATCCCGAAG
8680 TAGAGTGGTGGCTCCCAGAATCCC 8609
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```
   CG--   TC  C AA AGAA-- G
TTTCGG   CTGGG GCC A GC    TG A
||||||   ||||| ||| | ||    ||
GAAGCC   GACCC CGG T TG    GC G
   CTAA   T- -GG AGATAG A
GAM546 TTTCGGCGCTGGGTCGCCCAAAGCAGAATGGAGACGGATAGAGTGGTGGCTCCCAGAATCCCGAAG
8681 TAGAGTGGTGGCTCCCAGAATCCC 8609
   CG--   TC  C AA AGAA-- G
TTTCGG   CTGGG GCC A GC    TG A
||||||   ||||| ||| | ||    ||
GAAGCC   GACCC CGG T TG    GC G
   CTAA   T- -GG AGATAG A
GAM546 TTTCGGCGCTGGGTCGCCCAAAGCAGAATGGAGACGGATAGAGTGGTGGCTCCCAGAATCCCGAAG
8682 TAGAGTGGTGGCTCCCAGAATCCC 8609
   CG--   TC  C AA AGAA-- G
TTTCGG   CTGGG GCC A GC    TG A
||||||   ||||| ||| | ||    ||
GAAGCC   GACCC CGG T TG    GC G
   CTAA   T- -GG AGATAG A
GAM546 TTTCGGCGCTGGGTCGCCCAAAGCAGAATGGAGACGGATAGAGTGGTGGCTCCCAGAATCCCGAAG
8683 TAGAGTGGTGGCTCCCAGAATCCC 8609
   CG--   TC  C AA AGAA-- G
TTTCGG   CTGGG GCC A GC    TG A
||||||   ||||| ||| | ||    ||
GAAGCC   GACCC CGG T TG    GC G
   CTAA   T- -GG AGATAG A
GAM546 TTTCGGCGCTGGGTCGCCCAAAGCAGAATGGAGACGGATAGAGTGGTGGCTCCCAGAATCCCGAAG
8684 TAGAGTGGTGGCTCCCAGAATCCC 8609
   CG--   TC  C AA AGAA-- G
TTTCGG   CTGGG GCC A GC    TG A
||||||   ||||| ||| | ||    ||
GAAGCC   GACCC CGG T TG    GC G
   CTAA   T- -GG AGATAG A
GAM546 TTTCGGCGCTGGGTCGCCCAAAGCAGAATGGAGACGGATAGAGTGGTGGCTCCCAGAATCCCGAAG
8685 TAGAGTGGTGGCTCCCAGAATCCC 8609
   CG--   TC  C AA AGAA-- G
TTTCGG   CTGGG GCC A GC    TG A
||||||   ||||| ||| | ||    ||
GAAGCC   GACCC CGG T TG    GC G
   CTAA   T- -GG AGATAG A
GAM546 TTTCGGCGCTGGGTCGCCCAAAGCAGAATGGAGACGGATAGAGTGGTGGCTCCCAGAATCCCGAAG
8686 TAGAGTGGTGGCTCCCAGAATCCC 8609
   CG--   TC  C AA AGAA-- G
TTTCGG   CTGGG GCC A GC    TG A
||||||   ||||| ||| | ||    ||
GAAGCC   GACCC CGG T TG    GC G
   CTAA   T- -GG AGATAG A
GAM546 TTTCGGCGCTGGGTCGCCCAAAGCAGAATGGAGACGGATAGAGTGGTGGCTCCCAGAATCCCGAAG
8687 TAGAGTGGTGGCTCCCAGAATCCC 8609
   CG--   TC  C AA AGAA-- G
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TTTCGG   CTGGG GCC A GC    TG A
||||||   ||||| ||| | ||    ||
GAAGCC   GACCC CGG T TG    GC G
    CTAA    T- - GG AGATAG A
GAM546 TTTCGGCGCTGGGTCGCCCAAAGCAGAATGGAGACGGATAGAGTGGTGGCTCCCAGAATCCCGAAG
8689 TAGAGTGGTGGCTCCCAGAATCCC 8609
    CG--   TC  C AA AGAA-- G
TTTCGG   CTGGG GCC A GC    TG A
||||||   ||||| ||| | ||    ||
GAAGCC   GACCC CGG T TG    GC G
    CTAA    T- - GG AGATAG A
GAM546 TTTCGGCGCTGGGTCGCCCAAAGCAGAATGGAGACGGATAGAGTGGTGGCTCCCAGAATCCCGAAG
8690 TAGAGTGGTGGCTCCCAGAATCCC 8609
    CG--   TC  C AA AGAA-- G
TTTCGG   CTGGG GCC A GC    TG A
||||||   ||||| ||| | ||    ||
GAAGCC   GACCC CGG T TG    GC G
    CTAA    T- - GG AGATAG A
GAM546 TTTCGGCGCTGGGTCGCCCAAAGCAGAATGGAGACGGATAGAGTGGTGGCTCCCAGAATCCCGAAG
8691 TAGAGTGGTGGCTCCCAGAATCCC 8609
    CG--   TC  C AA AGAA-- G
TTTCGG   CTGGG GCC A GC    TG A
||||||   ||||| ||| | ||    ||
GAAGCC   GACCC CGG T TG    GC G
    CTAA    T- - GG AGATAG A
GAM546 TTTCGGCGCTGGGTCGCCCAAAGCAGAATGGAGACGGATAGAGTGGTGGCTCCCAGAATCCCGAAG
8692 TAGAGTGGTGGCTCCCAGAATCCC 8609
    CG--   TC  C AA AGAA-- G
TTTCGG   CTGGG GCC A GC    TG A
||||||   ||||| ||| | ||    ||
GAAGCC   GACCC CGG T TG    GC G
    CTAA    T- - GG AGATAG A
GAM546 TTTCGGCGCTGGGTCGCCCAAAGCAGAATGGAGACGGATAGAGTGGTGGCTCCCAGAATCCCGAAG
8693 TAGAGTGGTGGCTCCCAGAATCCC 8609
    CG--   TC  C AA AGAA-- G
TTTCGG   CTGGG GCC A GC    TG A
||||||   ||||| ||| | ||    ||
GAAGCC   GACCC CGG T TG    GC G
    CTAA    T- - GG AGATAG A
GAM546 TTTCGGCGCTGGGTCGCCCAAAGCAGAATGGAGACGGATAGAGTGGTGGCTCCCAGAATCCCGAAG
8695 TAGAGTGGTGGCTCCCAGAATCCC 8609
    CG--   TC  C AA AGAA-- G
TTTCGG   CTGGG GCC A GC    TG A
||||||   ||||| ||| | ||    ||
GAAGCC   GACCC CGG T TG    GC G
    CTAA    T- - GG AGATAG A
GAM546 TTTCGGCGCTGGGTCGCCCAAAGCAGAATGGAGACGGATAGAGTGGTGGCTCCCAGAATCCCGAAG
8696 TAGAGTGGTGGCTCCCAGAATCCC 8609
    CG--   TC  C AA AGAA-- G
TTTCGG   CTGGG GCC A GC    TG A
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||||||   |||||  |||| ||    ||
GAAGCC  GACCC CGG T TG    GC G
    CTAA   T- -GG AGATAG A
GAM546 TTTCGGCGCTGGGTCGCCCAAAGCAGAATGGAGACGGATAGAGTGGTGGCTCCCAGAATCCCGAAG
8697 TAGAGTGGTGGCTCCCAGAATCCC 8609
    CG--   TC  C AA AGAA-- G
TTTCGG  CTGGG GCC A GC    TG A
||||||   |||||  |||| ||    ||
GAAGCC  GACCC CGG T TG    GC G
    CTAA   T- -GG AGATAG A
GAM546 TTTCGGCGCTGGGTCGCCCAAAGCAGAATGGAGACGGATAGAGTGGTGGCTCCCAGAATCCCGAAG
8698 TAGAGTGGTGGCTCCCAGAATCCC 8609
    CG--   TC  C AA AGAA-- G
TTTCGG  CTGGG GCC A GC    TG A
||||||   |||||  |||| ||    ||
GAAGCC  GACCC CGG T TG    GC G
    CTAA   T- -GG AGATAG A
GAM546 TTTCGGCGCTGGGTCGCCCAAAGCAGAATGGAGACGGATAGAGTGGTGGCTCCCAGAATCCCGAAG
8699 TAGAGTGGTGGCTCCCAGAATCCC 8609
    CG--   TC  C AA AGAA-- G
TTTCGG  CTGGG GCC A GC    TG A
||||||   |||||  |||| ||    ||
GAAGCC  GACCC CGG T TG    GC G
    CTAA   T- -GG AGATAG A
GAM546 TTTCGGCGCTGGGTCGCCCAAAGCAGAATGGAGACGGATAGAGTGGTGGCTCCCAGAATCCCGAAG
8700 TAGAGTGGTGGCTCCCAGAATCCC 8609
    CG--   TC  C AA AGAA-- G
TTTCGG  CTGGG GCC A GC    TG A
||||||   |||||  |||| ||    ||
GAAGCC  GACCC CGG T TG    GC G
    CTAA   T- -GG AGATAG A
GAM546 TTTCGGCGCTGGGTCGCCCAAAGCAGAATGGAGACGGATAGAGTGGTGGCTCCCAGAATCCCGAAG
8701 TAGAGTGGTGGCTCCCAGAATCCC 8609
    CG--   TC  C AA AGAA-- G
TTTCGG  CTGGG GCC A GC    TG A
||||||   |||||  |||| ||    ||
GAAGCC  GACCC CGG T TG    GC G
    CTAA   T- -GG AGATAG A
GAM546 TTTCGGCGCTGGGTCGCCCAAAGCAGAATGGAGACGGATAGAGTGGTGGCTCCCAGAATCCCGAAG
8702 TAGAGTGGTGGCTCCCAGAATCCC 8609
    CG--   TC  C AA AGAA-- G
TTTCGG  CTGGG GCC A GC    TG A
||||||   |||||  |||| ||    ||
GAAGCC  GACCC CGG T TG    GC G
    CTAA   T- -GG AGATAG A
GAM546 TTTCGGCGCTGGGTCGCCCAAAGCAGAATGGAGACGGATAGAGTGGTGGCTCCCAGAATCCCGAAG
8703 TAGAGTGGTGGCTCCCAGAATCCC 8609
    CG--   TC  C AA AGAA-- G
TTTCGG  CTGGG GCC A GC    TG A
||||||   |||||  |||| ||    ||
```

GAAGCC   GACCC CGG T TG    GC G
   CTAA   T- -GG AGATAG A
GAM546 TTTCGGCGCTGGGTCGCCCAAAGCAGAATGGAGACGGATAGAGTGGTGGCTCCCAGAATCCCGAAG
8704 TAGAGTGGTGGCTCCCAGAATCCC 8609
   CG--   TC  C AA AGAA-- G
TTTCGG   CTGGG GCC A GC    TG A
||||||  |||||  ||| | ||    ||
GAAGCC   GACCC CGG T TG    GC G
   CTAA   T- -GG AGATAG A
GAM546 TTTCGGCGCTGGGTCGCCCAAAGCAGAATGGAGACGGATAGAGTGGTGGCTCCCAGAATCCCGAAG
8705 TAGAGTGGTGGCTCCCAGAATCCC 8609
   CG--   TC  C AA AGAA-- G
TTTCGG   CTGGG GCC A GC    TG A
||||||  |||||  ||| | ||    ||
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   CTAA   T- -GG AGATAG A
GAM546 TTTCGGCGCTGGGTCGCCCAAAGCAGAATGGAGACGGATAGAGTGGTGGCTCCCAGAATCCCGAAG
8706 TAGAGTGGTGGCTCCCAGAATCCC 8609
   CG--   TC  C AA AGAA-- G
TTTCGG   CTGGG GCC A GC    TG A
||||||  |||||  ||| | ||    ||
GAAGCC   GACCC CGG T TG    GC G
   CTAA   T- -GG AGATAG A
GAM546 TTTCGGCGCTGGGTCGCCCAAAGCAGAATGGAGACGGATAGAGTGGTGGCTCCCAGAATCCCGAAG
8707 TAGAGTGGTGGCTCCCAGAATCCC 8609
   CG--   TC  C AA AGAA-- G
TTTCGG   CTGGG GCC A GC    TG A
||||||  |||||  ||| | ||    ||
GAAGCC   GACCC CGG T TG    GC G
   CTAA   T- -GG AGATAG A
GAM546 TTTCGGCGCTGGGTCGCCCAAAGCAGAATGGAGACGGATAGAGTGGTGGCTCCCAGAATCCCGAAG
8709 TAGAGTGGTGGCTCCCAGAATCCC 8609
   CG--   TC  C AA AGAA-- G
TTTCGG   CTGGG GCC A GC    TG A
||||||  |||||  ||| | ||    ||
GAAGCC   GACCC CGG T TG    GC G
   CTAA   T- -GG AGATAG A
GAM546 TTTCGGCGCTGGGTCGCCCAAAGCAGAATGGAGACGGATAGAGTGGTGGCTCCCAGAATCCCGAAG
8711 TAGAGTGGTGGCTCCCAGAATCCC 8609
   CG--   TC  C AA AGAA-- G
TTTCGG   CTGGG GCC A GC    TG A
||||||  |||||  ||| | ||    ||
GAAGCC   GACCC CGG T TG    GC G
   CTAA   T- -GG AGATAG A
GAM546 TTTCGGCGCTGGGTCGCCCAAAGCAGAATGGAGACGGATAGAGTGGTGGCTCCCAGAATCCCGAAG
8713 TAGAGTGGTGGCTCCCAGAATCCC 8609
   CG--   TC  C AA AGAA-- G
TTTCGG   CTGGG GCC A GC    TG A
||||||  |||||  ||| | ||    ||
GAAGCC   GACCC CGG T TG    GC G

```
    CTAA    T-  -GG  AGATAG  A
GAM547
TTTGAATGACTTGTAATGATGGCTGCTAAGCATATCCTGTACTGTGGCTATGTCAATTTGCGAATCCTCCTCAAA
8715 TGACTTGTAATGATGGCTGCTAAG 8716
    AT-- C    --  --  TG TAA  TA
TTTGA  GA TTGTAA TGAT GGC C GCA T
|||||  || |||||| |||| ||| | |||
AAACT  CT AGCGTT ACTG TCG G TGT /
   CCTC A    TA   TA  GT TCA  CC
GAM548
TTTGAGATGTACGACCTGGACGGCGACGGGCGCATCACGCGCCTGGAGATGCTGGAGATCATCGAGGCAATCT
ACAAG 8724 TGTACGACCTGGACGGCGACGGGC 8725
   -  - A- CCTGGA-  A---    AT
TTTG AGAT GT CGA    CGGCG  CGGGCGC C
|||| |||| || |||      |||||  |||||||
GAAC TCTA CG GCT     GTCGT  GTCCGCG /
   A  A GA ACTAGAG   AGAG    CA
GAM549  TTTGTTAATGTTTCAAACATACTTTCTTGGTTTTCTAATGGAGTATATAGTTTAGTCATTTCACAGA 8728
GGAGTATATAGTTTAGTCATTTCA 8729
    T-  TTTC  ---    TC   T
TTTGT AATG  AAAC  ATACTT TTGG T
||||| ||||   |||| |||||| ||||
AGACA TTAC  TTTG  TATGAG AATC T
   CT  TGA-  ATA    GT   T
GAM550
TTTTTTTCAGTGAACATGTTTTTATTGAACACCAACTTAATTTCAGGAACATTTCAGGTACATTGTCAGAAA 8744
TTTCAGGAACATTTCAGGTACATT 8745
    TT  A -----    ---   ACA
TTTTT CAGTG AC   ATGTTTTT ATTGA C
||||| |||||| ||   ||||||||| |||||
AAAGA GTTAC TG   TACAAGGA  TAATT C
   CT  A GACTT     CTT   CAA
```

GAM-NAME TARGET-GENE TAREGT-SEQ TARGET-ID TARGET-DRAW

GAM24  A1BG          CACGCCATTGCACTCCAG-CCT    3    AACA    C        CT
                              CGCCA TGCACTCCAGTC
                              ||||| |||||||||||
                              GCGGT ACGTGAGGTCGG
                              _____      A        AC

GAM24  APPL          CACACCACTGCACTCCAG-CCT    4    AACA              CT
                              CGCCACTGCACTCCAGTC
                              ||||||||||||||||||
                              GTGGTGACGTGAGGTCGG
                              _____               AT

GAM24  ATP6V1A1       CACGCCATTGCACTCCAG-CCT    3    AACA    C        CT
                              CGCCA TGCACTCCAGTC
                              ||||| |||||||||||
                              GCGGT ACGTGAGGTCGG
                              _____      A        AC

GAM24  CASP8          CACGCCACTGCACTCCAG-CCT    5    AACA              CT
                              CGCCACTGCACTCCAGTC
                              ||||||||||||||||||
                              GCGGTGACGTGAGGTCGG
                              _____               AC

GAM24  CNN2           CGCCACTGCACTCCAG-CCT    6    AACACGCC          C
                              ACTGCACTCCAGTC
                              ||||||||||||||
                              TGACGTGAGGTCGG
                              _____          A

GAM24  CR1            ACGCCACTGCACTCCAG-CCT    7    AACACG            C
                              CCACTGCACTCCAGTC
                              ||||||||||||||||
                              GGTGACGTGAGGTCGG
                              _____           A

GAM24  CYP1A2         CGCCACTGCACTCCAG-CCT    6    AACACGCC          C
                              ACTGCACTCCAGTC
                              ||||||||||||||
                              TGACGTGAGGTCGG
                              _____          A

GAM24  CYP2B6         CACGCCACTGCACTCCAG-CCT    5    AACA              CT
                              CGCCACTGCACTCCAGTC
                              ||||||||||||||||||
                              GCGGTGACGTGAGGTCGG
                              _____               AC

GAM24  EIF2S3         CACGCCACTGCACTCCAG-CCT    5    AACA              CT
                              CGCCACTGCACTCCAGTC
                              ||||||||||||||||||
                              GCGGTGACGTGAGGTCGG
                              _____               AC

GAM24  EVC            CACGCCACTGCACTCCAG-CCT    5    AACA              CT
                              CGCCACTGCACTCCAGTC
                              ||||||||||||||||||
                              GCGGTGACGTGAGGTCGG

```
                         AC
GAM24  F2RL3      CACGCCACTGCACTCCAG-CCT   5   AACA            CT
                      CGCCACTGCACTCCAGTC
                      |||||||||||||||||
                      GCGGTGACGTGAGGTCGG
                         AC
GAM24  FCAR       GCCACTGCACTCCAG-CCT     8   AACACGCCAC
                      TGCACTCCAGTC
                      ||||||||||||
                      ACGTGAGGTCGG


GAM24  FUT1       CACGCCACTGCACTCCAG-CCT   5   AACA            CT
                      CGCCACTGCACTCCAGTC
                      ||||||||||||||||
                      GCGGTGACGTGAGGTCGG
                         AC
GAM24  LZTS1      CATGCCACTGCACTCCAG-CCT   9   AACAC           CT
                      GCCACTGCACTCCAGTC
                      ||||||||||||||||
                      CGGTGACGTGAGGTCGG
                   A     AC
GAM24  PAICS      CACGCCACTGCACTCCAG-CCT   5   AACA            CT
                      CGCCACTGCACTCCAGTC
                      |||||||||||||||||
                      GCGGTGACGTGAGGTCGG
                         AC
GAM24  PCDHB9     CGCCACTGCACTCCAG-CCT    6   AACACGCC         C
                      ACTGCACTCCAGTC
                      |||||||||||||
                      TGACGTGAGGTCGG
                          A
GAM24  PPP1R12B   CACACCACTGCACTCCAG-CCT   4   AACA            CT
                      CGCCACTGCACTCCAGTC
                      ||||||||||||||||
                      GTGGTGACGTGAGGTCGG
                         AC
GAM24  PSMB2      ACGCCACAGCACTCCAG-CCT    10  AACACG    T     C
                      CCAC GCACTCCAGTC
                      |||| ||||||||||
                      GGTG CGTGAGGTCGG
                          T     A
GAM24  RABL2B     CGCCACTGCACTCCAG-CCT    6   AACACGCC         C
                      ACTGCACTCCAGTC
                      |||||||||||||
                      TGACGTGAGGTCGG
                          A
GAM24  TBXA2R     CGCCACTGCACTCCAG-CCT    6   AACACGCC         C
                      ACTGCACTCCAGTC
                      |||||||||||||
                      TGACGTGAGGTCGG
```

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                          _____          A
GAM24  TERF1      CGCCACTGCACTCCAG-CCT    6   AACACGCC          C
                          ACTGCACTCCAGTC
                          ||||||||||||||
                          TGACGTGAGGTCGG

                          _____          A
GAM24  TERF2      CACGCCACTGCACTCCAG-CCT   5   AACA            CT
                          CGCCACTGCACTCCAGTC
                          ||||||||||||||||||
                          GCGGTGACGTGAGGTCGG

                          _____             AC
GAM24  TMPRSS3      CGCCACTGCACTCCAG-CCT    6   AACACGCC         C
                          ACTGCACTCCAGTC
                          ||||||||||||||
                          TGACGTGAGGTCGG

                          _____          A
GAM24  VHL       CGCCACTGCACTCCAG-CCT      6   AACACGCC         C
                          ACTGCACTCCAGTC
                          ||||||||||||||
                          TGACGTGAGGTCGG

                          _____          A
GAM25  AMACR        ACAGGCAACCCTA-AAACTG    21  TGAACA      ACAAAA
                          GGCAACCT    TGG
                          ||||||||    |||
                          CCGTTGGG    ACT

                          _____           ATTTTG
GAM25  ATRX       AACAGGT----TACAAAATG     18  TGAA   CAACC
                          CAGG    TACAAAAT
                          ||||    ||||||||
                          GTCC    ATGTTTTA

                          ____   A____
GAM25  BMP1       ACAGACACCAT-CAAAATGGG    23  TGAACA   A  TA
                          GGCA CC CAAAATGG
                          |||| || ||||||||
                          CTGT GG GTTTTACC

                          _____   _  TA
GAM25  CBR1      CAGGACAAGGTACAAAATGGG     27  TGAACAG    CC
                          GCAA TACAAAATGGG
                          |||| |||||||||||
                          TGTT ATGTTTTACCC

                          _____      CC
GAM25  COL14A1      TGAACAGGCAA---ACAAAA    34        CCT    TG
                          TGAACAGGCAA ACAAAA
                          |||||||||| ||||||
                          ACTTGTCCGTT TGTTTT

                          ___       II
GAM25  CRKL       AATAGCCACAGCAACAAAATGG  13  TGAACA  A CT__      G
                          GGC AC  ACAAAATGG
                          ||| ||  |||||||||
                          TCG TG  TGTTTTACC
```

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                              A_____   G  TCGT      G
GAM25  FKBP6      AACAGAGAACCCTACAAAAT    14  TGAA   CAA_        G
                          CAGG   CCTACAAAATG
                          ||||   |||||||||||
                          GTCT   GGATGTTTTAT
                          ____   CTTG       G
GAM25  IGF2R      GAACAGGCAAACTCTCCAAAA    28  TG     __  A   GGG
                          AACAGGCAA C CT CAAAAT
                          ||||||||| | || ||||||
                          TTGTCCGTT G GA GTTTTG
                           __      T A  G       |||
GAM25  IKBKAP      GAACAATCATTCTCACAAAATGG  30  TG   G AC _      GI
                          AACAG CA  CT ACAAAATGG
                          ||||| ||  || |||||||||
                          TTGTT GT  GA TGTTTTACC
                           __     A  AA  G       AI
GAM25  ITGB1      AACAGGCAA-ATAGCAAAAT    15  TGAA     CCTA
                          CAGGCAA   CAAAATGG
                          |||||||   |||||||||
                          GTCCGTT   GTTTTATT
                          ____      TATC
GAM25  LIMK1      AGGCAAAGTGACAAAATGG     24  TGAAC_____  CAA

                              AGG   CCTACAAAATGG
                              |||   |||||||||||||
                              TCC   GGATGTTTTACC
                          TTCACTGTTTTACCGGGAGIIIGGGTAAAACA  AAC
GAM25  MEN1      AGGCAACCTAGTCACCATGG    25  TGAACAGGCA   __  AA
                          ACCTA CA  ATGG
                          ||||| ||  ||||
                          TGGAT GT  TACC
                          _____   CA GG
GAM25  MEN1      AAAAGGCAACCTATAAACTGG    19  TGAAC       C  A
                          AGGCAACCTA AAA TGGG
                          |||||||||| ||| ||||
                          TCCGTTGGAT TTT ACCT
                          T____       A  G
GAM25  NPR2L      AAAAAGCAAAATACAAAATG    16  TGAAC   CC      G
                          AGGCAA TACAAAATG
                          |||||| ||||||||||
                          TTCGTT ATGTTTTAC
                          T____   TT      A
GAM25  PLAG1      AACTGGC--CCTACAAAAAGG    20  TGAACA AA       T
                          GGC  CCTACAAAA GG
                          |||  |||||||||| ||
                          CCG  GGATGTTTT CC
                          GA____  __       T
GAM25  PPP2R2B     GAGCGGGCAGCCGCGACAAAATGG  29  TGAACA  A T__      GI
                          GGCA CC  ACAAAATGG
                          |||| ||  |||||||||
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                         CCGT GG  TGTTTTACC
                    TCGC__    C CGC      AI
GAM25 RAD1      ACATGCCCTCTACAAAATGG    22 TGAACAG AAC
                      GC  CTACAAAATGG
                      II  IIIIIIIIIII
                      CG  GATGTTTTACC
                    A_____    GGA
GAM25 RRM2B      AAAAGGAAATGTACAAAATG    17 TGAAC C CC
                     AGG AA TACAAAATGG
                     III II IIIIIIIIII
                     TCC TT ATGTTTTACT
                    T____   T AC
GAM25 SLC12A7    TGACCA--CAACCTACAAA     33  A AG        ATG
                     TGA C GCAACCTACAAA
                     III I IIIIIIIIIIII
                     ACT G TGTTGGATGTTT
                     _G_        III
GAM25 SLC14A1    TGAA-AGGAAAA-TACAAAATG  35   C C CC      G
                     TGAA AGG AA TACAAAATG
                     IIII III II IIIIIIIII
                     ACTT TCC TT ATGTTTTAC
                     _  _  TT      I
GAM25 SLC6A5     TGACACAGGCAACAGACTGAACTGG 32  _     CT AAAA_ GII
                     TGA ACAGGCAAC AC   TGG
                     III IIIIIIIII II   III
                     ACT TGTCCGTTG TG   ACC
                      G     TC ACTTG  III
GAM25 SYT1      AGGAATTCTACAAAATTGG     26 TGAACAGGCAAC      _
                        CTACAAAAT GG
                        IIIIIIIII II
                        GATGTTTTA CC
                    AA_____      A
GAM25 TBXAS1     GAACAGGCAACCAAGCAAA     31 TG      TA_ ATGG
                        AACAGGCAACC CAAA
                        IIIIIIIIII IIII
                        TTGTCCGTTGG GTTT
                       __       TTC  GIII
GAM26 CSPG3      AGACCTTTGTTCAAAGGAATA   38 TATTAGAC   _ T TA
                         CTTTGT CAGA GGA
                         IIIIII IIII III
                         GAAACA GTTT CCT
                        _____   A _ TA
GAM26 DTNB      TATTAGCCCTTTGTCAGATG    44    A       GAT
                         TATTAG CCTTTGTCAGATG
                         IIIIII IIIIIIIIIIII
                         ATAATC GGAAACAGTCTAC
                           G       III
GAM26 NPHP1     TACTAGACCTTTATCAGTTAGAT  45            A  AI
                         TATTAGACCTTTGTCAG TGGAT
                         IIIIIIIIIIIIIIIII IIIII
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                    ATGATCTGGAAATAGTC ATCTA
                         A     II
GAM26  NYX         TATTAGGAAACCCTTTGTCAG    43      A____        ATGGATA
                    TATTAG    CCTTTGTCAG
                    ||||||    ||||||||||
                    ATAATC    GGAAACAGTC
                      CTTTG       IIIATAG
GAM26  RDX         TACACATTTGTCAGACGTGATA   42  TATTAG  C          _
                    AC TTTGTCAGATG GATA
                    II IIIIIIIIIII IIII
                    TG AAACAGTCTGC CTAT
                    _____     T      A
GAM26  RPL10        TAGACCTTTGGTCAGGTGG    41  TATTAG    _   A  AT
                    ACCTTTG TCAG TGG
                    ||||||| |||| |||
                    TGGAAAC AGTC ACC
                    _____      C   C  AC
GAM26  SHC1         ATTAGACCTAAG--AGATGG    40  TA      TTGTC    A
                    TTAGACCT   AGATGG
                    ||||||||   ||||||
                    AATCTGGA   TCTACC
                    __      TTC__     A
GAM26  SLC22A5      AGGCCTTTGTCACTGAAGGA   39  TATTAGAC     __ T
                    CTTTGTCA GA GGAT
                    |||||||| || ||||
                    GAAACAGT CT CCTG
                    _____      GA  T
GAM27  APPBP2       AAAAAAAAAAAAATTTCCTGGC  53      CT        TT
                    AAAAAAGA GAATTTCCTGGC
                    |||||||| ||||||||||||
                    TTTTTTTT TTTAAAGGACCG
                    TT          II
GAM27  MYO6         AAAAAAGACACTAGGAATTTC   48      T____      CTGGCTT
                    AAAAAAGAC   GAATTTC
                    |||||||||   |||||||
                    TTTTTTCTG   CTTAAAG
                    TGATC       IIITTCG
GAM27  RABL2A       AAAAAACACCTAAATTTCCTG   49    G _       GCTT
                    AAAAAA AC TGAATTTCCTG
                    |||||| || ||||||||||||
                    TTTTTT TG ATTTAAAGGAC
                    G  G       IIIT
GAM27  RABL2B       AAAAAACACCTAAATTTCCTG   49    G _       GCTT
                    AAAAAA AC TGAATTTCCTG
                    |||||| || ||||||||||||
                    TTTTTT TG ATTTAAAGGAC
                    G  G       IIIT
GAM27  SET          AAAAAAGACTGCAACTTGCT    50      _   C GGCT
                    AAAAAAGACTG AATTT CT
                    |||||||||| ||||| ||
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                        TTTTTTCTGAC TTGAA GA
                          G    C  IIIT
GAM27  SLC4A8       AAAAAAGACAGAAAGTCCT       51        T  TT   GGCT
                        AAAAAAGAC GAA  TCCT
                        IIIIIIIII III  IIII
                        TTTTTTCTG CTT  AGGA
                          T    TC   IIIT
GAM27  SLC6A3       AACATAAACAGAATTTCCTGG    52  AAAAA  T       CTT
                          AGAC GAATTTCCTGG
                          IIII IIIIIIIIIII
                          TTTG CTTAAAGGACC
                        TTGTA   T      III
GAM28  AASS       TATTTATAAAATACAGGGT     58       ACC_       TTTGG
                        TATTTA ATACAGGGT
                        IIIIII IIIIIIIIII
                        ATAAAT  TATGTCCCA
                          ATTT       IIITG
GAM28  CYP19      ATTTCACCA--CAGGGTTT     57  TATTTA  AT      G
                          ACC ACAGGGTTTT
                          III IIIIIIIIII
                          TGG TGTCCCAAAG
                        AAAG__  __      I
GAM28  DAAM1      TTTAACCATAC---GTATAGGT   66  TATT     A___     TGG
                          TAACCATAC  GGGTTT
                          IIIIIIIII  IIIIII
                          ATTGGTATG  TCCAGA
                        ____       CATA    III
GAM28  HIF1A     TAATAAACCATACAGCATTT     60  TATT     G  TGG
                          AACCATACAG GTTT
                          IIIIIIIIII IIII
                          TTGGTATGTC TAAA
                        ATTAT      G   III
GAM28  KCNAB1     TTTAACCATGCAGCTTCTGTGGT   63  TATT    A GG  _  I
                          TAACCAT CAG  TTT TGGT
                          IIIIIIII III  III IIII
                          ATTGGTA GTC  AGA ACCA
                        ____       C  GA  C  A
GAM28  MBNL      TTAATTCAAAGAGG-TTTTGGT   61  TATTTAAC TACA
                          CA   GGGTTTTGGT
                          II   IIIIIIIIII
                          GT   TCCAAAACCA
                        TAA_____ TTC_
GAM28  PRKY     TTTAA---TACAGGGTCTTG    64  TATTTAA C
                          C ATACAGGGTTTTG
                          I IIIIIIIIIIII
                          A TATGTCCCAGAAC
                        _____ T
GAM28  PRPS2      TAATTAATTCTATACAGGGTTTT   59  TATTTAACC__       GGTI
                          ATACAGGGTTTT
                          IIIIIIIIIIII
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                          TATGTCCCAAAA
                     ATTAATTAAGA          IIIT
GAM28  RAI14     ATATTACCATATCAGGGTTTT  56  TATTTA    _       GGT
                     ACCATA CAGGGTTTT

                     IIIIII IIIIIIIIII
                     TGGTAT GTCCCAAAA
                     ATAA__    A      AII
GAM28  SFRS2IP       TTTAATAGAGACAGGGTTTTG  62  TATTTAACCAT       GT
                           ACAGGGTTTTG

                           IIIIIIIIIII
                           TGTCCCAAAAC
                     ATTATCTC___        GG
GAM28  ZNF264        TTTTAGTAGACAGGGTTTTG  65  TATTTAACCAT        G
                           ACAGGGTTTTG

                           IIIIIIIIIII
                           TGTCCCAAAAC
                     AATCATC____        G
GAM29  ABCC2       AAGTACCT-G--GTGACATTT  76  A   CGTC       C
                     AAG ACCT   GTGACATTT

                     III IIII   IIIIIIIII
                     TTC TGGA   CACTGTAAA
                       A   C___      I
GAM29  ANK3       ACTTCCTGCTGACATTTCT      80  AAGAA  C CG
                       CCT GT TGACATTTCT

                       III II IIIIIIIIII
                       GGA CG ACTGTAAAGA

GAM29  APOH        AAGAAACAAGT-GTGACATTT  75     CCTC C     CT
                     AAGAA  GT GTGACATTT

                     IIIII  II IIIIIIIII
                     TTCTT  CA CACTGTAAA
                       TGTT _       II
GAM29  ARHGEF7       AGGACATTGTCTGTGACATTT  82  AAGAACCTC  _      CTC
                           GTC GTGACATTT

                           III IIIIIIIII
                           CAG CACTGTAAA
                     CCTGTAA__  A    TII
GAM29  ASGR1      CCCTGCGGCAGGTCGAGGCATT  84         TG___   CTIII
                     CCCTGCGGC   GAGGC

                     IIIIIIIII   IIIII
                     GGGACGCCG   CTCCG
                     TCCAG    TAAII
GAM29  ASGR1      CCCTGCGGCAGGTCGAGGCATT  84  TGTCCC    TG___    CTTTI
                        TGCGGC   GAGGC

                        IIIIII   IIIII
                        ACGCCG   CTCCG
                     _____    TCCAG    TAACT
GAM29  CLCN6      TCCCTGCGGCACAGGAGGCC  89       T__   III
                     TCCCTGCGGC GGAGGC

                     IIIIIIIIII IIIIII
```

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                        AGGGACGCCG  CCTCCG
                           TGT     GII
GAM29  CLCN6        TCCCTGCGGCACAGGAGGCC    89  TGTC    T__      T
                       CCTGCGGC  GGAGGCCTT
                       |||||||| |||||||||
                       GGACGCCG  CCTCCGGGA
                       ____       TGT     I
GAM29  FXYD7        TCCCAGGAGCTGGAGGCCT     90   TGC          II
                       TCCC  GGCTGGAGGCC
                       ||||  ||||||||||
                       AGGG  TCGACCTCCGG
                        TCC          AI
GAM29  FXYD7        TCCCAGGAGCTGGAGGCCT     90  TGTC TGC        T
                        CC  GGCTGGAGGCCT
                        ||  ||||||||||||
                        GG  TCGACCTCCGGA
                       ____   TCC         C
GAM29  GGA3        TGTCCCCACGGCTGGAGGCACGCTTT 94     TG        CTTTIII
                       TGTCCC  CGGCTGGAGGC
                       ||||||  |||||||||||
                       ACAGGG  GCCGACCTCCG
                         GT        TGCGAAA
GAM29  GGA3        TGTCCCCACGGCTGGAGGCACGCTTT 94  C TG        CTTI
                        CC  CGGCTGGAGGC
                        ||  |||||||||||
                        GG  GCCGACCTCCG
                        _  GT        TGCG
GAM29  HMGCL      AAGAACCTC--CATGACCTGTGTC    77        GT    ATTTCTC
                       AAGAACCTC  CGTGAC
                       |||||||||  ||||||
                       TTCTTGGAG  GTACTG
                          __       GACACAG
GAM29  JRKL       AAGAACCTCCGTCTTCAAGTTTCT    73     _  GTGACA    CI
                       AAGAACCTC GTC    TTTCT
                       ||||||||| |||    |||||
                       TTCTTGGAG CAG    AAAGA
                          G  AAGTTC     II
GAM29  LAMC2       AAGAACCTCAGTTGAGAAAT     74       TCG  CATTTCT
                       AAGAACCTCG  TGA
                       ||||||||||  |||
                       TTCTTGGAGT  ACT
                         CA_    CTTTAII
GAM29  LIPE       GTCCCTGCGGC-GGTCGCC     88        T AG  I
                       GTCCCTGCGGC GG  GC
                       ||||||||||| || ||
                       CAGGGACGCCG CC  CG
                         _  AG  G
GAM29  LIPE       GTCCCTGCGGC-GGTCGCC     88  TG      T AG  TT
                       TCCCTGCGGC GG  GCC
                       |||||||||| || |||
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                              AGGGACGCCG CC  CGG
                              __        _  AG  CI
GAM29  LMO1       AATAAAATCG-CATTACATTTCTC  78  AAGAACC  T  G       I
                              TCG CGT ACATTTCTC
                              ||| ||| |||||||||
                              AGC GTA TGTAAAGAG
                          TTATTTT  _  A      I
GAM29  LTBP2      CCTGTGACTGGAGGCCATT       85      C         TTII
                          CCTG GGCTGGAGGCC
                          |||| |||||||||||
                          GGAC CTGACCTCCGG
                             A      TAAI
GAM29  LTBP2      CCTGTGACTGGAGGCCATT       85  TGTCCCTGC       TT
                             GGCTGGAGGCC
                             |||||||||||
                             CTGACCTCCGG
                          A_____        TA
GAM29  MGAT1       AAGCTCAGGACGTGGACATTTCT  69  AAGAAC  T__  _     CI
                          CTCG  CGTG ACATTTCT
                          ||||  |||| ||||||||
                          GAGT  GCAC TGTAAAGA
                          _____   CCT  C     CC
GAM29  MLC1       TGTCCCTGCAGCCTGGCAGG       91          _  _   CCTTT
                          TGTCCCTGCGGC TGG AGG
                          ||||||||||| ||| |||
                          ACAGGGACGTCG ACC TCC
                            G  G  IIITT
GAM29  MLC1       TGTCCCTGCAGCCTGGCAGG       91          _  AGIII
                          TGTCCCTGCGGC TGG
                          |||||||||||| |||
                          ACAGGGACGTCG ACC
                            G  GTCCI
GAM29  NEUROD2     TGTCCCTGCGCTCTGGGGGC      92       G_  A  CTTT
                          TGTCCCTGCG CTGG GGC
                          |||||||||| |||| |||
                          ACAGGGACGC GACC CCG
                            GA  C  IIIT
GAM29  NEUROD2     TGTCCCTGCGCTCTGGGGGC      92       G_  A  II
                          TGTCCCTGCG CTGG GG
                          |||||||||| |||| ||
                          ACAGGGACGC GACC CC
                            GA  C  GI
GAM29  PAX5       TGCCCCTCCCTCAGGAGGCCTT    96      GCGGCT       TI
                          TGTCCCT  GGAGGCCTT
                          |||||||  |||||||||
                          ACGGGGA  CCTCCGGAA
                            GGGAGT      II
GAM29  PAX5       TGCCCCTCCCTCAGGAGGCCTT    96      GCGGCT       I
                          GTCCCT  GGAGGCCT
                          ||||||  ||||||||
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                        CGGGGA      CCTCCGGA
                        GGGAGT        I
GAM29  PPP2R5C       AAGACACTTGGAATAGTGACATTTCT 72      AC  C___  C        CII
                        AAGA  CT   GT GTGACATTTCT
                        IIII II   II IIIIIIIIIII
                        TTCT  GA   TA CACTGTAAAGA
                        GT  ACCT  T          III
GAM29  PSD           ACCTCGTCGTCCACATCTTCT   79 AAGAACCT    GA  T  C
                        CGTCGT  CAT TCT
                        IIIIII  III III
                        GCAGCA  GTG AGA
                        _____      G_  T  A
GAM29  RGS19IP1      TGTCCCT---GCTGGGGGCC    95        GGC  A  T
                        TGTCCCTGC  TGG GGCC
                        IIIIIIIII  III IIII
                        ACAGGGACG  ACC CCGG
                             ___  C  I
GAM29  RGS19IP1      TGTCCCT---GCTGGGGGCC    95 _      GGC  A
                        GTCCCTGC  TGG GGC
                        IIIIIIII  III III
                        CAGGGACG  ACC CCG
                        A      ___  C
GAM29  RNPEPL1       GTCCCAG--GCTGGAGGCC    87      TGC        I
                        GTCCC  GGCTGGAGGC
                        IIIII  IIIIIIIIII
                        CAGGG  CCGACCTCCG
                            T__       G
GAM29  RNPEPL1       GTCCCAG--GCTGGAGGCC    87 TG  TGC
                        TCCC  GGCTGGAGGCCT
                        IIII  IIIIIIIIIIII
                        AGGG  CCGACCTCCGGG
                        __    T__
GAM29  ROR2         AGGACCTCGTCGTCGTCCTCTTCTC 83 AAGA        GACA__    II
                        ACCTCGTCGT    TTTCTC
                        IIIIIIIIII    IIIIII
                        TGGAGCAGCA    GAAGAG
                        CC__        GCAGGA    GI
GAM29  SFTPC        TGTCCCTGCGG-TGTGGGC    93        C  GA  CTT
                        TGTCCCTGCGG TG GGC
                        IIIIIIIIIII II III
                        ACAGGGACGCC AC CCG
                          _ AC  III
GAM29  SFTPC        TGTCCCTGCGG-TGTGGGC    93        C  GA  I
                        TGTCCCTGCGG TG GG
                        IIIIIIIIIII II II
                        ACAGGGACGCC AC CC
                          _ AC  G
GAM29  SORD         AACCTCA-CATGACATTTC     71 AAGAAC  T
                        CTCG CGTGACATTTC
                        IIII IIIIIIIIIII
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                        GAGT GTACTGTAAAG
                        _____  _
GAM29  SRRM1       GAACAGAGCCATGACATTTC   86  AAGAACCTC         T
                        GTCGTGACATTTC
                        |||||||||||||
                        CGGTACTGTAAAG
                   TGTCT____          T
GAM29  TBXAS1      AATCACTTCAGTGACATTTTC  70  AAGA C  TC       CTC
                        AC TCG GTGACATTT
                        || |||  |||||||||
                        TG AGT CACTGTAAA
                        G___ A  ___      AAG
GAM29  TM4SF4      AGAACCTCGATGGCAATGGACATTT 81  AA      TC_  ____     CTCII
                        GAACCTCG GT  GACATTT
                        |||||||| ||  |||||||
                        CTTGGAGC CG  CTGTAAA
                        __     TAC TTAC    TIIIC
GAM30  ADAMTS5     GTTGAATGTGTTGGACATGATAG  106       AA  IIIC
                        GTTGAATGTGTT GATA
                        |||||||||||| ||||
                        CAACTTACACAA CTGT
                        C_    ACTA
GAM30  ADH7        TAATAGTTTCAATGTGTTAAG    111     G_        ATAG
                        TAATAGTT AATGTGTTAAG
                        |||||||| |||||||||||
                        ATTATCAA TTACACAATTC
                        AG      IIIG
GAM30  ADH7        TAATAGTTTCAATGTGTTAAG    111 A   G_       I
                        ATAGTT AATGTGTTAA
                        |||||| |||||||||||
                        TATCAA TTACACAATT
                        _    AG        I
GAM30  AF1Q        TAATAGTAGGAATGCATGTTAAGAT 110      T_   __    AGII
                        TAATAGT GAATGT GTTAAGAT
                        ||||||| |||||| ||||||||
                        ATTATCA CTTACG CAATTCTA
                        TC    TA    IIIG
GAM30  AF1Q        TAATAGTAGGAATGCATGTTAAGAT 110 AAT T_   __    I
                        AGT GAATGT GTTAAGA
                        ||| |||||| ||||||||
                        TCA CTTACG CAATTCT
                        ___ TC   TA   I
GAM30  AKT1        TAA-AGTTGAATGTTGTAA      113 TAAT      GTTAAGAT
                        AGTTGAATGT
                        ||||||||||
                        TCAACTTACA
                        ATT_        ACATTIII
GAM30  AKT1        TAA-AGTTGAATGTTGTAA      113 TAAT      GTTAI
                        AGTTGAATGT
                        ||||||||||
```

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                          TCAACTTACA
                      ATT_        ACATT
GAM30  C8orf1   TAATAGTTGAATTTATTTAGA    115        G   A  TAG
                      TAATAGTTGAAT TGTT AGA
                      IIIIIIIIIII IIII III
                      ATTATCAACTTA ATAA TCT
                          A    A   III
GAM30  C8orf1   TAATAGTTGAATTTATTTAGA    115        G   AAGI
                      AATAGTTGAAT TGTT
                      IIIIIIIIII IIII
                      TTATCAACTTA ATAA
                          A   ATCI
GAM30  CSN2    TACTAGTTGAA----TTAAGAT   116 AA_      ATGT
                      TAGTTGA  GTTAAGA
                      IIIIIII  IIIIIII
                      ATCAACT  TAATTCT
                      ATG      ____
GAM30  CSN2    TACTAGTTGAA----TTAAGAT   116 TAA     ATGT
                      TAGTTGA  GTTAAGAT
                      IIIIIII  IIIIIIII
                      ATCAACT  TAATTCTA
                      ATG      ____
GAM30  CYBB    TAATAGTTGAGCACAGTTTTAAGA 112        AT___ G   TAGI
                      TAATAGTTGA    GT TTAAGA
                      IIIIIIIIII    II IIIIII
                      ATTATCAACT    CA AATTCT
                          CGTGT A     IIIG
GAM30  DAZ    AACAGTTTCA-GTGTTAAGATA    102 _     GAAT       I
                      ATAGTT  GTGTTAAGAT
                      IIIIII  IIIIIIIIII
                      TGTCAA  CACAATTCTA
                      T   AGT_      I
GAM30  DAZ    AACAGTTTCA-GTGTTAAGATA    102 TA    GAAT
                      ATAGTT  GTGTTAAGATAG
                      IIIIII  IIIIIIIIIII
                      TGTCAA  CACAATTCTATT
                      __   AGT_
GAM30  GALR1  TTGAATTCTTGTTAAGATA    118       G__       III
                      TTGAAT TGTTAAGAT
                      IIIIII IIIIIIIII
                      AACTTA ACAATTCTA
                          AGA      TII
GAM30  HGF    TAGTTGAATGT-TGAATGATA    117        GTTAA  I
                      AGTTGAATGT   GAT
                      IIIIIIIII    III
                      TCAACTTACA   CTA
                          ACTTA  I
GAM30  HGF    TAGTTGAATGT-TGAATGATA    117 TAATAG    GTTAA
                      TTGAATGT  GATA
                      IIIIIIII  IIII
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                       AACTTACA   CTAT
                       _____      ACTTA
GAM30  HMGE          TAACTAGTTGAATATGATTTAAATA 107 A        TTAAGATI
                       TAGTTGAATGTG
                       |||||||||||
                       ATCAACTTATAC
                       G        TAAATTTI
GAM30  HMGE          TAACTAGTTGAATATGATTTAAATA 107 TAA_        _ A   GII
                       TAGTTGAATGTG TT AGATA
                       ||||||||||| || |||||
                       ATCAACTTATAC AA TTTAT
                       ATTG       T A   III
GAM30  IL1RAP        AATAGTTGAGCACTGAGGTTAACATAG100 TA      A___ T_   G   III
                       ATAGTTGA   TG GTTAA ATAG
                       ||||||||  ||  ||||| ||||
                       TATCAACT   AC CAATT TATC
                       __        CGTG  TC   G   GII
GAM30  LMO2          AATAGTTGAACAACTTTTTAAGAT 99 TA       TG___     AGI
                       ATAGTTGAATG   TTAAGAT
                       |||||||||||   |||||||
                       TATCAACTTGT   AATTCTA
                       __           TGAAA    AII
GAM30  MEF2A         ATAGCAGAATGTGTTCAAAAGTAG 104 A T     _   TAI
                       GT GAATGTGT TAAGA
                       || ||||||||| |||||
                       CG CTTACACA GTTTT
                       _ T     A   CAI
GAM30  MEF2A         ATAGCAGAATGTGTTCAAAAGTAG 104 TAAT  T     _ _  I
                       AGT GAATGTGT TAAGA TAG
                       ||| ||||||||| ||||| |||
                       TCG CTTACACA GTTTT ATC
                       ____     T    A   C A
GAM30  PAFAH1B2      TAATAATTCAATGAATGTGTTACACATA109       ____      AG  GIII
                       TAATAGT  TGAATGTGTTA ATA
                       |||||||  ||||||||||| |||
                       ATTATTA  ACTTACACAAT TGT
                       AGTT       G_   ATII
GAM30  PAFAH1B2      TAATAATTCAATGAATGTGTTACACATA109 AATAGT      AI
                       TGAATGTGTTA
                       |||||||||||
                       ACTTACACAAT
                       TT____        GT
GAM30  PPP1CB        TAATAGTTGGTGAATGTCTGTAAAG 108       AAT_  AAGATAGII
                       TAATAGTTG  GTGTT
                       |||||||||  |||||
                       ATTATCAAC  TACAG
                       CACT    ACATTTCII
GAM30  SCG3          TAATAG--GAA-GTGTTAAGA       114   TT T    T
                       TAATAG GAA GTGTTAAGA
                       |||||| ||| |||||||||
```

```
                              ATTATC CTT CACAATTCT
                                __  _           I
GAM30  SCG3        TAATAG--GAA-GTGTTAAGA   114 _    TT  T
                             AATAG GAA GTGTTAAG
                             ||||| ||| ||||||||
                             TTATC CTT CACAATTC
                             A     __  _
GAM30  SNX5        ATGGTTAAATG--TTAAGAT    105 TA_   AT      I
                             GTTGA GTGTTAAGA
                             ||||| |||||||||
                             CAATT TACAATTCT
                             TAC       __    I
GAM30  SNX5        ATGGTTAAATG--TTAAGAT     105 TAATA  AT
                             GTTGA GTGTTAAGAT
                             ||||| ||||||||||
                             CAATT TACAATTCTA
                             C____      __
GAM30  TNFSF4      ATAGTTGAAGGTGTACTTAAGA    103       T  TAAGIII
                             ATAGTTGAA GTGT
                             ||||||||| ||||
                             TATCAACTT CACA
                                 C   TGAATTC
GAM30  TNFSF4      ATAGTTGAAGGTGTACTTAAGA    103 TAAT   T  ___    TAG
                             AGTTGAA GTGT  TAAGA
                             ||||||| |||| |||||
                             TCAACTT CACA  ATTCT
                             ____      C TGA   CCI
GAM30  TOB1        AATAGTTG-ATGTCTTTAAGAT    101      A  G_   I
                             ATAGTTGA TGT TTAAGA
                             |||||||| ||| ||||||
                             TATCAACT ACA AATTCT
                               _  GA    I
GAM30  TOB1        AATAGTTG-ATGTCTTTAAGAT    101 TA     A G_     AG
                             ATAGTTGA TGT TTAAGAT
                             |||||||| ||| |||||||
                             TATCAACT ACA AATTCTA
                               __    _ GA    CI
GAM31  AF3P21      GCGCCGAGCCGCGCCGCGGT    123  _  AAC      II
                             GCGC GAG CGCCGCGG
                             |||| ||| ||||||||
                             CGCG CTC GCGGCGCC
                             G GGC     AI
GAM31  AF3P21      GCGCCGAGCCGCGCCGCGGT    123 TATGCG  AAC      G
                             CGAG CGCCGCGGT
                             |||| |||||||||
                             GCTC GCGGCGCCA
                             G_____ GGC     A
GAM31  AKAP13      GCCCGAGCA--GCCGCGGTG    127 G  AACC      I
                             GC CGAG  GCCGCGG
                             || ||||  |||||||
```

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                    CG GCTC  CGGCGCC
                     G  GT__     A
GAM31  AKAP13        GCCCGAGCA--GCCGCGGTG   127 TATGCG  AACC
                     CGAG  GCCGCGGT
                     ||||  ||||||||
                     GCTC  CGGCGCCA
                     _____    GT__
GAM31  CDKN2C        TGCTGGGAGAGC-GCCGCGGTG  130  GC_  AC      I
                     GC  GAGA CGCCGCGGT
                     ||  ||||  ||||||||||
                     CG  CTCT GCGGCGCCA
                      ACC  C_      I
GAM31  CDKN2C        TGCTGGGAGAGC-GCCGCGGTG  130 TATGCGC  AC       T
                     GAGA CGCCGCGGTG
                     ||||  ||||||||||
                     CTCT GCGGCGCCAC
                      GACC___  C_      C
GAM31  CYP7B1        GCGCGCGCTAGGCCGCGGTG    129   AGAACC    I
                     GCGCG    GCCGCGG
                     |||||    |||||||
                     CGCGC    CGGCGCC
                      GATC__      A
GAM31  CYP7B1        GCGCGCGCTAGGCCGCGGTG    129 TAT  G AACC
                     GCGC AG   GCCGCGGTG
                     |||| ||   |||||||||
                     CGCG TC  CGGCGCCAC
                      G__  A  ____
GAM31  DTNB          ATGGG-GAGAACCGCTGGGG    121 ATGCGC      CGCI
                     GAGAACCGC
                     |||||||||
                     CTCTTGGCG
                      ACCC__     ACCC
GAM31  DTNB          ATGGG-GAGAACCGCTGGGG    121 TATGCGC      CGC TG
                     GAGAACCGC  GG
                     |||||||||  ||
                     CTCTTGGCG  CC
                      ACCC___     ACC CI
GAM31  ECEL1         GCGCCGAGG-CCGCCGCGGTG   124  _  AA      I
                     CGC GAG CCGCCGCGGT
                     ||| ||| ||||||||||
                     GCG CTC GGCGGCGCCA
                      G  C_      I
GAM31  ECEL1         GCGCCGAGG-CCGCCGCGGTG   124 TATGCG  AA
                     CGAG CCGCCGCGGTG
                     |||| ||||||||||
                     GCTC GGCGGCGCCAC
                      G_____   C_
GAM31  FBXL4         GCGCGAGAA-GGCCTGGGTG    128 _     CC  GC  I
                     CGCGAGAA GCC GGT
                     |||||||| ||| |||
```

```
                        GCGCTCTT CGG CCA
                        C    C_  AC  I
GAM31  FBXL4            GCGCGAGAA-GGCCTGGGTG      128  TATGCG    CC  GC
                        CGAGAA GCC GGTG
                        |||||| ||| ||||
                        GCTCTT CGG CCAC
                        _____      C_  AC
GAM31  MAPRE3           CGCTGAGG-CCGCCGCGGT       122  _  AA       II
                        CGC GAG  CCGCCGCGG
                        ||| |||  |||||||||
                        GCG CTC  GGCGGCGCC
                        A  C_       AI
GAM31  MAPRE3           CGCTGAGG-CCGCCGCGGT       122  TATGCGC  AA
                        GAG  CCGCCGCGGT
                        |||  ||||||||||
                        CTC  GGCGGCGCCA
                        _____       C_
GAM31  MARK3           GCGCAAGACAGGCCGCCGCGG      125      A___       III
                        GCGCGAGA  CCGCCGCG
                        ||||||||  ||||||||
                        CGCGTTCT  GGCGGCGC
                        GTCC     CII
GAM31  MFI2            GCGCGAGAGGCCGCCGCGG        126      A_     II
                        GCGCGAGA CCGCCGCG
                        |||||||| ||||||||
                        CGCGCTCT GGCGGCGC
                        CC      CI
GAM31  MFI2            GCGCGAGAGGCCGCCGCGG        126  TATGCG   A_      TG
                        CGAGA CCGCCGCGG
                        ||||| |||||||||
                        GCTCT GGCGGCGCC
                        _____     CC     TT
GAM31  PRKCI          TGCCGGAGAACCGCGGCCGT        132  TATG C     C G G
                        CG GAGAACCGC GC GT
                        || ||||||||| || ||
                        GC CTCTTGGCG CG CA
                        G___ _      C G G
GAM31  PRKCI          TGCCGGAGAACCGCGGCCGT        132  TG C     C GI
                        CG GAGAACCGC GC
                        || ||||||||| ||
                        GC CTCTTGGCG CG
                        G_ _      C GC
GAM31  RPS6KA1        TGCGACCCGAACCGCCGCG         131  _GA       II
                        TGCG C GAACCGCCGC
                        |||| | ||||||||||
                        ACGC G CTTGGCGGCG
                        T GG       CI
GAM31  RPS6KA1        TGCGACCCGAACCGCCGCG         131  TAT C GA       GTG
                        G GC GAACCGCCGCG
                        | || ||||||||||
```

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                              G TG  CTTGGCGGCGC
                           ___ C  GG        GGI
GAM31  SLC18A3       TGGGCG-GAGGCGCCGCGGTG   133 ___   C   AAC      I
                           GCG GAG  CGCCGCGGT
                           ||| |||  |||||||||
                           CGC CTC  GCGGCGCCA
                           ACC _  C__        I
GAM31  SLC18A3       TGGGCG-GAGGCGCCGCGGTG   133 TAT  C   AAC
                           GCG GAG  CGCCGCGGTG
                           ||| |||  |||||||||
                           CGC CTC  GCGGCGCCAC
                           C__ _  C__
GAM32  B3GALT3       TCACTATCCTTTTTATCTTGTA  155     AT        A   AA
                          TCAC  TTCTTTTTATC TGTA
                          |||| |||||||||| ||||
                          AGTG AGGAAAAATAG ACAT
                           AT        A   II
GAM32  B3GALT3       TCACTATCCTTTTTATCTTGTA  155     AT        A   I
                          CAC  TTCTTTTTATC TGT
                          ||| |||||||||| |||
                          GTG  AGGAAAAATAG ACA
                           AT        A   I
GAM32  BACH1         CATTTCTTTGTCTCTTGTA     145         TTA A  II
                          CATTTCTTT  TC TGT
                          ||||||||| || |||
                          GTAAAGAAA  AG ACA
                           CAG  A  TI
GAM32  CAPZA1        CACCTTTCTTTTTTTGACATGTA  141 ACA       AT__    I
                          TTTCTTTTT  CATGT
                          |||||||||  |||||
                          AAAGAAAAA  GTACA
                          G__       AACT   I
GAM32  CAPZA1        CACCTTTCTTTTTTTGACATGTA  141 TC A       AT__    AAI
                          AC TTTCTTTTT  CATGTA
                          || |||||||||  ||||||
                          TG AAAGAAAAA  GTACAT
                          __ G       AACT   AII
GAM32  COG3          TCACATTTCTTGTGACCATTTAAA 157          TTT  G    I
                          TCACATTTCTT ATCAT TAAA
                          ||||||||||| ||||| ||||
                          AGTGTAAAGAA TGGTA ATTT
                           CAC  A  I
GAM32  COG3          TCACATTTCTTGTGACCATTTAAA 157          TTT  GTAAI
                          CACATTTCTT ATCAT
                          |||||||||| |||||
                          GTGTAAAGAA TGGTA
                           CAC  AATTI
GAM32  COL4A4        CACATTTTTCTTTTTACCA-GAAAA 139 ACA         TGI
                          TTTCTTTTTATCA
                          |||||||||||||
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                             AAAGAAAAATGGT
                        A__          CTT
GAM32  COL4A4      CACATTTTTCTTTTTACCA-GAAAA 139 TC   __         TGTAAAI
                        ACATT TCTTTTTATCA
                        ||||| ||||||||||||
                        TGTAA AGAAAAATGGT
                          __    AA          CTTTTAI
GAM32  COX15       ACATTTCTTTCTCTACAT-TAAA  136        AT_ GTAAI
                        CATTTCTTTTT  CAT
                        |||||||||| |||
                        GTAAAGAAAGA  GTA
                            GAT  ATTII
GAM32  EIF5A2      CATTGCATAGTATCATGTAAA    146 ATTTCTTTT        I
                            TATCATGTAA
                            ||||||||||
                            ATAGTACATT
                        TAACGTATC         I
GAM32  EIF5A2      CATTGCATAGTATCATGTAAA    146 TCACATTTCTTTT
                            TATCATGTAAA
                            |||||||||||
                            ATAGTACATTT
                        ACGTATC_____
GAM32  FANCD2      TCACATTCTATTTTTGTATGT  149         _  ATC   AAA
                        TCACATTCT TTTT  ATGT
                        |||||||||| ||||   ||||
                        AGTGTAAAGA AAAA  TACA
                          T   ACA   III
GAM32  FZD6        CACATTCTGTTT-TCAGGTA    144 _     T  A  T  I
                          ACATTTCT TTT TCA GT
                          |||||||| ||| ||| ||
                          TGTAAAGA AAA AGT CA
                            G     C  _  C I
GAM32  FZD6        CACATTTCTGTTT-TCAGGTA     144 TC     T  A  T  A
                          ACATTTCT TTT TCA GTA
                          |||||||| ||| ||| |||
                          TGTAAAGA AAA AGT CAT
                            __      C  _  C  A
GAM32  GPR23       CACATTTCTTATTAATAATGT    140 TC     T  TC_  AAA
                          ACATTTCTT TTA  ATGT
                          ||||||||| |||  ||||
                          TGTAAAGAA AAT  TACA
                              __     T  TAT  AII
GAM32  LTBR        TCCCATT-CTTTTTATTGCATGT 150  A  T      ___    AAAI
                          TC CATT CTTTTTAT  CATGT
                          || |||| |||||||||  |||||
                          AG GTAA GAAAAATA  GTACA
                              G  _    AAC   IIIA
GAM32  MS4A3       TCACATTTTCTTTTTATTTTCATTTAA147         _   ___    GTAAAIII
                          TCACATTT CTTTTTA  TCAT
                          |||||||| |||||||   ||||
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                     AGTGTAAA GAAAAAT  AGTA
                       A      AAA    AATTIIIA
GAM32  MS4A3     TCACATTTTCTTTTTATTTTCATTTAA147 CA         ___      GTAI
                     TTTCTTTTTA  TCAT
                     IIIIIIIIII IIII
                     AAAGAAAAAT  AGTA
                       A_       AAA    AIII
GAM32  NEDD4     TCACATTTCAGATTTCTATCAGGT 148         ___       T AAAI
                     TCACATTTC  TTTTTATCA GT
                     IIIIIIIII  IIIIIIIII II
                     AGTGTAAAG  AAAGATAGT CA
                        TCT       C  IIIA
GAM32  PDK4      TCACATTTCTCTGTA-CAT       151           T  CAI
                     TCACATTTCTTT TAT
                     IIIIIIIIIIII III
                     AGTGTAAAGAGA ATG
                          C  TAI
GAM32  PDK4      TCACATTTCTCTGTA-CAT       151           T  CATGTA
                     TCACATTTCTTT TAT
                     IIIIIIIIIIII III
                     AGTGTAAAGAGA ATG
                          C  TAIIIA
GAM32  PGK1      TCAC-TTTCTTTTTAACAGGCAAA 156     A       T T   I
                     TCAC TTTCTTTTTA CA GTAAA
                     IIII IIIIIIIIII II IIIII
                     AGTG AAAGAAAAAT GT CGTTT
                       _       T C   I
GAM32  PGK1      TCAC-TTTCTTTTTAACAGGCAAA 156 _   A       T T   I
                     CAC TTTCTTTTTA CA GTAA
                     III IIIIIIIIII II IIII
                     GTG AAAGAAAAAT GT CGTT
                       A _       T C   I
GAM32  PIGA      ATTTCTTTTATATCAGTGCAA       137       _  _   III
                     ATTTCTTTT TATCA TGTA
                     IIIIIIIII IIIII IIII
                     TAAAGAAAA ATAGT ACGT
                        T   C   TII
GAM32  PLS3      CACATTTCTTTGTTTCAGGTGTAAA 143 TC       TTA __    II
                     ACATTTCTTT TCA TGTAAA
                     IIIIIIIIII III IIIIII
                     TGTAAAGAAA AGT ACATTT
                        __       CAA  CC    TI
GAM32  PRPF18    TTTCTTTTTAATCATCTAA       159        _  G II
                     TTTCTTTTTA TCAT TA
                     IIIIIIIIII IIII II
                     AAAGAAAAAT AGTA AT
                        T   G TI
GAM32  RAI14     TCACATTTCTTTGGAGCAT       152               TTATCAII
                     TCACATTTCTTT
                     IIIIIIIIIIII
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                       AGTGTAAAGAAA
                        CCTCGTAI
GAM32  RAI14     TCACATTTCTTTGGAGCAT      152        TTATCATGTAA
                        TCACATTTCTTT
                        ||||||||||||
                        AGTGTAAAGAAA
                         CCTCGTAIIIA
GAM32  RASGRP1    ATGTCT-TTTATCATATAAA    138  TCACATTTCT
                        TTTTATCATGTAA
                        ||||||||||||
                        AAAATAGTATATT
                    G_____
GAM32  RASGRP1     ATGTCT-TTTATCATATAAA   138  TTTC          I
                        TTTTATCATGTAA
                        ||||||||||||
                        GAAAATAGTATATT
                    TACA           I
GAM32  SLC21A9     TCCCTTTTCTTTT-ATCATGT  153  ACA      T    AA
                        TC  TTTCTTTT ATCATGT
                        ||  |||||||| |||||||
                        AG  AAAGAAAA TAGTACA
                     GGA       _     II
GAM32  SLC21A9     TCCCTTTTCTTTT-ATCATGT  153  CACA_     T   I
                        TTTCTTTT ATCATG
                        |||||||| ||||||
                        AAAGAAAA TAGTAC
                     AGGGA       _    I
GAM32  TFAP2C    CACTTTTCTTTTTTTCAAGGTAAA 142  TC A      A T_  I
                        AC TTTCTTTTT TCA GTAAA
                        || ||||||||| ||| |||||
                        TG AAAGAAAAA AGT  CATTT
                      __ A     A TC  A
GAM32  TFAP2C    CACTTTTCTTTTTTTCAAGGTAAA 142  ACA       A T_  I
                        TTTCTTTTT TCA GTAA
                        ||||||||| ||| ||||
                        AAAGAAAAA AGT  CATT
                      GA_      A TC  I
GAM32  TIMM23    TCATGTTTCTTTTTCTCCTTTAAA 158  CA       A ATG  I
                        TCA TTTCTTTTT TC  TAAA
                        ||| ||||||||| || ||||
                        AGT AAAGAAAAA AG  ATTT
                      AC       G GAA  I
GAM32  ZNF253    TCACATTTCTTTATAT-TTGTA    154        T  CA  AA
                        TCACATTTCTTT TAT TGTA
                        |||||||||||| ||| ||||
                        AGTGTAAAGAAA ATA ACAT
                       T  A_  II
GAM32  ZNF253    TCACATTTCTTTATAT-TTGTA    154  _      T CATGTI
                        CACATTTCTTT TAT
                        ||||||||||| |||
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                              GTGTAAAGAAA ATA
                              A      T  AACAII
GAM33  ALEX3      AGCATTGATGATACAA---TATGA 163    A_         GTATI
                              AGCA GATGATACAATG
                              IIII IIIIIIIIIII
                              TCGT CTACTATGTTAT
                               AA         ACTII
GAM33  ALEX3      AGCATTGATGATACAA---TATGA 163 TA A_       ATG
                              GCA GATGATACA  GTATGA
                              III IIIIIIIII  IIIIII
                              CGT CTACTATGT  TATACT
                              __  AA         ___
GAM33  ATRX       CAGGAAGA---AATGGTATG    167 TAGC  TGATAC
                              AAGA    AATGGTAT
                              IIII    IIIIIIII
                              TTCT    TTACCATA
                              C___    _____
GAM33  DPP4       AAGATGATA----GGTATGA    162 _     CAAT
                              AGATGATA GGTATG
                              IIIIIIII IIIIII
                              TCTACTAT CCATAC
                              T        ____
GAM33  LARS2      TAGCCTAATGTGCCAATGGTATGA 176   AA  ATA       I
                              TAGC GATG CAATGGTATGA
                              IIII IIII IIIIIIIIIII
                              ATCG TTAC GTTACCATACT
                               GA  ACG       I
GAM33  LARS2      TAGCCTAATGTGCCAATGGTATGA 176   AA  ATA       I
                              AGC GATG CAATGGTATG
                              III IIII IIIIIIIIII
                              TCG TTAC GTTACCATAC
                               GA  ACG       I
GAM33  MLLT7      TAGCAC-ATGATACAATCTGGGTA 173    AG       ___  TGAI
                              TAGCA ATGATACAAT GGTA
                              IIIII IIIIIIIIII IIII
                              ATCGT TACTATGTTA CCAT
                               G_        GAC  IIIA
GAM33  MLLT7      TAGCAC-ATGATACAATCTGGGTA 173 AGCAAG       ___ I
                              ATGATACAAT GGT
                              IIIIIIIIII III
                              TACTATGTTA CCA
                              GTG___       GAC I
GAM33  MYO1D      AGGAAGATGATACCAAAGG      164 C       AATGII
                              AG AAGATGATAC
                              II IIIIIIIIII
                              TC TTCTACTATG
                               C      GTTTCC
GAM33  MYO1D      AGGAAGATGATACCAAAGG      164 TAGC      AAT_ ATG
                              AAGATGATAC GGT
                              IIIIIIIIII III
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                        TTCTACTATG  CCG
                        CC__        GTTT  III
GAM33  NEK2      AGCAAGATG-T-C-ATGGTAT   165 _      ATACA
                        GCAAGATG  ATGGTA
                        |||||||  ||||||
                        CGTTCTAC  TACCAT
                        T      AG___
GAM33  NEK2      AGCAAGATG-T-C-ATGGTAT   165 TA     ATACA
                        GCAAGATG  ATGGTAT
                        |||||||  |||||||
                        CGTTCTAC  TACCATA
                        __      AG___
GAM33  NFE2      CAAGATGATGACAGT-ATATG   166      ACA    I
                        AAGATGAT  ATGGTAT
                        |||||||  |||||||
                        TTCTACTA  TGTCATA
                        C__     T
GAM33  OTC      GCAAGATGATAGAGAAGGTAT   168 C      CAAT_  I
                        AAGATGATA  GGTA
                        |||||||||  ||||
                        TTCTACTAT  CCAT
                        _       CTCTT  I
GAM33  OTC      GCAAGATGATAGAGAAGGTAT   168 TAGC     CAAT_   A
                        AAGATGATA  GGTATG
                        |||||||||  ||||||
                        TTCTACTAT  CCATAT
                        ____       CTCTT   C
GAM33  PTGIS   TAGTAACAATAATCACAATGGTA  170 _    GATGA     I
                        AGCAA  TACAATGGT
                        |||||  |||||||||
                        TTGTT  GTGTTACCA
                        A   ATTA_     I
GAM33  PTGIS   TAGTAACAATAATCACAATGGTA  170 ___    GATGA     TGAI
                        TAGCAA  TACAATGGTA
                        ||||||  ||||||||||
                        ATTGTT  GTGTTACCAT
                        ATC   ATTA_      IIIA
GAM33  PYGB    TAGCAAGATGTGTGCAAAGTTCTG  172      ATA_  T ATGAI
                        TAGCAAGATG  CAA GGT
                        ||||||||||  ||| |||
                        ATCGTTCTAC  GTT TCA
                        ACAC  _  AGACI
GAM33  PYGB    TAGCAAGATGTGTGCAAAGTTCTG  172 A     ATA_  T ATI
                        GCAAGATG  CAA GGT
                        |||||||  ||| |||
                        CGTTCTAC  GTT TCA
                        _     ACAC  _  AGA
GAM33  RAI3    GCAAGATGAGAGAA--GTAT   169         TACAATGGTI
                        GCAAGATGA
                        |||||||||
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                           CGTTCTACT
                           CTCTTCATAI
GAM33  RAI3        GCAAGATGAGAGAA--GTAT   169 TAGC     TACAAT
                           AAGATGA    GGTAT
                           |||||||    |||||
                           TTCTACT    TCATA
                           ____     CTCT__
GAM33  TFRC        TACCAAGATGATGGGATGGAAT   174 G      ACA   TATGA
                           TA CAAGATGAT  ATGG
                           || ||||||||| ||||
                           AT GTTCTACTA  TACC
                            G      CCC  TTAII
GAM33  TFRC        TACCAAGATGATGGGATGGAAT   174 G      ACA   TI
                           CAAGATGAT  ATGG
                           ||||||||| ||||
                           GTTCTACTA  TACC
                           G      CCC  TI
GAM33  UBQLN2      TAGCAAAAAAGAT-CAATGGTAT   171      T_  A     GA
                           TAGCAAGA GAT CAATGGTAT
                           |||||||| ||| |||||||||
                           ATCGTTTT CTA GTTACCATA
                            TT  _      II
GAM33  UBQLN2      TAGCAAAAAAGAT-CAATGGTAT   171      T_  A     I
                           AGCAAGA GAT CAATGGTA
                           ||||||| ||| ||||||||
                           TCGTTTT CTA GTTACCAT
                            TT  _      I
GAM33  VIPR1       TATCCAGATGATAC-ATGAGATG   175 GCA      A  TI
                           AGATGATACA TGG
                           |||||||||| |||
                           TCTACTATGT ACT
                           AGG      _  CT
GAM33  VIPR1       TATCCAGATGATAC-ATGAGATG   175 TAGCA      A  GT  A
                           AGATGATACA TG ATG
                           |||||||||| || |||
                           TCTACTATGT AC TAC
                           ATAGG      _  TC  I
GAM34  BTC         GCTATCAAAC----AAATCA    184       TTGGAAAT
                           GCTATCAAAC
                           ||||||||||
                           CGATAGTTTG
                           TTTAGTII
GAM34  CYBB        TATCAAACTTTAAGAAATC    185       __     III
                           TATCAAACTT GGAAAT
                           |||||||||| ||||||
                           ATAGTTTGAA TCTTTA
                            AT     GII
GAM34  DAAM1       TCAGCTATCAA------AAATCAT  187       CTTGGAI
                           TCAGCTATCAAA
                           ||||||||||||
```

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                        AGTCGATAGTTT
                          TTAGTAI
GAM34  DAAM1        TCAGCTATCAA------AAATCAT  187        AACTTG
                     TCAGCTATCA     GAAATC
                     IIIIIIIIII     IIIIII
                     AGTCGATAGT     TTTTAG
                                    _____

GAM34  ECT2         CTATCAAACT---AAATCA     183       TGG
                     CTATCAAACT AAATC
                     IIIIIIIIII IIIII
                     GATAGTTTGA TTTAG
                                 __

GAM34  FACL5       TATTAAGGTTGGAAATCAT       186 TATCAAAC       II
                             TTGGAAATCA
                             IIIIIIIIII
                             AACCTTTAGT
                     ATAATTCC       AI
GAM34  FZD3         CAGCTATCAGTCATGCAAA      182        AACTTGGAAII
                         CAGCTATCA
                         IIIIIIIII
                         GTCGATAGT
                           CAGTACGTTTI
GAM34  FZD3         CAGCTATCAGTCATGCAAA      182 TC    AACT G  TCA
                         AGCTATCA   TG AAA
                         IIIIIIII   II III
                         TCGATAGT   AC TTT
                     __       CAGT G  TII
GAM34  GAS7        CAGCAACCAA-CTTGGAACACCAT 181   T   A    _   I
                     AGC ATCAA CTTGGAA ATCA
                     III IIIII IIIIIII IIII
                     TCG TGGTT GAACCTT TGGT
                       T  _   G  I
GAM34  GAS7        CAGCAACCAA-CTTGGAACACCAT 181 TC T   A    _   I
                     AGC ATCAA CTTGGAA ATCAT
                     III IIIII IIIIIII IIIII
                     TCG TGGTT GAACCTT TGGTA
                     __  T  _   G  A
GAM34  GDF8        AGCTCAAAAACTCTGGAAATCAT  179 _  CTATC   _       I
                        TCAG   AAACT TGGAAATCAT
                        IIII   IIIII IIIIIIIIII
                        AGTT   TTTGA ACCTTTAGTA
                        G   _____   G    T
GAM34  GDF8        AGCTCAAAAACTCTGGAAATCAT  179 GCTA  __ _       I
                        TCAA ACT TGGAAATCA
                        IIII III IIIIIIIII
                        AGTT TGA ACCTTTAGT
                        G___  TT G    I
GAM34  STK4        CAGCTATCACTCAACTAGGA     180        ___ T III
                     CAGCTATCA  AACT GG
                     IIIIIIIII  IIII II
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                        GTCGATAGT  TTGA CC
                        GAG    T TII
GAM34  STK4        CAGCTATCACTCAACTAGGA      180  TC       ___     T  AATCA
                        AGCTATCA  AACT GGA
                        ||||||||  |||| |||
                        TCGATAGT  TTGA CCT
                          __    GAG   T  CIIIT
GAM35  ANXA9        CCCAGCATCTCTTCTCCCAG      197  TACC       AAA_   CT
                        CAGCATCTTT  CCAG
                        ||||||||||  ||||
                        GTCGTAGAGA  GGTC
                        ____      AGAG   CT
GAM35  COG6        TACCCA---TCTTTAAACACCAGGCTT206     GCA       __  _  I
                        TACCCA  TCTTTAA  ACCAG CTT
                        ||||||  |||||||  ||||| |||
                        ATGGGT  AGAAATT  TGGTC GAA
                          ___      TG    C  I
GAM35  DDB2        CCCAGGGCTTGTTCAAACCAGCTT  196  TACCCA ATC          I
                        GC  TTTAAACCAGCTT
                        ||  ||||||||||||
                        CG  AAGTTTGGTCGAA
                        GTCC__  AAC          C
GAM35  DHCR24        TACCCAGCACCTTCAATGTGACCAG 205              ____    CTTII
                        TACCCAGCATCTTTAA  ACCAG
                        ||||||||||||||||  |||||
                        ATGGGTCGTGGAAGTT  TGGTC
                          ACAC    IIITT
GAM35  EPHB6        CCCAGCATCTAGACTCCAG      198  TACC       TTAAA  CT
                        CAGCATCT    CCAG
                        ||||||||    ||||
                        GTCGTAGA    GGTC
                        ____        TCTGA   AC
GAM35  GALNT7        TACCAACATCATCTTTAAAACA   200    __  G      C  GCTT
                        TACC  CA CATCTTTAAA CA
                        ||||  || |||||||||| ||
                        ATGG  GT GTAGAAATTT GT
                          TT  A        T  IIIT
GAM35  GBP1        TACACAGCATCTTTTAAAGTCCATCTT203    C        _  __  G  III
                        TAC CAGCATCTTT AAA CCA CTT
                        ||| |||||||||| ||| ||| |||
                        ATG GTCGTAGAAA TTT GGT GAA
                          T       A CA A  III
GAM35  ICOS        TACCCCTGGCATCTTTAAAACA   201    A__        C  GCTT
                        TACCC  GCATCTTTAAA CA
                        |||||  |||||||||| ||
                        ATGGG  CGTAGAAATTT GT
                          GAC        T  IIIT
GAM35  KCNJ16        TACCCAGCATCATCATAAAACA   204              TT__   C  GCTT
                        TACCCAGCATC   TAAA CA
                        |||||||||||   |||| ||
```

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                    ATGGGTCGTAG   ATTT GT
                     TAGT    T  IIIT
GAM35  MSH3       CCAACAATCTTTAAA-CTGCTT   195 TACCCA  _        CA
                    GCA TCTTTAAAC GCTT
                    ||| |||||||| ||||
                    TGT AGAAATTTG CGAA
                    _____  T     A_
GAM35  NCAM2        GACTAGTTTTAGTACACTGG   199      A GAG   CGA
                    GACTAGTTT AG  ACTGG
                    ||||||||| ||  |||||
                    CTGATCAAA TC  TGACC
                      A ATG    |||
GAM35  NOS1       ACCTCATCCACTTTA-ACCAGCTT  190 TA _ G_ T   A    I
                    CC CA  CA CTTTAA CCAGCTT
                    || ||  || |||||| |||||||
                    GG GT  GT GAAATT GGTCGAA
                    __ A AG _   _     G
GAM35  PACE       ACCCAGCATCTTACAAAACCAGC   191 TA        T__      TI
                    CCCAGCATCTT AAACCAGCT
                    ||||||||||| |||||||||
                    GGGTCGTAGAA TTTGGTCGG
                       __         TGT      ||
GAM35  PCDHA9        ACTAGCTCTAAGGAGACTGG    194 GA    _        CGA
                    CTAGTTT AAGGAGACTGG
                    ||||||| |||||||||||
                    GATCGAG TTCCTCTGACC
                       __     A     TII
GAM35  RCV1      TACCCAGCACTCCACAAAGGAGCTT 202         _ T  CC   II
                    TACCCAGCA TCT TAAA  AGCTT
                    ||||||||| ||| ||||  |||||
                    ATGGGTCGT AGG GTTT  TCGAA
                        G  T  CC   II
GAM35  SUV39H1      TACCCAGCA-CTGTAAGCACGAGC 207         CTTTAA_ C TTI
                    TACCCAGCAT    AC AGC
                    ||||||||||    || |||
                    ATGGGTCGTG    TG TCG
                     ACATTCG  C  III
GAM35  USP9Y      ACCCAGTCTCATTCAAACCAGCT   193 TA   CA _          I
                    CCCAG TC TTTAAACCAGCTT
                    ||||| || |||||||||||||
                    GGGTC AG AAGTTTGGTCGAG
                     __    AG  T         I
GAM35  VCAM1      ACCCGGCATCTTTACAAAACC    192 TA A         ___   AGCTT
                    CCC GCATCTTTA  AACC
                    ||| |||||||||  ||||
                    GGG CGTAGAAAT  TTGG
                     __  C       GTT  AIIIT
GAM36  ABP1       GGGTCGTTCTGGTGGTAGAT    212  _         ||
                    GGGTT TTCTGGTGGTGGA
                    ||||| |||||||||||||
```

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                        CCCAG AAGACCACCATCT
                          C        AI
GAM36  ABP1         GGGTCGTTCTGGTGGTAGAT    212 TAGCGGGTT
                          TTCTGGTGGTGGAT
                          llllllllllll
                          AAGACCACCATCTA
                        GC_____
GAM36  APM1         GGGTTTTCT-GTTGTGAAT       213        GTG    I
                          GGGTTTTCTG GTGGA
                          llllllllll  lllll
                          CCCAAAAGAC CACTT
                            AA_  A
GAM36  APM1         GGGTTTTCT-GTTGTGAAT        213 TAGCGGGT    GTG
                          TTTCTG GTGGA
                          llllll  lllll
                          AAAGAC CACTT
                        _____    AA_
GAM36  INPP5A       GCAGGTTTTCTGGGTCGTCGA     211 C       _G GGI
                          GGGTTTTCTGG T GT
                          lllllllllll l ll
                          TCCAAAAGACC A CA
                          _       C G GCI
GAM36  INPP5A       GCAGGTTTTCTGGGTCGTCGA     211 TAGC      _G G TC
                          GGGTTTTCTGG T GT GA
                          lllllllllll l ll ll
                          TCCAAAAGACC A CA CT
                        ____        C G G TC
GAM36  TIRAP        GCTGCTTTCTCTT-TGGTGGATC  210 CGG     GG_     I
                          GTTTTCT TGGTGGAT
                          lllllll llllllll
                          CGAAAGA ACCACCTA
                        GA_    GAA     I
GAM36  TIRAP        GCTGCTTTCTCTT-TGGTGGATC  210 TAGCGG    GG_
                          GTTTTCT TGGTGGATC
                          lllllll lllllllll
                          CGAAAGA ACCACCTAG
                        A_____      GAA
GAM37  ADAT1        TGACCTCAAGT-GATCTGCCTGCC 231          ATA    I
                          TGACCTCAAGTGG TGCCTGCC
                          lllllllllll llllllll
                          ACTGGAGTTCACT ACGGACGG
                            AG_    I
GAM37  C21orf5      TGACCTCAAGT-GATCTGCCTGCC 231          ATA    I
                          TGACCTCAAGTGG TGCCTGCC
                          lllllllllll llllllll
                          ACTGGAGTTCACT ACGGACGG
                            AG_    I
GAM37  CASP10       TGACCTCAAGT-GATCTGCCTGCC 231          ATA    I
                          TGACCTCAAGTGG TGCCTGCC
                          lllllllllll llllllll
```

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                          ACTGGAGTTCACT  ACGGACGG
                              AG_      I
GAM37  CPT2      TGACCTCAAGT-GATCCACCCGCC 227         ATA     I
                          TGACCTCAAGTGG  TGCCTGCC
                          ||||||||||||  ||||||||
                          ACTGGAGTTCACT  GTGGGCGG
                              AG_      I
GAM37  CTSS      TGGCCTCAAGTTGATATGCCTGCC 234  A     G      I
                          TG CCTCAAGT GATATGCCTGCC
                          || |||||||| |||||||||||
                          AC GGAGTTCA CTATACGGACGG
                             C      A      I
GAM37  DAPP1     TGACCTCAAGT-GATCTGCTTG  222         ATA C CC
                          TGACCTCAAGTGG  TGC TG
                          |||||||||||  ||| ||
                          ACTGGAGTTCACT  ACG AC
                              AG_      A II
GAM37  DMC1      TGACCTCAAGT-GATCCACCTGCC 228         ATA     I
                          TGACCTCAAGTGG  TGCCTGCC
                          |||||||||||  ||||||||
                          ACTGGAGTTCACT  GTGGACGG
                              AG_      I
GAM37  DNASE2    TGACCTCAAGT-GATCTGCC    220         ATA TGC
                          TGACCTCAAGTGG  TGCC
                          |||||||||||  ||||
                          ACTGGAGTTCACT  ACGG
                              AG_    III
GAM37  FCMD      TGGCCTCAAGT-GATCCACCTGCC 232  A       ATA    I
                          TG CCTCAAGTGG  TGCCTGCC
                          || |||||||||  ||||||||
                          AC GGAGTTCACT  GTGGACGG
                             C      AG_    I
GAM37  FPRL1     TGACCTCAAGGCTGCAAATGC    218      TGGATA  C__  C
                          TGACCTCAAG   TGC TGC
                          |||||||||   ||| |||
                          ACTGGAGTTC   ACG ACG
                             CG____  TTT I
GAM37  GGCX      TGGCCTCAAGT-GATCTGCC    221  A     ATA TGC
                          TG CCTCAAGTGG  TGCC
                          || |||||||||  ||||
                          AC GGAGTTCACT  ACGG
                             C      AG_  III
GAM37  HCS       GACCTCAAGT-GATCTGCCTGCC 217 TG      ATA
                          ACCTCAAGTGG  TGCCTGCC
                          ||||||||||  ||||||||
                          TGGAGTTCACT  ACGGACGG
                          __       AG_
GAM37  HOXB5     TGACCTCAAGAGGTAATTCATGC  223       T A____   CTGCCI
                          TGACCTCAAG GG   TATGC
                          |||||||||| ||   |||||
```

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                          ACTGGAGTTC CC   GTACG
                             T ATTAA    IIICCG
GAM37  IL10          TGACCTCAAGT-GATCCACCCGCC 227        ATA    I
                        TGACCTCAAGTGG TGCCTGCC
                        ||||||||||| ||||||||
                        ACTGGAGTTCACT GTGGGCGG
                                  AG_    I
GAM37  MSL3L1          TGGCCTCAAGT-GATCCTCCTGCC 233  A       G ATG    I
                        TG CCTCAAGTG AT  CCTGCC
                        || |||||||| ||  ||||||
                        AC GGAGTTCAC TA  GGACGG
                           C    _ GGA    I
GAM37  NUP62          TGACCTCAAGT-CATCTGCCCGCC 226          GGATA    I
                        TGACCTCAAGT   TGCCTGCC
                        ||||||||||    ||||||||
                        ACTGGAGTTCA   ACGGGCGG
                                 GTAG_    I
GAM37  OPA3          TGACCTCAAGT-GATCCGCCCGCC 229        ATA    I
                        TGACCTCAAGTGG TGCCTGCC
                        ||||||||||| ||||||||
                        ACTGGAGTTCACT GCGGGCGG
                                  AG_    I
GAM37  PAICS          TGACCTCAAGT-GATCTGCTTGC 224        ATA C C
                        TGACCTCAAGTGG  TGC TGC
                        |||||||||||  ||| |||
                        ACTGGAGTTCACT  ACG ACG
                                  AG_  A I
GAM37  PHKB          ACCTCAAGT-GATCCACCTGCC   216 TGAC       ATA
                           CTCAAGTGG  TGCCTGCC
                           ||||||||  ||||||||
                           GAGTTCACT  GTGGACGG
                           ____       AG_
GAM37  POLK          TGACCTCAAGT-GATCTGCC      220        ATA  TGC
                        TGACCTCAAGTGG  TGCC
                        |||||||||||  ||||
                        ACTGGAGTTCACT  ACGG
                                  AG_  III
GAM37  SUDD          TGACCTCAAGT-GATCCACCCGCC 227        ATA    I
                        TGACCTCAAGTGG  TGCCTGCC
                        |||||||||||  ||||||||
                        ACTGGAGTTCACT GTGGGCGG
                                  AG_    I
GAM37  TNFRSF10A        TGACCTCAAGT-GATCCACCCGCC 227          ATA    I
                        TGACCTCAAGTGG  TGCCTGCC
                        |||||||||||  ||||||||
                        ACTGGAGTTCACT GTGGGCGG
                                  AG_    I
GAM37  TPM4          TGACCTCAAGT-GATCTGTCCTG 219        ATA _  CC
                        TGACCTCAAGTGG  TG CCTG
                        |||||||||||  || ||||
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                    ACTGGAGTTCACT  AC GGAC
                        AG_ A  II
GAM37 TRPM8      TGACCTCAAGT-GATCTGCC     220        ATA  TGC
                    TGACCTCAAGTGG  TGCC
                    |||||||||||  ||||
                    ACTGGAGTTCACT  ACGG
                        AG_   III
GAM37 ZNF136    TGACCTCAAGT-GATCCTCCTGCC 230       G ATG   I
                    TGACCTCAAGTG AT  CCTGCC
                    |||||||||| ||  ||||||
                    ACTGGAGTTCAC TA  GGACGG
                         _ GGA   I
GAM37 ZNF14     TGACCTCAAAT-GATCTGCCCGCC 225       ATA    I
                    TGACCTCAAGTGG  TGCCTGCC
                    ||||||||||  ||||||||
                    ACTGGAGTTTACT  ACGGGCGG
                        AG_   I
GAM38 ANK1      TCTGGCAGCCAG---GTCCCCGGC 243   AAAA  AGC
                    TCTG  CCAG  GTCCCCGGC
                    ||||  ||||  |||||||||
                    AGAC  GGTC  CAGGGGCCG
                     CGTC    ___
GAM38 ANK1      TCTGGCAGCCAG---GTCCCCGGC 243 _ AAAA  AGC
                     CTG  CCAG  GTCCCCGG
                    |||  ||||  ||||||||
                     GAC  GGTC  CAGGGGCC
                    A CGTC    ___
GAM38 CD3Z      AAACCAGAGGGCCCAAGGC      238       C  CC II
                    AAACCAGAG GTCC  GG
                    ||||||||| ||||  ||
                    TTTGGTCTC CGGG  CC
                         C  TT GI
GAM38 DPH2L1    TCTGAAAACCACCAGCCTC      241       G_  G CCCGG
                    TCTGAAAACCA AGC TC
                    ||||||||||| ||| ||
                    AGACTTTTGGT TCG AG
                     GG  G IIICG
GAM38 DPH2L1    TCTGAAAACCACCAGCCTC      241       G_  GTII
                    TCTGAAAACCA AGC
                    ||||||||||| |||
                    AGACTTTTGGT TCG
                     GG  GAGI
GAM38 HAS3      TCTGAAAA-CACAGAATCCCCTGC 242       _  GC   G I
                    TCTGAAAAC CAGA  GTCCCC GC
                    |||||||| ||||  |||||| ||
                    AGACTTTTG GTCT  TAGGGG CG
                         T  __  A I
GAM38 HAS3      TCTGAAAA-CACAGAATCCCCTGC 242 _    _  GC   GGI
                     CTGAAAAC CAGA  GTCCCC
                    |||||||| ||||  ||||||
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                          GACTTTTG GTCT  TAGGGG
                          A      T  __     ACI
GAM38  JAM2       TGAAAACCAGACGAGGCGTCCGCCGG 244  TCTG      ____    _   CII
                          AAAACCAGA   GCGTCC CCGG
                          ||||||||||   |||||| ||||
                          TTTTGGTCT   CGCAGG GGCC
                          ____        GCTC   C  CAI
GAM38  SLBP       GAAACCC---GCGTCCCCG      240  GA   AGA
                           AAACC  GCGTCCCC
                           |||||  ||||||||
                           TTTGG  CGCAGGGG
                           C_     G__
GAM38  TGFB3       GAAAACCAGGCGGCCTCCCC      239      A__  G  III
                          GAAAACCAG  GC TCCC
                          |||||||||  || ||||
                          CTTTTGGTC  CG AGGG
                           CGC  G   GII
GAM38  TGFB3       GAAAACCAGGCGGCCTCCCC      239  TCTGAA    A__  G
                           AACCAG  GC TCCCCGG
                           ||||||  || |||||||
                           TTGGTC  CG AGGGGTC
                          _____      CGC  G
GAM38  TRPV3      AAAACCAGAGGCTTCACCCGG      237        _ G _   III
                          AAAACCAGAG C TC CCCG
                          |||||||||| | || ||||
                          TTTTGGTCTC G AG GGGC
                           C A  T  CII
GAM39  ADAR      AGTCTGGCTGGTTCTAGACTTC   252  GT    AC   CTTI
                           CTGGCTG TCTG
                           ||||||| ||||
                           GACCGAC AGAT
                           __     CA   CTGA
GAM39  ARCN1      GTGTGAGTG-CTCTGCTTC       254   C GC A     I
                          GT TG  TG CTCTGCTT
                          || ||  || |||||||||
                          CA AC  AC GAGACGAA
                           C TC _      G
GAM39  CNGB3      GAAAG-CTTCATGATCTCTGCTTC 253    T GGC  _     I
                          AAAG CT  TGA CTCTGCTT
                          |||| ||  ||| ||||||||
                          TTTC GA  ACT GAGACGAA
                           _ AGT  A     I
GAM39  CNGB3      GAAAG-CTTCATGATCTCTGCTTC 253  TG   T GGC  _      I
                          AAAG CT  TGA CTCTGCTTC
                          |||| ||  ||| |||||||||
                          TTTC GA  ACT GAGACGAAG
                          __  _ AGT  A      G
GAM39  DAPK1     TGACAGCTCCTGGCTGACTC    255  A  __        TGCTT
                          TGA AGT CTGGCTGACTC
                          ||| ||| |||||||||||
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                               ACT TCG  GACCGACTGAG
                                G  AG        IIICT
GAM39  DAPK1        TGACAGCTCCTGGCTGACTC    255   A  __         III
                               TGA AGT  CTGGCTGACT
                               III III  IIIIIIIIII
                               ACT TCG  GACCGACTGA
                                G  AG       GII
GAM39  EPB41        TGAAAGTCTGAAGTCTGACTATG  256        ___    C  CTTCI
                               TGAAAGTCTGG  CTGACT TG
                               IIIIIIIIIII  IIIIII II
                               ACTTTCAGACT  GACTGA AC
                                  TCA    T IIICT
GAM39  EPB41        TGAAAGTCTGAAGTCTGACTATG  256 ___  A       ACTCI
                               TGAA GTCTGGCTG
                               IIII IIIIIIIII
                               ACTT CAGACTGAT
                               CAG  _       ACIII
GAM39  FMOD         AAAGTCTGGCCTTTCCTCTTCT   248 AA      GA__   GCI
                               GTCTGGCT  CTCT
                               IIIIIIII  IIII
                               CAGACCGG  GAGA
                                __   AAAG   AGI
GAM39  FMOD         AAAGTCTGGCCTTTCCTCTTCT   248 TGAA      GA__  G TC
                               AGTCTGGCT  CTCT CT
                               IIIIIIIII  IIII II
                               TCAGACCGG  GAGA GA
                               ____       AAAG  A CT
GAM39  IDH3A        AAGTACTAGCT--CTCTGCTTC   251 _  _     GA    I
                               AGT CTGGCT  CTCTGCTT
                               III IIIIII  IIIIIIII
                               TCA GATCGA  GAGACGAA
                                T  T    __    I
GAM39  IDH3A        AAGTACTAGCT--CTCTGCTTC   251 TGAAAGT    GA
                               CTGGCT  CTCTGCTT
                               IIIIII  IIIIIIII
                               GATCGA  GAGACGAA
                               AT_____      __
GAM39  IL5RA        TGAAAGTCTGAGGTGAGTC      257       _C  C  TGCTT
                               TGAAAGTCTG G TGA TC
                               IIIIIIIIII I III II
                               ACTTTCAGAC C ACT AG
                                T C   C IIICT
GAM39  IL5RA        TGAAAGTCTGAGGTGAGTC      257       _C  CTII
                               TGAAAGTCTG G TGA
                               IIIIIIIIII I III
                               ACTTTCAGAC C ACT
                                T C  CAGI
GAM39  RNMT         TGAAATTCAAGTCTTATCTCTGCTTC 258   G  T _ GA_     II
                               TGAAA TC GG CT  CTCTGCTTC
                               IIIII II II II  IIIIIIIII
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                          ACTTT AG TC GA   GAGACGAAG
                           A  T A ATA      II
GAM39  RNMT       TGAAATTCAAGTCTTATCTCTGCTTC 258 GA___    GGCTGA     I
                           AAGTCT    CTCTGCTT
                           IIIIII    IIIIIIII
                           TTCAGA    GAGACGAA
                           TTAAG    ATA___     I
GAM39  TMEM2      AAAGACCTCAGGCTGACTCT   247  T ___      III
                           AAAG CT  GGCTGACTC
                           IIII II  IIIIIIIII
                           TTTC GG  CCGACTGAG
                            T AGT      AII
GAM39  TMEM2      AAAGACCTCAGGCTGACTCT    247 T AAG  T     GCTT
                            GA  TC GGCTGACTCT
                            II  II IIIIIIIIII
                            CT  AG CCGACTGAGA
                            T GG_ T      GTII
GAM39  WARS       AAAGCCACCCTGACTCTGC     250      TGG      II
                           AAAGTC  CTGACTCTG
                           IIIIII  IIIIIIIII
                           TTTCGG  GACTGAGAC
                            TGG      GI
GAM39  WARS       AAAGCCACCCTGACTCTGC     250 TGAA   TGG      TT
                            AGTC  CTGACTCTGC
                            IIII  IIIIIIIIII
                            TCGG  GACTGAGACG
                            ____    TGG       TC
GAM39  ZNF144     AAAGTCTGG--GATCTGTGCTT  249 _     CT _ C  I
                           AAGTCTGG GA CT TGCT
                           IIIIIIII II II IIII
                           TTCAGACC CT GA ACGA
                            T    __ A C  I
GAM39  ZNF144     AAAGTCTGG--GATCTGTGCTT   249 TGAA    CT _ C
                           AGTCTGG GA CT TGCTT
                           IIIIIII II II IIIII
                           TCAGACC CT GA ACGAA
                            ____      __ A C
GAM40  GNRH1      AAAAAGCTAGCATCTGTATCA    261       AC__  GTTCIII
                           AAAAAGCTA  CTG
                           IIIIIIIII  III
                           TTTTTCGAT  GAC
                           CGTA  ATAGTII
GAM40  GNRH1      AAAAAGCTAGCATCTGTATCA    261 TA    AC__  GT AAAT
                           AAAAGCTA  CTG TCA
                           IIIIIIII  III III
                           TTTTCGAT  GAC AGT
                            __     CGTA AT GIII
GAM40  MNDA       AAAGCTAACAAGG--AAAAAT    262      CT TTCAAAI
                           AAAGCTAAC GG
                           IIIIIIIII II
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                          TTTCGATTG CC
                          TT TTTTTAI
GAM41  AGTR1      AATTTGTTGCAAACACTATATCAA  276  TAAAATTTCTCAA       TI
                          ACTATATCAA
                          |||||||||
                          TGATATAGTT
                          AACAACGTTTG__        TA
GAM41  BCAT1      AAATTTTCTCAAATTAGCTTTCAA  269  TAAAA     C TA__   TI
                          TTTCTCAAA TA   TCAA
                          ||||||||| ||   ||||
                          AAAGAGTTT AT   AGTT
                          TTA__        A CGAA  TI
GAM41  FACL4      AAATTTCCTCAAACTACAT       274  TAAAA          CAA
                          TTTCTCAAACTATAT
                          |||||||||||||||
                          AAGGAGTTTGATGTA
                          TA___           AGI
GAM41  GALNT2     AAAATTAC-CAAACTATAT       271  TA    T T     CA
                          AAATT C CAAACTATAT
                          ||||| | ||||||||||
                          TTTAA G GTTTGATATA
                          __    T _     AI
GAM41  ITIH2      TATAATTTCCCAAACTATA       281  TAA          TCAA
                          AATTTCTCAAACTATA
                          ||||||||||||||||
                          TTAAAGGGTTTGATAT
                          ATA           |||T
GAM41  LHCGR      AAAATTTCT-AAACACTCTCAA    273  TA    C  TATA
                          AAATTTCT AAAC   TCAAT
                          |||||||| ||||   |||||
                          TTTAAAGA TTTG   AGTTG
                          __     _  TGAG
GAM41  MDM1       AAAATTTCTATTCAAACTTTTTAAA 265  TA     ___     ATATCAATII
                          AAATTTC  TCAAACT
                          |||||||  |||||||
                          TTTAAAG  AGTTTGA
                          __     ATA     AAAATTTTII
GAM41  NDUFA5     AAAATTTCTCCAATAACCTGTATGCAAT267  TA     AAA____ A _   III
                          AAATTTCTC      CT TAT CAAT
                          |||||||||      || ||| ||||
                          TTTAAAGAG      GA ATA GTTA
                          __      GTTATTG C C  C||
GAM41  PDGFRA     TAAAAGTTTCTCTCAAACT       277  TAAAA___        ATATCAA
                          TTTCTCAAACT
                          |||||||||||
                          AGAGAGTTTGA
                          ATTTTCAA      |||TAAC
GAM41  PITPNB     AAAATGTCATCACTAACTATATC   266  TA T _ __       AATI
                          AAAT TC TCA  AACTATATC
                          |||| || |||  |||||||||
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                           TTTA AG AGT  TTGATATAG
                           __   C T  GA       GIII
GAM41  RANBP2L1        AAAATTTCTCAACAATTTATAACAAT 268 TA         AC___   T  II
                           AAATTTCTCAA    TATA CAAT
                           |||||||||||    |||| ||||
                           TTTAAAGAGTT    ATAT GTTA
                           __          GTTAA  T  GI
GAM41  RAX            AAAGTTTCTCAAACTCTAT    272 TAAAA      A  CAA
                           TTTCTCAAACT TAT
                           ||||||||||| |||
                           AAAGAGTTGA ATA
                           TTC__        G  AII
GAM41  RNF6          AAAATAGTTCAAACTATAT     270 TAAAATTTC        CAA
                           TCAAACTATAT
                           |||||||||||
                           AGTTTGATATA
                           TTTATCA__          TII
GAM41  SAS        TAAACTTTCTCAAACTGGATC      282    A      AT AAT
                           TAAA TTTCTCAAACT ATC
                           |||| ||||||||||| |||
                           ATTT AAAGAGTTGA  TAG
                             G       CC  III
GAM41  SCN3A         TATAAATTCTCAATAACTATATCA 280 TAAAAT     __       ATI
                           TTCTCAA ACTATATCA
                           ||||||| |||||||||
                           AAGAGTT TGATATAGT
                           ATATTT    AT       III
GAM41  SIP1      TAAAATTTCATCATACAATTCTAT 279        _ A T A AATII
                           TAAAATTTC TCA AC AT TC
                           ||||||||| ||| || || ||
                           ATTTTAAAG AGT TG TA AG
                             T  A T A ATAII
GAM41  SMARCC1       AAAAGTCTCAAACTTTACCA    275 TAAAATT     A   A
                           TCTCAAACT TATCA
                           ||||||||| |||||
                           AGAGTTGA ATGGT
                           TTC____       A   A
GAM41  SORCS1        TACAATGGTTCTCAAACTTTA   278 TAAAAT__      ATATCAAT
                           TTCTCAAACT
                           ||||||||||
                           AAGAGTTGA
                           ATGTTACC         AATIIITA
GAM42  ACTN2       AAGGCTT---TTTTTTTTTCCCC   288     CAG  C
                           AGGGTT  TTT TTTTTCCC
                           |||||| ||| |||||||||
                           TTCCGA  AAA AAAAAGGG
                            AA_ _
GAM42  ACTN2       AAGGCTT---TTTTTTTTTCCCC   288 TAA    CAG  C
                           GGGTT  TTT TTTTTCCC
                           ||||| ||| |||||||||
```

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                        TCCGA  AAA AAAAGGGG
                         ___    AA_  A
GAM42  ADD2       GGGTTCGGAATTTCTTTTTC    292    __          III
                     GGGTTC AGTTTCTTTTT
                     |||||| ||||||||||||
                     CCCAAG TTAAAGAAAAA
                        CC          GII
GAM42  ADD2       GGGTTCGGAATTTCTTTTTC    292 TAA  TTCA       CC
                     GGG  GTTTCTTTTTC
                     |||  ||||||||||||
                     CCT  TAAAGAAAAAG
                        AAG  ____       AA
GAM42  BCRP2      GGGTT-ATTTT-TTTTTCCCC   294 _  CA   C     I
                     GGTT GTTT TTTTTCCC
                     |||| |||| ||||||||
                     CCAA TAAA AAAAAGGG
                        C  __   A     I
GAM42  BCRP2      GGGTT-ATTTT-TTTTTCCCC   294 TAAGGGTTCA  C
                         GTTT TTTTTCCC
                         |||| |||||||||
                         TAAA AAAAAGGG
                        AA_____  A
GAM42  CDH13      AGGGTTCAGGTGTCTTAGTTTCC 290 __ _ C_    TTTTI
                        AGG GTT AGTTTCT
                        ||| ||| ||||||||
                        TCC CAG TCAAAGG
                        AG A AA    IIITT
GAM42  CDH13      AGGGTTCAGGTGTCTTAGTTTCC 290 TAAG    TT_ __    CCI
                        GGTTCAG TCTT TTTCC
                        ||||||| |||| |||||
                        CCAAGTC AGAA AAAGG
                         ____    CAC  TC   TGI
GAM42  CLCA3      GGGTTCAGTATAATTTTTCC    293        TTC_  II
                        GGGTTCAGT  TTTTTC
                        |||||||||  ||||||
                        CCCAAGTCA  AAAAAG
                          TATT    GI
GAM42  CLCA3      GGGTTCAGTATAATTTTTCC    293 TAAGGG  TTC_   C
                        TTCAGT  TTTTTCC
                        ||||||  |||||||
                        AAGTCA  AAAAAGG
                          _____   TATT    T
GAM42  CSPG3      TAAGGGTTCAGTTTACACTTCTT 298        CTT  CCCI
                        TAAGGGTTCAGTTT  TTTC
                        ||||||||||||||  ||||
                        ATTCCCAAGTCAAA  GAAG
                          TGT   AAII
GAM42  CSPG3      TAAGGGTTCAGTTTACACTTCTT 298 AAG       ___   I
                        GGTTCAGTTT  CTTTT
                        ||||||||||  |||||
```

```
                              CCAAGTCAAA  GAAGA
                              ___        TGT    I
GAM42  CSPG3         AAGGTGTTGTGCTTTCTTTTT   285 TA  _ CAG_     CCCC
                          AGG GTT   TTTCTTTTT
                          ||| |||  |||||||||
                          TCC CAA   AAAGAAAAA
                          __ A CACG      AIII
GAM42  PLA2G2A       GGATCTGTTGCTCTTTTCC    295 TAAGGGTTCA  T    C
                              GTT CTTTTTCC
                              ||| ||||||||
                              CGA GAAAAAGG
                          GACAA_____ _     A
GAM42  RGL          AGGTTCTCAGTTTCTTCTATTTCCC 289 GGGT       ___  I
                          TCAGTTTCTTT  TTCC
                          |||||||||||  ||||
                          AGTCAAAGAAG  AAGG
                          G___        ATA  I
GAM42  RGL          AGGTTCTCAGTTTCTTCTATTTCCC 289 TAA GG       ___  CII
                          G TTCAGTTTCTTT  TTCCC
                          | |||||||||||  |||||
                          C GAGTCAAAGAAG  AAGGG
                          ___ AA        ATA  ACI
GAM42  SET          AAGGGAGCAGGTTTTTCTTTTTTCCC 286 A___    CAG     _ CI
                          GGGTT  TTTCTTTTT CC
                          |||||  |||||||||| ||
                          TCCAA  AAAGAAAAA GG
                          CTCG    ___       A II
GAM42  SET          AAGGGAGCAGGTTTTTCTTTTTTCCC 286 TA   TT ___      _ CII
                          AGGG CAG  TTTCTTTTT CCC
                          |||| |||  |||||||||| |||
                          TCCC GTC  AAAGAAAAA GGG
                          __ TC  CAA      A TII
GAM42  STAU          TAGGGGTTATGCTTTCTTTTT    297 AA   CA  _   I
                          GGGTT  GTTT  CTTTT
                          |||||  ||||  |||||
                          CCCAA  CGAA  GAAAA
                          C_  TA  A    I
GAM42  STAU          TAGGGGTTATGCTTTCTTTTT    297 TAA   CA  _   CCCC
                          GGGTT  GTTT  CTTTTT
                          |||||  ||||  ||||||
                          CCCAA  CGAA  GAAAAA
                          ATC    TA  A    IIIC
GAM42  TIMM23       TTCATGTTTCTTTTTCTCC        299  _       _ II
                          TTCA GTTTCTTTTTC CC
                          |||| ||||||||||| ||
                          AAGT CAAAGAAAAAG GG
                          A       A II
GAM42  TMEM2        GTTCACATTTTTTTTCCCC        296  _  C     II
                          GTTCA GTTT TTTTCCC
                          ||||| |||| |||||||
```

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                              CAAGT TAAA AAAAGGGG
                                G   A        II
GAM42  TMEM2      GTTCACATTTTTTTTCCCC   296 TAAGGGTTCA   C
                             GTTT TTTTTCCC
                             |||| |||||||||
                             TAAA AAAAGGGG
                          G_____       A
GAM42  XKRY      AAAGGT--AGTTTCTTTTT   287    TC       I
                          AAGGGT AGTTTCTTTT
                          |||||| |||||||||||
                          TTTCCA TCAAAGAAAA
                          __            A
GAM42  XKRY      AAAGGT--AGTTTCTTTTT   287 TA  TC      CC
                          AGGGT AGTTTCTTTTT
                          ||||| |||||||||||
                          TTCCA TCAAAGAAAAA
                          __  __       AI
GAM42  ZNF135    AGGGTTCAGACTTATGTTTTCCC  291 GG   _  CT_  I
                          GTTCAG TTT  TTTTCC
                          |||||| |||  ||||||
                          CAAGTC GAA  AAAAGG
                          __   T  TAC   I
GAM42  ZNF135    AGGGTTCAGACTTATGTTTTCCC  291 TAAG  _  CT_  CI
                          GGTTCAG TTT  TTTTCCC
                          ||||||| |||  |||||||
                          CCAAGTC GAA  AAAAGGG
                          ____      T  TAC   AA
GAM43  ADCY9     ACACTCTTTGAAACGTTGAGCTTG 302 TGACACCG  ____     TCAI
                          TTGA  TTGAGCTTG
                          ||||  |||||||||
                          AACT  AACTCGAAC
                TGAGA___  TTGC    CAII
GAM43  DYRK1A    GAC-CCGTTGATT--GCTTCTCA  305 TG A     GA  G
                          AC CCGTTGATT GCTT TC
                          || ||||||||| |||| ||
                          TG GGCAACTAA CGAA AG
                          __  _      __  G
GAM43  FUS1      ACACC-TTGATTGAGCCTG    303 TGAC  G       T
                          ACC TTGATTGAGCTTG
                          ||| ||||||||||||||
                          TGG AACTAACTCGGAC
                          ____  _      C
GAM43  KRT15     GACACTGTACAAATGAGCTTGT  304 TG  C _ T    CA
                          ACAC GT TGA TGAGCTTGT
                          |||| || ||| |||||||||
                          TGTG CA GTT ACTCGAACA
                          __  A T    AI
GAM43  PHYH      TGACACCGTTCCTATGCCCTTG  307      GA A GTCA
                          TGACACCGTT TTG GCTT
                          |||||||||| ||| ||||
```

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                        ACTGTGGCAA  GAT CGGG
                           G_   A    AACI
GAM43   RGL         TGGCAC--TTGATTGAGAAAGTCA  308   A  CG        CTT
                        TG CAC  TTGATTGAG  GTCA
                        || ||| ||||||||  ||||
                        AC GTG  AACTAACTC  CAGT
                           C   __        TTT
GAM43   SCD         TGTCAC--TTGAATTGAGCTT    306 TGA  CG  _      GTC
                          CAC  TTGA TTGAGCTT
                          ||| |||| |||||||||
                          GTG  AACT AACTCGAA
                        ACA  __  T   III
GAM44   BCL2        GTTTCTTACTCAGACAGAGC      328              AGIII
                        GTTTCTTACTCGGG
                        ||||||||||||||
                        CAAAGAATGAGTCT
                           GTCTC
GAM44   BCL2        GTTTCTTACTCAGACAGAGC      328 TGAGTT      ___  TG
                        TCTTACTCGG  GAGC  G
                        |||||||||| |||| |
                        AGAATGAGTC  CTCG  C
                        _____       TGT  GT
GAM44   CIAS1       GCTACTCAGGAAGTTGAGGT      320 TGGC  T  _      C
                        TACTC GGA GTTGAGGTG
                        ||||| ||| ||||||||||
                        ATGAG CCT CAACTCCAT
                        ____     T  T     C
GAM44   CRYAA         GCTA-TCTAAAGGAGTGTGAGGTGCG 318 TGG  CTCT   _      II
                        CTA   GGAGT TGAGGTGCG
                        |||   ||||| |||||||||
                        GAT   CCTCA ACTCCACGC
                        ATA  TT__   C    CA
GAM44   CX3CR1      GCTACT--GGAGTTGGGGT       323 TGGCTACT       A  G
                        CTGGAGTTG GGT
                        ||||||||| |||
                        GACCTCAAC CCA
                        AT_____     C  A
GAM44   FUS1        GAGTTTCTTGC-CGGG-GCAGG    316 TG    A T  A T
                        AGTTTCTT C CGGG GC GG
                        |||||||| | |||| || ||
                        TCAAAGAA G GCCC CG CC
                          __    C _  _ T
GAM44   FUS1        GAGTTTCTTGC-CGGG-GCAGG    316         A T  A TI
                        GAGTTTCTT C CGGG GC
                        ||||||||| | |||| ||
                        CTCAAAGAA G GCCC CG
                           C _  _ TC
GAM44   GFAP        TGAGTTTCTTGTTAGTTGGAGTTG  331          ACTCG__  C GCI
                        TGAGTTTCTT    GGAG TG
                        ||||||||||    |||| ||
```

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                              ACTCAAAGAA      CCTC AC
                                CAATCAA   A III
GAM44   GFAP        TGAGTTTCTTGTTAGTTGGAGTTG 331 A      ACTCG__   CTI
                           GTTTCTT      GGAG
                           |||||||     ||||
                           CAAAGAA     CCTC
                        _       CAATCAA   AII
GAM44   GNGT2         CTACTCTGGCGTGGAAATGC    314 TGGCTA    A T
                           CTCTGG GT GAGGTGC
                           |||||| || ||||||||
                           GAGACC CA CTTTACG
                        _____      G C
GAM44   HEM1         TGGCTA-T-TGGAGTTGAGG     335    CTC      TG
                           TGGCTA  TGGAGTTGAGG
                           ||||||  |||||||||||
                           ACCGAT  ACCTCAACTCC
                             A__         II
GAM44   HSPB2        GCTACCTCTGGAGTGGTGG     317 TGGCTA     TGA T
                           CTCTGGAGT  GG GC
                           |||||||||  || ||
                           GAGACCTCA  CC CG
                           ATG___      CCA _
GAM44   HTR1D        GCTACTCTGGAGGCTGAGG     319 TGGC      _    C
                           TACTCTGGAG TTGAGGTG
                           |||||||||| ||||||||
                           ATGAGACCTC GACTCCGT
                           ____        C   I
GAM44   IMPA2      ACTTTGCAAGGCTGAGGTGCG     311 TGGCTACTCT A
                           GG GTTGAGGTGCG
                           || |||||||||||
                           TC CGACTCCACGC
                        CGT_____  _
GAM44   LTF         TGAGGCTTTCTTG---GGGAGCTGG 330   __    ACTC     C
                           TGAG TTTCTT  GGGAGCTGG
                           |||| ||||||  |||||||||
                           ACTC AAAGAA  CCCTCGACC
                             CG   C___      I
GAM44   LTF         TGAGGCTTTCTTG---GGGAGCTGG 330 _ __     ACTC    I
                           GAG TTTCTT  GGGAGCTG
                           ||| ||||||  ||||||||
                           CTC AAAGAA  CCCTCGAC
                           A CG   C___      I
GAM44   MAFF        TGGACACTGACAGGGGTTGAGGTG 333   C  CT__ A     CGI
                           TGG TACT  GG GTTGAGGTG
                           ||| ||||  || |||||||||
                           ACC GTGA  CC CAACTCCAC
                            T  CTGT C       III
GAM44   METTL1      CTCCTC---AGTTGAGGTGC     315 TGGCTA TGG
                           CTC AGTTGAGGTG
                           ||| |||||||||
```

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                              GAG   TCAACTCCAC
                             _____  ___
GAM44  MME         GTTTCTTA--CAGGTGCTGGC   329 _      TC  A   I
                        TTTCTTAC GGG GCTGG
                        |||||||| ||| |||||
                        AAAGAATG TCC CGACC
                            C      __ A   I
GAM44  MME         GTTTCTTA--CAGGTGCTGGC   329 TGAGTT   TC  A
                         TCTTAC GGG GCTGG
                         |||||| ||| |||||
                         AGAATG TCC CGACC
                             _____  __  A
GAM44  MPP2       TGGCGCCTCTGGAGTTGTGTGTG  334   TA     AG  CGI
                      TGGC CTCTGGAGTTG GTG
                      |||| ||||||||||| |||
                      ACCG GAGACCTCAAC CAC
                        CG       A_  ACI
GAM44  MTR        GCTACTCTGGAGGCTGAGG      319 TGGC       _     C
                      TACTCTGGAG TTGAGGTG
                      |||||||||| ||||||||
                      ATGAGACCTC GACTCCGT
                      ____       C    I
GAM44  NFRKB       GCTGCTG-GGAGTTGAGGTAGCG  324 TG  ACTCT       _
                       GCT   GGAGTTGAGGT GCG
                       |||   |||||||||| |||
                       CGA   CCTCAACTCCA CGC
                       A_  C____         T
GAM44  PPP2R2B      AGTTTCTTAGAACTGGGGAGCTGG  313 GTT  ___  C     I
                       TCTT ACT GGGAGCTG
                       |||| ||| ||||||||
                       AGAA TGA CCCTCGAC
                       ___  TCT C    I
GAM44  PPP2R2B      AGTTTCTTAGAACTGGGGAGCTGG  313 TGAG   ___  C    CI
                       TTTCTT ACT GGGAGCTGG
                       |||||| ||| |||||||||
                       AAAGAA TGA CCCTCGACC
                       ____   TCT C    CT
GAM44  RENT1       GGCTACTCT-GAGATGAGG      326 TG   G T   TG
                       GCTACTCTG AG TGAGG
                       ||||||||| || |||||
                       CGATGAGAC TC ACTCC
                       __      _ T   CI
GAM44  REQ         GCCACTCTGGAGGAAAGAGGTG   321 TGGC     TT__  CG
                       TACTCTGGAG  GAGGTG
                       ||||||||||  ||||||
                       GTGAGACCTC  CTCCAC
                       ____          CTTT   TC
GAM44  SIM2        AGTCTGCGTCCTGGGGAGCTGGC  312 ___ T  ACTC       I
                        GT TCTT  GGGAGCTGG
                        || |||| |||||||||
```

```
                              CG AGGA   CCCTCGACC
                             AGA C  C___        I
GAM44  SLC24A1      GGCTACTCTGGGATTCAGGT    327 TG      AG G   GC
                        GCTACTCTGG TT AGGT
                        |||||||||| || ||||
                        CGATGAGACC AA TCCA
                           __      CT G   AI
GAM44  SLC6A3       GGC-ACACTGGGAGTTGAGG    325 TG T T  _     TGC
                        GC AC CTGG AGTTGAGG
                        || || |||| ||||||||
                        CG TG GACC TCAACTCC
                        __ _ T  C    TII
GAM44  TCF2         TGAGTCGATGACTCGGGAGC    332     TCTT     TGG
                        TGAGTT  ACTCGGGAGC
                        ||||||  ||||||||||
                        ACTCAG  TGAGCCCTCG
                          CTAC       III
GAM44  TCF2         TGAGTCGATGACTCGGGAGC    332     TCTT    I
                        GAGTT  ACTCGGGAG
                        |||||  |||||||||
                        CTCAG  TGAGCCCTC
                         CTAC        I
GAM44  TEM5         TGGC-AGTCAGCTGTTGAGGTGC 336    TAC TGGA      G
                        TGGC TC  GTTGAGGTGC
                        |||| ||  |||||||||||
                        ACCG AG  CAACTCCACG
                         TC_ TCGA       I
GAM44  TNFRSF11A      GCTACTCCGAAGGTTGAGGTG  322 TGGC      _     CG
                        TACTCTGGAG TTGAGGTG
                        |||||||||| ||||||||
                        ATGAGGCTTC AACTCCAC
                          ____      C    CC
GAM45  ADORA1        AGTGTTCTCCTCTCCATCAG    349 TACAGT   GTA  A
                        GTTCTC  TCCA CAG
                        ||||||  |||| |||
                        CAAGAG  AGGT GTC
                         _____    GAG   A
GAM45  BTG3         TACAGGGTTCTCGTATCCAACAGA 358    T          I
                        TACAG GTTCTCGTATCCAACAGA
                        ||||| ||||||||||||||||||
                        ATGTC CAAGAGCATAGGTTGTCT
                          C            I
GAM45  BTG3         TCAAAGGGGCTAAAACAAATCGTC 363     T          I
                        TCAAAGG GCTAGAACAAATCGTC
                        ||||||| |||||||||||||||
                        AGTTCC CGATTTTGTTTAGCAG
                          C            I
GAM45  CLASP1       ACAGTGTTCCCAAGGATCTCAGCAG 344 TA      T__ _ A AII
                        CAGTGTTCTCG  ATC CA CAG
                        |||||||||  ||| || |||
```

```
                         GTCACAAGGGT  TAG GT GTC
                         __        TCC  A  C  AII
GAM45  CPD        CAGTGTTCTC----CCAAGAG   355 TACA     GTAT  C
                         GTGTTCTC   CCAA A
                         IIIIIIII   IIII I
                         CACAAGAG   GGTT T
                         ____       ____   C
GAM45  DGKI       CACTGTATCCTGTATCCAACAG  351 TACA    C       A
                         GTGTTCT GTATCCAACAG
                         IIIIIII IIIIIIIIII
                         CATAGGA CATAGGTTGTC
                         GA__    _       A
GAM45  FAAH       CAGT-TTCTGGTGCATCCAACAGA 353 TACAGTG   C__        I
                         TTCT  GTATCCAACAGA
                         IIII  IIIIIIIIIII
                         AAGA  CGTAGGTTGTCT
                         CA_____  CCA        C
GAM45  FCMD     TCAAAGGTGCATGAAACAAT    360       TA_  ATCGT
                         TCAAAGGTGC  GAACAA
                         IIIIIIIIII  IIIIII
                         AGTTTCCACG  TTTGTT
                         TAC    AIIIC
GAM45  FZD4     AAAGGTGCT-GAACAGAATC   340 TCAA    A  _  GT
                         AGGTGCT GAACA AATC
                         IIIIIII IIIII IIII
                         TCCACGA CTTGT TTAG
                         ____       _    C  AG
GAM45  GNRHR      GTGTATTGGTAATCCAACAGA   356 TACAGTGTTCTC  _
                         GTA TCCAACAGA
                         III IIIIIIIII
                         CAT AGGTTGTCT
                         TAAC_____   T
GAM45  HGF       ACAGTGTTCT--T-TTCAAGAGA 346 TA      CGTATC  C
                         CAGTGTTCT    CAA AG
                         IIIIIIIII    III II
                         GTCACAAGA    GTT TC
                         __         AAA___  C
GAM45  HNRPDL      TCAAAGGTG-TGGTAGAAATC   362     C__  CAA GT
                         TCAAAGGTG  TAGAA  ATC
                         IIIIIIIII  IIIII  III
                         AGTTTCCAC  ATCTT  TAG
                         ACC       ___  II
GAM45  HS2ST1     AGTGATTATC-TCTCCAACAGA  347 TACAGTGT  GTA
                         TCTC  TCCAACAGA
                         IIII  IIIIIIIII
                         AGAG  AGGTTGTCT
                         CTAAT___   ___
GAM45  MEN1       CAAATGAG---GAACAAATC    350 TCAA    CTA    G
                         AGGTG  GAACAAATC
                         IIIII  IIIIIIIII
```

```
                     TTTAC  CTTGTTTAG
                     ____        TC_        G
GAM45  MLLT2         ACAGTGTTCTTCCATTTCCTAC   343 TA      __   A  A  AGA
                     CAGTGTTCT CGT TCC AC
                     |||||||| ||| ||| ||
                     GTCACAAGA GTA AGG TG
                             __   AG   A   A  AII
GAM45  NAB1          TCAAAGGTG-TAGAA-AAAT     359      C   CAAATCG
                     TCAAAGGTG TAGAA
                     ||||||||| |||||
                     AGTTTCCAC ATCTT
                              _    TTTAIII
GAM45  NPTX2         AGAGTTCTCGTAGCATACA      348 TACAGT      TC _
                     GTTCTCGTA CA ACAG
                     ||||||||| || ||||
                     CAAGAGCAT GT TGTT
                     _____        C_  A
GAM45  SH3BP2        AAGGTGCTAAGAA-AAATC      342 TCAAAG    _  C    G
                     GTGCTA GAA AAATC
                     |||||| ||| |||||
                     CACGAT CTT TTTAG
                     _____      T  _  T
GAM45  SNRP70        TCCAAGGGGCCAGAACAAAT     361 A  T       CGT
                     TC AAGG GCTAGAACAAAT
                     || |||| |||||||||||||
                     AG TTCC CGGTCTTGTTTA
                          G   C         III
GAM45  SOX11         AAAGGTGTCACAGAACAAAT     339 TCAA   C__        CGT
                     AGGTG  TAGAACAAAT
                     |||||  |||||||||||
                     TCCAC  GTCTTGTTTA
                     ____     AGT        CGI
GAM45  TMEM2         TCCAAGGTGCTACAATAGCTGGTC 364 A      G CAAATC  I
                     TC AAGGTGCTA AA    GTC
                     || ||||||||| ||    |||
                     AG TTCCACGAT TT    CAG
                       G     G ATCGAC  I
GAM45  UBQLN1        TACAGTGTTCCTTCAGTCTGCACAAAGA357        CG _ CA_   III
                     TACAGTGTTCT TA TC  ACAGA
                     ||||||||||| || ||  |||||
                     ATGTCACAAGG GT AG  TGTTT
                          AA C ACG    CTI
GAM45  VAT1          AAGGCACTGAGAACAAATC      341 TCAAAG TG _      GT
                     G  CT AGAACAAATC
                     |  || ||||||||||
                     C  GA TCTTGTTTAG
                     _____GT C      GT
GAM45  VSX1          ACACTGTTTCCAGCTATCCAACA  345 TA G  CT __       AI
                     CA TGTT CG TATCCAACAG
                     || |||| || |||||||||||
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                        GT ACAA  GT  ATAGGTTGTT
                        __  G  AG CG        II
GAM45   WNT2        CAGTGTTCTTGCAGATCCAA    352 TACA     C __      CAG
                        GTGTTCT GT  ATCCAA
                        ||||||| || ||||||
                        CACAAGA CG  TAGGTT
                        ____      A  TC    ACI
GAM45   ZNF137       CAGTGTTC---TATACAAC    354 TACA     CGT__    AAC
                        GTGTTCT    ATCC
                        |||||||    ||||
                        CACAAGA    TGGG
                        ____       TATGT   III
GAM46   AQP6        TGACTGG-GACCCTCTCTTGGCC  384      T G         C
                        TGACTGG GG TCTCTTGGCC
                        ||||||| || |||||||||||
                        ACTGACC CT GGAGAGAACCGG
                            _  G       I
GAM46   AQP6        TGACTGG-GACCCTCTCTTGGCC  384 _    T G        I
                        GACTGG GG TCTCTCTTGGC
                        |||||| || |||||||||||
                        CTGACC CT GGAGAGAACCG
                            A  _  G       I
GAM46   ATP4A       ACTGGTGGGGCTGGGACTCTTGG  370       T ____    IIIC
                        ACTGGTGGG CT  CTCTTG
                        ||||||||| ||  ||||||
                        TGACCACCC GA   GAGAAC
                            C CCCT    CIII
GAM46   ATP4A       ACTGGTGGGGCTGGGACTCTTGG  370 TGAC     T ____    CCCI
                        TGGTGGG CT   CTCTTGG
                        ||||||| ||  |||||||
                        ACCACCC GA   GAGAACC
                        ____      C  CCCT    AAII
GAM46   C8G         ACTGGTGGGGTCGTCTCTCGG    368        _ _       III
                        ACTGGTGGG TC TCTCTTG
                        ||||||||| || |||||||
                        TGACCACCC AG AGAGAGC
                            C C     CII
GAM46   C8G         ACTGGTGGGGTCGTCTCTCGG    368 TGAC     _ _       CCC
                        TGGTGGG TC TCTCTTGG
                        ||||||| || |||||||||
                        ACCACCC AG AGAGAGCC
                        ____       C C     CCI
GAM46   CALM3       CTGGAATGCCTCTCTTGGC      374 TGG         II
                        CTGG  GTCTCTCTTGG
                        ||||  ||||||||||
                        GACC  CGGAGAGAACC
                            TTA       GI
GAM46   CALM3       CTGGAATGCCTCTCTTGGC      374 TGACTGGTGG        _
                        GTCTCTCTTGGC C
                        |||||||||||| I
```

```
                              CGGAGAGAACCG G
                    CTTA_____          T
GAM46  CUTL1       CTGGCTGGGGCTCTCTCTCTTGG  372   _ ____        IIIC
                    CTGG TGGG   TCTCTCTTG
                    IIII IIII   IIIIIIIII
                    GACC ACCC   AGAGAGAAC
                      G   CGAG        CIII
GAM46  CUTL1       CTGGCTGGGGCTCTCTCTCTTGG  372  TGA  T G__       CCCI
                    CTGG GG   TCTCTCTTGG
                    IIII II   IIIIIIIIII
                    GACC CC  AGAGAGAACC
                     C__  _ GAG        CCAI
GAM46  ELAVL3      TGCCTG-TGCTGTCTCTCTTGGGCC 380  A  _ GG        CI
                     CTG GT  GTCTCTCTTGG
                     III II  IIIIIIIIIII
                     GAC CG  CAGAGAGAACC
                      G   A A_       CI
GAM46  ELAVL3      TGCCTG-TGCTGTCTCTCTTGGGCC 380  TGA _ GG       _ CI
                     CTG GT  GTCTCTCTTGG CC
                     III II  IIIIIIIIIII II
                     GAC CG  CAGAGAGAACC GG
                      ACG  A A_       C II
GAM46  HTR2A       GGTTGGTCTCAAACTCTTGGCC   377   G   ____       IIIG
                     GGT GGTCTC   TCTTGGC
                     III IIIIII   IIIIIII
                     CCA CCAGAG   AGAACCG
                      A    TTTG      GIII
GAM46  ITGAM       TGGTTGGGTCTCTTCTGCCCC    385  GG      CT G I
                     TGGGTCTCT TG CC
                     IIIIIIIII II II
                      ACCCAGAGA AC GG
                      CA     AG G I
GAM46  ITGAM       TGGTTGGGTCTCTTCTGCCCC    385  TGACTGG      CT G
                     TGGGTCTCT TG CCC
                     IIIIIIIII II III
                     ACCCAGAGA AC GGG
                     _____       AG G
GAM46  KCNQ1       GGTGGGGCCACTCTTGGCC      376      _ T    II
                     GGTGGG TC CTCTTGGC
                     IIIIII II IIIIIIIII
                     CCACCC GG GAGAACCG
                       C  T    GI
GAM46  KCNQ1       GGTGGGGCCACTCTTGGCC      376  TGACTGGTG  T
                     GGTC CTCTTGGCC
                     IIII IIIIIIIII
                     CCGG GAGAACCGG
                     _____    T
GAM46  MDK         ACTGGTGGGTCACATCTCGGGCC  371           TC_   CCI
                     TGGTGGGTC TCTTGG
                     IIIIIIIII IIIIII
```

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                          ACCACCCAG  AGAGCC
                              TGT    CII
GAM46  MDK          ACTGGTGGGTCACATCTCGGGCC  371 TGAC       TC_     _ CI
                          TGGTGGGTC  TCTTGG CC
                          |||||||||  |||||| ||
                          ACCACCCAG  AGAGCC GG
                          ____        TGT    C AC
GAM46  NFATC3        TGGTGGGTCCCACTCCTGGCCC   386 GG      __        I
                          TGGGTCT CTCTTGGCC
                          ||||||| |||||||||
                          ACCCAGG GAGGACCGG
                          __      GT      I
GAM46  NRAP         CTGCTGGCTC-CTCTTGGCC      375 _ G  G T     I
                          TG TGG TC CTCTTGGC
                          || ||| || ||||||||
                          AC ACC AG GAGAACCG
                          G  G  G _     I
GAM46  NRAP         CTGCTGGCTC-CTCTTGGCC      375 TGACTGG  G T
                          TGG TC CTCTTGGCC
                          ||| || |||||||||
                          ACC AG GAGAACCGG
                          G_____ G _
GAM46  PAIP2        TGACTGGTGCTTCTTTCCTTGC    382      GG  C  G CC
                          TGACTGGTG  TCT TCTT GC
                          |||||||||  ||| |||| ||
                          ACTGACCAC  AGA AGGA CG
                          GA  A  A II
GAM46  PAIP2        TGACTGGTGCTTCTTTCCTTGC    382      GG  C  GGI
                          GACTGGTG  TCT TCTT
                          ||||||||  ||| ||||
                          CTGACCAC  AGA AGGA
                          GA  A  ACI
GAM46  POLR2E        ACAGGTGGCTTCTCTCTTG      369 T  G_      II
                          AC GGTGG  TCTCTCTT
                          || |||||  ||||||||
                          TG CCACC  AGAGAGAA
                          T  GA      CI
GAM46  POLR2E        ACAGGTGGCTTCTCTCTTG      369 TGACT  G_      G
                          GGTGG  TCTCTCTTG CC
                          |||||  |||||||||| ||
                          CCACC  AGAGAGAAC GG
                          T____     GA        _
GAM46  PTGS1        CTGTTGGGTCTCTGGTCTTG      373 G      CTTIII
                          CTG TGGGTCTCT
                          ||| |||||||||
                          GAC ACCCAGAGA
                          A      CCAGAA
GAM46  PTGS1        CTGTTGGGTCTCTGGTCTTG      373 TGACTGG     ___     CC
                          TGGGTCTC TCTTGG
                          |||||||| |||||
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                          ACCCAGAG   AGAACT
                        A_____        ACC     CT
GAM46  RAD17          TGACTGGTAC-TATAATCTTGGCCC 381        GGTCTC       I
                        TGACTGGTG    TCTTGGCCC
                        ||||||||     |||||||||
                        ACTGACCAT    AGAACCGGG
                           GATATT        I
GAM46  RAD17          TGACTGGTAC-TATAATCTTGGCCC 381        GGTCTC       I
                        GACTGGTG     TCTTGGCC
                        ||||||||     ||||||||
                        CTGACCAT     AGAACCGG
                           GATATT        I
GAM46  SLC21A9          ACTGCTGTGGCTGCTACTCTTGGCC 367 A  G  __ CT       CII
                        TG CTG TGG GT CTCTTGGCC
                        || ||| ||| || |||||||||
                        AC GAC ACC CG GAGAACCGG
                         _  _  GA AT       TCI
GAM46  SLC21A9          ACTGCTGTGGCTGCTACTCTTGGCC 367 C_   GG CT        I
                         TGGT GT CTCTTGGC
                         |||| || |||||||||
                         ACCG CG GAGAACCG
                         AC  A_ AT       I
GAM46  TBL1X          TGATCTGTTGATTCTCTCTTG    379  _  G GG      GCCC
                        TGA CTG TG TCTCTCTTG
                        ||| ||| || ||||||||||
                        ACT GAC AC AGAGAGAAC
                         A   A  TA      IIIC
GAM46  TBL1X          TGATCTGTTGATTCTCTCTTG    379 GA  G GG      I
                         CTG TG TCTCTCTT
                         ||| || |||||||||
                         GAC AC AGAGAGAA
                         TA  A  TA      I
GAM46  TBX5          TGTCTGTGGGGT-TCTCTTGGC   383 GA_  G TC       I
                         CTG TGGG TCTCTTGG
                         ||| |||| |||||||||
                         GAC ACCC AGAGAACC
                         ACA  _  CA      I
GAM46  TBX5          TGTCTGTGGGGT-TCTCTTGGC   383 TGA  G TC      CC
                         CTG TGGG TCTCTTGGC
                         ||| |||| ||||||||||
                         GAC ACCC AGAGAACCG
                         ACA  _  CA      II
GAM46  TNFRSF6B        GGTGGGT---TCTTGGCCC      378       CTC
                        GGTGGGT  TCTTGGCC
                        |||||||  ||||||||
                        CCACCCA  AGAACCGG
                          ___
GAM47  ATM          TGAGCCGCTGCGCCCAGCC        415    A       II
                        TGAGCC CTGCGCCCAGC
                        |||||| ||||||||||||
```

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                      ACTCGG GACGCGGGTCG
                         C        GI
GAM47  ATM            TGAGCCGCTGCGCCCAGCC     415 CATG   A
                          AGCC CTGCGCCCAGCCTG
                          |||| ||||||||||||
                          TCGG GACGCGGGTCGGGC
                          ____        C
GAM47  CHST5          CATGAGCCACCGCACCCGGCCTGG  401           A    I
                         CATGAGCCACTGCGCCC GCCTGG
                         ||||||||||||||| ||||||
                         GTACTCGGTGGCGTGGG CGGACC
                                     C    I
GAM47  CHST5          CATGAGCCACCGCACCCGGCCTGG  401           A    I
                         ATGAGCCACTGCGCCC GCCTG
                         |||||||||||||| |||||
                         TACTCGGTGGCGTGGG CGGAC
                                    C    I
GAM47  CLECSF12        GCCGTTGCACTCCAGCCTGG      408  AC   _     II
                        GCC  TGCGC CCAGCCTG
                        |||  ||||| |||||||||
                        CGG  ACGTG GGTCGGAC
                         CA    A     CI
GAM47  CLECSF12       TGTGCCACTGCACTCCAGCCTGG  413 CATGA      _      I
                           GCCACTGCGC CCAGCCTGG
                           |||||||||| |||||||||
                           CGGTGACGTG GGTCGGACC
                          A____       A     C
GAM47  CLECSF12       TGTGCCACTGCACTCCAGCCTGG  413 GA        _     I
                           GCCACTGCGC CCAGCCTG
                           |||||||||| ||||||||
                           CGGTGACGTG GGTCGGAC
                          A_        A     I
GAM47  CROT          CATGAGCCACTGCACCCAGCC     393              TGG
                         CATGAGCCACTGCGCCCAGCC
                         ||||||||||||||||||||
                         GTACTCGGTGACGTGGGTCGG
                                  III
GAM47  CROT          CATGAGCCACTGCACCCAGCC     393                  I
                         ATGAGCCACTGCGCCCAGC
                         |||||||||||||||||||
                         TACTCGGTGACGTGGGTCG
                                  I
GAM47  DFFB        GCCACTACACTCCAGCCTGG        406        _     II
                         GCCACTGCGC CCAGCCTG
                         |||||||||| ||||||||
                         CGGTGATGTG GGTCGGAC
                          A    CI
GAM47  FANCC        TGAGCCACTGCACCCAGCCAGG      420              TGI
                         GAGCCACTGCGCCCAGCC
                         ||||||||||||||||||
```

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                          CTCGGTGACGTGGGTCGG
                                  TCI
GAM47   FANCC          TGAGCCACTGCACCCAGCCAGG   420  CATG              T
                          AGCCACTGCGCCCAGCC GG
                          |||||||||||||||| ||
                          TCGGTGACGTGGGTCGG CC
                          ____              T
GAM47   FANCD2         CATGAGCCACTGCG-CCAGCC    394           C   TG
                          CATGAGCCACTGCGCC AGCC
                          ||||||||||||| ||||
                          GTACTCGGTGACGCGG TCGG
                              _     II
GAM47   FANCD2         CATGAGCCACTGCG-CCAGCC    394  _        C   I
                          ATGAGCCACTGCGCC AGC
                          ||||||||||||| |||
                          TACTCGGTGACGCGG TCG
                          G         _  I
GAM47   FGF2           CATGAGCCACTGCACCCGGCCT   398           A   GG
                          CATGAGCCACTGCGCCC GCCT
                          ||||||||||||||| ||||
                          GTACTCGGTGACGTGGG CGGA
                                 C  II
GAM47   FGF2           CATGAGCCACTGCACCCGGCCT   398           A   I
                          ATGAGCCACTGCGCCC GCC
                          |||||||||||||| |||
                          TACTCGGTGACGTGGG CGG
                                 C  I
GAM47   FUT1           GCCACTGCACTCCAGCCTGG     407          _    II
                          GCCACTGCGC CCAGCCTG
                          |||||||||| |||||||||
                          CGGTGACGTG GGTCGGAC
                              A       CI
GAM47   GNE            TGAGCCACTGCACTCCAGCCTGG  409  CATG        _      I
                          AGCCACTGCGC CCAGCCTGG
                          ||||||||||| |||||||||
                          TCGGTGACGTG GGTCGGACC
                          ____         A      C
GAM47   GNE            TGAGCCACTGCACTCCAGCCTGG  409  G           _      I
                          AGCCACTGCGC CCAGCCTG
                          ||||||||||| |||||||||
                          TCGGTGACGTG GGTCGGAC
                              _     A    I
GAM47   GNE            TGAGCCACTGTGCCCGGCCTGG   421       C   A   I
                          GAGCCACTG GCCC GCCTG
                          ||||||||| |||| |||||
                          CTCGGTGAC CGGG CGGAC
                                 A   C    I
GAM47   GNE            TGAGCCACTGTGCCCGGCCTGG   421  CATG       C   A
                          AGCCACTG GCCC GCCTGG
                          ||||||||| |||| |||||
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                      TCGGTGAC CGGG CGGACC
                           A   C
GAM47  GP2        CATGAGCCACTGCGCCCAGCC    395        C  CA  I
                      GAGCCACTG GCC  GCC
                      ||||||||| ||| |||
                      CTCGGTGAC CGG  CGG
                           A  AC  I
GAM47  GP2        CATGAGCCACTGCGCCCAGCC    395 CATG    C  CA
                       AGCCACTG GCC  GCCTG
                       |||||||| ||| |||||
                       TCGGTGAC CGG  CGGAC
                           A  AC
GAM47  IFIT4      CATGAGCCACTGCGCCCGGCC    396          A  TGG
                      CATGAGCCACTGCGCCC GCC
                      ||||||||||||||||| |||
                      GTACTCGGTGACGCGGG CGG
                           C  III
GAM47  IFIT4      CATGAGCCACTGCGCCCGGCC    396          A  I
                       ATGAGCCACTGCGCCC GC
                       |||||||||||||||| ||
                       TACTCGGTGACGCGGG CG
                           C  I
GAM47  IL18       TGAGCCACTGCGCCCGGCATG    417          A  CTI
                       GAGCCACTGCGCCC GC
                       |||||||||||||| ||
                       CTCGGTGACGCGGG CG
                           C  TAI
GAM47  IL18       TGAGCCACTGCGCCCGGCATG    417 CATG        A  C
                       AGCCACTGCGCCC GC TGG
                       ||||||||||||| || |||
                       TCGGTGACGCGGG CG ACT
                           C  T
GAM47  IPP        TGAGCCACCATGCCCAGCCT     416        GC    I
                      GAGCCACT GCCCAGCC
                      |||||||| ||||||||
                      CTCGGTGG CGGGTCGG
                           TA    I
GAM47  IPP        TGAGCCACCATGCCCAGCCT     416 CATG    GC
                       AGCCACT GCCCAGCCTG
                       ||||||| ||||||||||
                       TCGGTGG CGGGTCGGAT
                           TA
GAM47  IPP        CATGAGGCCACTGCGCCCAGCCT  390        _       GGI
                      CATGAG CCACTGCGCCCAGCCT
                      |||||| ||||||||||||||
                      GTACTC GGTGACGCGGGTCGGA
                           C        III
GAM47  IPP        CATGAGGCCACTGCGCCCAGCCT  390 A  _        I
                       TGAG CCACTGCGCCCAGCC
                       |||| |||||||||||||||
```

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                              ACTC GGTGACGCGGGTCGG
                               _    C           I
GAM47  KCNA7        CATGAGCCACCGCGCCCGGCCT   397          A    GG
                        CATGAGCCACTGCGCCC GCCT
                        |||||||||||||| ||||
                        GTACTCGGTGGCGCGGG CGGA
                                  C   II
GAM47  KCNA7        CATGAGCCACCGCGCCCGGCCT   397          A    I
                         ATGAGCCACTGCGCCC GCC
                         ||||||||||||| |||
                         TACTCGGTGGCGCGGG CGG
                                 C   I
GAM47  MEFV         CCACTGCACTCCAGCCTGG      402          _    II
                       CCACTGCGC CCAGCCTG
                       ||||||||| ||||||||
                       GGTGACGTG GGTCGGAC
                              A     CI
GAM47  MEFV         GCCACTGCACTCCAGCCTGG     407          _    II
                       GCCACTGCGC CCAGCCTG
                       |||||||||| ||||||||
                       CGGTGACGTG GGTCGGAC
                               A     CI
GAM47  MIR16        CATGAGCCACTGTGCCCAGC     391          C    CTG
                        CATGAGCCACTG GCCCAGC
                        ||||||||||| |||||||
                        GTACTCGGTGAC CGGGTCG
                                 A     III
GAM47  MIR16        CATGAGCCACTGTGCCCAGC     391          C    I
                         ATGAGCCACTG GCCCAG
                         |||||||||| ||||||
                         TACTCGGTGAC CGGGTC
                                A     I
GAM47  OPTN         CATGAGCCACTGTGCCCGGCCTG  399        C   A   GI
                        CATGAGCCACTG GCCC GCCTG
                        ||||||||||| |||| |||||
                        GTACTCGGTGAC CGGG CGGAC
                                 A   C   II
GAM47  OPTN         CATGAGCCACTGTGCCCGGCCTG  399        C   A   I
                         ATGAGCCACTG GCCC GCCT
                         |||||||||| |||| ||||
                         TACTCGGTGAC CGGG CGGA
                                A   C   I
GAM47  PCDHB9       ATGAGCCACTGAGCCCTGCCT    389        C   A   I
                        TGAGCCACTG GCCC GCC
                        ||||||||| |||| |||
                        ACTCGGTGAC CGGG CGG
                               T   A   I
GAM47  PCDHB9       ATGAGCCACTGAGCCCTGCCT    389 CA     C   A   GG
                        TGAGCCACTG GCCC GCCT
                        ||||||||| |||| ||||
```

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                    ACTCGGTGAC CGGG CGGA
                     __      T    A   GI
GAM47  PDE6B        GCCACGGCACTCCAGCCTGG    405    T  _      II
                    GCCAC GCGC CCAGCCTG
                    ||||| |||| ||||||||
                    CGGTG CGTG GGTCGGAC
                         C    A    CI
GAM47  PPEF2        GCCAATGCACTCCAGCCTGG    404    C  _      II
                    GCCA TGCGC CCAGCCTG
                    |||| ||||| ||||||||
                    CGGT ACGTG GGTCGGAC
                        T    A    CI
GAM47  PRKR         TGTGTCATTGCACTCCAGCCTGG   414  CATGAGC  C   _     I
                      CA TGCGC CCAGCCTGG
                      || ||||| ||||||||||
                      GT ACGTG GGTCGGACC
                    ACA____  A   A       C
GAM47  PRKR         TGTGTCATTGCACTCCAGCCTGG   414  GAGC   C   _     I
                      CA TGCGC CCAGCCTG
                      || ||||| |||||||||
                      GT ACGTG GGTCGGAC
                    ACA_  A   A       I
GAM47  RABL2B       TGCGCCACTGCACTCCAGCCTGG   410  GA        _     I
                      GCCACTGCGC CCAGCCTG
                      |||||||||| |||||||||
                      CGGTGACGTG GGTCGGAC
                        G_       A    I
GAM47  RABL2B       TGCGCCACTGCACTCCAGCCTGG   410  CATGA       _      I
                      GCCACTGCGC CCAGCCTGG
                      |||||||||| ||||||||||
                      CGGTGACGTG GGTCGGACC
                        G____    A    C
GAM47  RHD          TGCGGCACTGCACTCCAGCCTGG   411  _A C    _     I
                      G GC ACTGCGC CCAGCCTG
                      | || |||||||| ||||||||
                      C CG TGACGTG GGTCGGAC
                        G _ _    A    I
GAM47  RHD          TGCGGCACTGCACTCCAGCCTGG   411  CATGAGC      _      I
                      CACTGCGC CCAGCCTGG
                      |||||||| ||||||||||
                      GTGACGTG GGTCGGACC
                    GCC____      A    A
GAM47  SIM2         TGAGCCACTGAGCCCGGCCTGG   419       C  A  I
                    GAGCCACTG GCCC GCCTG
                    ||||||||| |||| |||||
                    CTCGGTGAC CGGG CGGAC
                        T    C   I
GAM47  SIM2         TGAGCCACTGAGCCCGGCCTGG   419  CATG    C  A
                    AGCCACTG GCCC GCCTGG
                    |||||||| |||| ||||||
```

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                          TCGGTGAC CGGG CGGACC
                          ____          T   C
GAM47  SLC17A5      CATGAGCCACCGTGCCCGGCC   392        C    A   TGG
                          CATGAGCCACTG GCCC GCC
                          |||||||||||| |||| |||
                          GTACTCGGTGGC CGGG CGG
                               A    C   III
GAM47  SLC17A5      CATGAGCCACCGTGCCCGGCC   392        C    A   I
                          ATGAGCCACTG GCCC GC
                          |||||||||||| |||| ||
                          TACTCGGTGGC CGGG CG
                               A   C  I
GAM47  TRIM14      TGAGCCACCGCGCCCAGCCAGG   418              TGI
                          GAGCCACTGCGCCCAGCC
                          ||||||||||||||||||
                          CTCGGTGGCGCGGGTCGG
                               TCI
GAM47  TRIM14      TGAGCCACCGCGCCCAGCCAGG   418 CATG          T
                          AGCCACTGCGCCCAGCC GG
                          ||||||||||||||||| ||
                          TCGGTGGCGCGGGTCGG CC
                          ____                  T
GAM47  TRPM1       CATGAGCCACTGTGCCCAGC   391        C    CTG
                          CATGAGCCACTG GCCCAGC
                          |||||||||||| |||||||
                          GTACTCGGTGAC CGGGTCG
                               A    III
GAM47  TRPM1       CATGAGCCACTGTGCCCAGC   391        C    I
                          ATGAGCCACTG GCCCAG
                          |||||||||||| ||||||
                          TACTCGGTGAC CGGGTC
                               A    I
GAM47  VENTX2     TGCGTCATTGCACTCCAGCCTGG   412 GAGC C   _       I
                          CA TGCGC CCAGCCTG
                          || ||||| |||||||||
                          GT ACGTG GGTCGGAC
                     GCA_  A   A     I
GAM47  VENTX2     TGCGTCATTGCACTCCAGCCTGG   412 CATGAGC C   _        I
                          CA TGCGC CCAGCCTGG
                          || ||||| ||||||||||
                          GT ACGTG GGTCGGACC
                     GCA____  A   A      C
GAM47  VHL        CATGAGCCACTGTGCTCGGCCTG   400        C CCA    GI
                          CATGAGCCACTG GC  GCCTG
                          |||||||||||| ||  |||||
                          GTACTCGGTGAC CG  CGGAC
                               A AGC   II
GAM47  VHL        CATGAGCCACTGTGCTCGGCCTG   400        C CCA   I
                          ATGAGCCACTG GC  GCCT
                          |||||||||||| ||  ||||
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                        TACTCGGTGAC CG  CGGA
                          A AGC   I
GAM47  VHL        CCTCTGCACTCCAGCCTGG    403  A   _      II
                  CC CTGCGC CCAGCCTG
                  || |||||| |||||||||
                  GG GACGTG GGTCGGAC
                    A    A      CI
GAM47  VHL        GCCACTGCACTCCAGCCTGG   407        _      II
                  GCCACTGCGC CCAGCCTG
                  |||||||||| |||||||||
                  CGGTGACGTG GGTCGGAC
                         A      CI
GAM47  YES1       GCCACTGCACTCCAGCCTGG   407        _      II
                  GCCACTGCGC CCAGCCTG
                  |||||||||| |||||||||
                  CGGTGACGTG GGTCGGAC
                         A      CI
GAM48  AP2B1      GTGGTGTAATGGTTTCCTGC   427    T_      II
                  GTGGTGT TGGTTTCCTG
                  ||||||| ||||||||||
                  CACCACA ACCAAAGGAC
                       TT      GI
GAM48  AP2B1      GTGGTGTAATGGTTTCCTGC   427 TG  T_       CC
                  TGGTGT TGGTTTCCTGCT
                  |||||| ||||||||||||
                  ACCACA ACCAAAGGACGG
                    __      TT         II
GAM48  GALGT   GTGGTGGTTCTGGCCGTTTCCTGC 426     __   ___     IIIG
                  GTGGTG TTTGGT TTCCTG
                  |||||| |||||| ||||||
                  CACCAC AGACCG AAGGAC
                      CA   GCA    GIII
GAM48  GALGT   GTGGTGGTTCTGGCCGTTTCCTGC 426 T_   G   ___     CCTI
                  GTGGT TTTGGT TTCCTGCT
                  ||||| |||||| |||||||||
                  CACCA AGACCG AAGGACGG
                  AC    _   GCA    IIIT
GAM48  HK1       GGTGTTTGGACTCTTTTCCTTCTC 424        _____     GCTIIIG
                  GGTGTTTGG  TTTCCT
                  |||||||||  ||||||
                  CCACAAACC  AAAGGA
                      TGAGA     AGAGIII
GAM48  SPTBN2      GTGGTAGGCGGCTTCCTGCTCCT  428    TT        I
                  TGGTG TGGTTTCCTGCTCC
                  ||||| ||||||||||||||
                  ACCAT GCCGAAGGACGAGG
                     CC          I
GAM48  SPTBN2      GTGGTAGGCGGCTTCCTGCTCCT  428 TG  TT         I
                  TGGTG TGGTTTCCTGCTCCT
                  ||||| |||||||||||||||
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```
                          ACCAT GCCGAAGGACGAGGA
                          __    CC          C
GAM48  TAL1       GGTGTTTGGAGCCTTTCCT    425        ____    IIIA
                          GGTGTTTGG  TTTCC
                          IIIIIIIII  IIIII
                          CCACAAACC  AAAGG
                           TCGG   AIII
GAM48  TAL1       GGTGTTTGGAGCCTTTCCT    425 TGTGGT    TTT  GC
                          GTTTGG  CCT TCC
                          IIIIII  III III
                          CAAACC  GGA AGG
                          _____     TC_  A_
GAM49  ACVR1B        AACGAGCCTTCAGAATGGT     432   AT_ A     II
                          AAC  CCT CAGAATGG
                          III  III IIIIIIII
                          TTG  GGA GTCTTACC
                           CTC  A     AI
GAM49  ACVR1B        AACGAGCCTTCAGAATGGT     432 TAACAT A     GAAA
                          CCT CAGAATGGT
                          III IIIIIIIII
                          GGA GTCTTACCA
                          TGCTC_  A     AIII
GAM49  APOL1       CATCCTGGCCAACATGGTGAAA    446 AT A__ A     I
                          CCT  CAG ATGGTGAA
                          III  III IIIIIIII
                          GGA  GTT TACCACTT
                          __  CCG  G     I
GAM49  APOL1       CATCCTGGCCAACATGGTGAAA    446 TAACAT A__ A      G
                          CCT  CAG ATGGTGAAA
                          III  III IIIIIIIII
                          GGA  GTT TACCACTTT
                          _____  CCG  G    G
GAM49  DAPP1       ACTTTCTATCAGAATGGTGA     438 ACATC  _      II
                          CTA CAGAATGGTG
                          III IIIIIIIIII
                          GAT GTCTTACCAC
                          TGAAA  A     TI
GAM49  DAPP1       ACTTTCTATCAGAATGGTGA     438 TAACATC  _       AA
                          CTA CAGAATGGTGA
                          III IIIIIIIIIII
                          GAT GTCTTACCACT
                          AAA____  A      AA
GAM49  FGF5       CATCCTGACCAACATGGTGAAA    444 AT _ AGA_     I
                          CCT AC  ATGGTGAA
                          III II  IIIIIIII
                          GGA TG  TACCACTT
                          __  C GTTG     I
GAM49  FGF5       CATCCTGACCAACATGGTGAAA    444 TAACAT _ AGA_      G
                          CCT AC  ATGGTGAAA
                          III II  IIIIIIIII
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                              GGA TG   TACCACTTT
                     _____   C GTTG      G
GAM49 FMN2       TAACATCCTAGA-AAAATTGAAA  451        C  TGG   G
                     TAACATCCTA AGAA  TGAAA
                     |||||||||| |||| |||||
                     ATTGTAGGAT TTTT  ACTTT
                              C  TA_  |
GAM49 FMN2       TAACATCCTAGA-AAAATTGAAA  451 _       C  TGG   |
                       AACATCCTA AGAA  TGAA
                       ||||||||| |||| ||||
                       TTGTAGGAT TTTT  ACTT
                              A   C  TA_  |
GAM49 GDF8      ATGCTACAGAAT--TGAAAG    442 TC_      GG   |
                         CTACAGAAT TGAAA
                         ||||||||| |||||
                         GATGTCTTA ACTTT
                       TAC        __   |
GAM49 GRM7      CATCCTGGCCAACATGGTGAAA   446 AT A__  A      |
                         CCT  CAG ATGGTGAA
                         |||  ||| ||||||||
                         GGA  GTT TACCACTT
                         __  CCG G     |
GAM49 GRM7      CATCCTGGCCAACATGGTGAAA   446 TAACAT A__  A      G
                         CCT  CAG ATGGTGAAA
                         |||  ||| |||||||||
                         GGA  GTT TACCACTTT
                     _____   CCG G     A
GAM49 MCP       ACATTCTATAGT-TGGTGAAAG   440 _  C  C AA     |
                         CAT CTA AG TGGTGAAA
                         ||| ||| || ||||||||
                         GTA GAT TC ACCACTTT
                       T A A A_    |
GAM49 MCP       ACATTCTATAGT-TGGTGAAAG   440 TAACATC  C AA
                         CTA AG TGGTGAAAG
                         ||| || |||||||||
                         GAT TC ACCACTTTC
                       TAA____  A A_
GAM49 NRIP1     TAACTTT-TACAAGAGATGGTGAAA 448    ATCC  _ _      GI
                         TAAC   TACA GA ATGGTGAAA
                         ||||   |||| || |||||||||
                         ATTG   ATGT CT TACCACTTT
                         AAA_   T C      II
GAM49 NRIP1     TAACTTT-TACAAGAGATGGTGAAA 448 AACATCC  _ _      I
                         TACA GA ATGGTGAA
                         |||| || ||||||||
                         ATGT CT TACCACTT
                       TGAAA__   T C    I
GAM49 PPARGC1    AAAATCCTACAGATCTATGCTGAAA 436 ACA        ___  G  I
                         TCCTACAGA  ATG TGAA
                         |||||||||  ||| ||||
```

```
                          AGGATGTCT  TAC ACTT
                          ___        AGA  G    I
GAM49  PPARGC1      AAAATCCTACAGATCTATGCTGAAA 436 TAAC      ___  G   GII
                        ATCCTACAGA  ATG TGAAA
                        IIIIIIIIII  III IIIII
                        TAGGATGTCT  TAC ACTTT
                        TT__        AGA  G   AII
GAM49  PRKWNK3      ACATTTCTACAGAATGATGA     437   C_          II
                        ACAT CTACAGAATGGTG
                        IIII IIIIIIIIIIII
                        TGTA GATGTCTTACTAC
                        AA        TI
GAM49  PRKWNK3      ACATTTCTACAGAATGATGA      437 TAACATC         AA
                          CTACAGAATGGTGA
                          IIIIIIIIIIIII
                          GATGTCTTACTACT
                        TAAA___          CG
GAM49  RHD         AACTATCCTAGCCAACATGGTGAAA 431 AC    __  A      I
                        ATCCTA CAG ATGGTGAA
                        IIIIII III IIIIIIII
                        TAGGAT GTT TACCACTT
                        __     CG  G       I
GAM49  RHD         AACTATCCTAGCCAACATGGTGAAA 431 TAAC    __  A      GII
                        ATCCTA CAG ATGGTGAAA
                        IIIIII III IIIIIIIII
                        TAGGAT GTT TACCACTTT
                        TGA_   CG  G      GII
GAM49  RPE        TAACGTTCTTAAGAATGGTG      450   A_ C C     AAA
                        TAAC TC TA AGAATGGTG
                        IIII II II IIIIIIIII
                        ATTG AG AT TCTTACCAC
                        CA  A  _        III
GAM49  RPE        TAACGTTCTTAAGAATGGTG       450 AACA_ C C     I
                          TC TA AGAATGGT
                          II II IIIIIIII
                          AG AT TCTTACCA
                        TTGCA  A  _     I
GAM49  RYR2       TCCTTCCAGGATGGTGAAA       452   A_  A    II
                        TCCT CAG ATGGTGAA
                        IIII III IIIIIIII
                        AGGA GTC TACCACTT
                        AG   C       TI
GAM49  RYR2       TCCTTCCAGGATGGTGAAA       452 TAACATCCTA  A
                        CAG ATGGTGAAA
                        III IIIIIIIII
                        GTC TACCACTTT
                        G_____      C
GAM49  SBF1      ACACACT-CAGGAATGGTGA      439   TC A  _    II
                        ACA CT CAG AATGGTG
                        III II III IIIIIII
```

```
                         TGT  GA GTC TTACCAC
                         GT _  C     TI
GAM49  SBF1        ACACACT-CAGGAATGGTGA    439  TAACATC A  _     AA
                         CT CAG AATGGTGA
                         || ||| |||||||||
                         GA GTC TTACCACT
                         TGT____ _  C     GG
GAM49  TERF1       AACATCCTGACCAGCATGGTGAAA  433  AC   A__  A     I
                         ATCCT  CAG ATGGTGAA
                         ||||| ||| |||||||||
                         TAGGA  GTC TACCACTT
                         __   CTG  G       I
GAM49  TERF1       AACATCCTGACCAGCATGGTGAAA  433  TA     A__  A    GI
                         ACATCCT  CAG ATGGTGAAA
                         |||||||| ||| |||||||||
                         TGTAGGA  GTC TACCACTTT
                         __    CTG  G       GI
GAM49  TLX1        TAAAATCCTACAG---GGTTCGAAAG 449  C    AAT  __   I
                         TAA ATCCTACAG  GGT GAAAG
                         ||| ||||||||| ||| |||||
                         ATT TAGGATGTC  CCA CTTTC
                         T         AG       I
GAM49  TLX1        TAAAATCCTACAG---GGTTCGAAAG 449  AC     AAT  GI
                         ATCCTACAG  GGT
                         ||||||||| |||
                         TAGGATGTC  CCA
                         T_        AG
GAM49  TUFT1       CAGCCTAGCCAGTATGGTGAAA    445  AT  __  A     I
                         CCTA CAG ATGGTGAA
                         |||| ||| |||||||||
                         GGAT GTC TACCACTT
                         __  CG  A       I
GAM49  TUFT1       CAGCCTAGCCAGTATGGTGAAA    445  TAACAT  __  A     G
                         CCTA CAG ATGGTGAAA
                         |||| ||| |||||||||
                         GGAT GTC TACCACTTT
                         _____  CG  A       G
GAM49  UBE4A       AACATCCTACTAGATTGGGTTTGGAAG435  T   _  A  TGAAAI
                         CCTAC AGA TGG
                         ||||| ||| |||
                         GGATG TCT ACC
                         _  A  A  CAAACI
GAM49  UBE4A       AACATCCTACTAGATTGGGTTTGGAAG435  TA    _  A  TGAAAGIII
                         ACATCCTAC AGA TGG
                         ||||||||| ||| |||
                         TGTAGGATG TCT ACC
                         __       A  A  CAAACCTTC
GAM49  UC28        ATCCAAACAGAATGG-GAAAG    441  T_   T  I
                         TCC  ACAGAATGG GAAA
                         ||| ||||||||| ||||
```

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                        AGG  TGTCTTACC CTTT
                         TT        _    I
GAM49  UC28          ATCCAAACAGAATGG-GAAAG   441 TAACATCCT      T
                         ACAGAATGG GAAA

                         |||||||| ||||
                         TGTCTTACC CTTT
                      TT_____       _
GAM49  VHL           CATCCTGGACAACATGGTGAAA   443 AT  __   A      I
                         CCT ACAG ATGGTGAA

                         ||| |||| ||||||||
                         GGA TGTT TACCACTT
                         __  CC  G      I
GAM49  VHL           CATCCTGGACAACATGGTGAAA   443 TAACAT  __   A      G
                         CCT ACAG ATGGTGAAA

                         ||| |||| |||||||||
                         GGA  TGTT TACCACTTT
                      _____    CC  G      G
GAM49  WASF3         TAAAATTCTGACCAAGTGGTGAAAG 447 AACA CT A A     I
                         TC  AC GA TGGTGAAA

                         || || || ||||||||
                         AG  TG TT ACCACTTT
                      TTTA AC G C      I
GAM49  WASF3         TAAAATTCTGACCAAGTGGTGAAAG 447 TAACA_ CT A A      II
                         TC  AC GA TGGTGAAAG

                         || || || |||||||||
                         AG  TG TT ACCACTTTC
                      ATTTTA AC G C       II
GAM49  WDR1          AACATCAAAGCATGATGGTGAAA   434 A  CTA_ GA     I
                         CATC  CA ATGGTGAA

                         ||||  || ||||||||
                         GTAG  GT TACCACTT
                      _  TTTC AC      I
GAM49  WDR1          AACATCAAAGCATGATGGTGAAA   434 TA   CTA_ GA      GI
                         ACATC  CA ATGGTGAAA

                         |||||  || |||||||||
                         TGTAG  GT TACCACTTT
                         __   TTTC AC      GI
GAM50  ACP1          TAGA-TGTTGACCT-GGGCC     457    A    CGA GA
                         TAGA TGTTGACCT  GCC

                         |||| ||||||||| |||
                         ATCT ACAACTGGA  CGG
                         _     CC_  II
GAM50  PACSIN1       AGAATGTTGTTCTGGGGGCCGTGG 455 TA    AC CGA_  A I
                         GAATGTTG CT  GCCG GG

                         |||||||| ||   |||| ||
                         CTTACAAC GA   CGGC CC
                         __      AA CCCC  A C
GAM50  SKI           TAGAATGTT-CCAGCAAGCAGAGG 458      GA T_  C I
                         TAGAATGTT CC CGAGC GAGG

                         |||||||| || ||||| ||||
```

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                        ATCTTACAA GG GTTCG CTCC
                            __  TC   T    I
GAM50  TAZ          AGATTGCGGAGCTGGAGCCGAGG  456 TA A  T C C       I
                        GA TGT GA CT GAGCCGAGG
                        || ||| || || |||||||||
                        CT ACG CT GA CTCGGCTCC
                            __  A  C  C      G
GAM51  ACATN           TATGATCAAATATACAGAAA   469 TATTAT    G
                            GATCAAG ATATGGAAA
                            ||||||| |||||||||
                            CTAGTTT TATGTCTTT
                            _____         A
GAM51  ATRN           TATGATCAAAAGAGATGGA    468 TATTAT   _ T   AA
                            GATCAAG GA ATGGA
                            ||||||| || |||||
                            CTAGTTT CT TACCT
                            _____       T C   GG
GAM51  CDKN2B         TATAATGATCAAGCAACCCTGGAAAT 472  T    _  A_    II
                        TAT ATGATCAAG GAT  TGGAAAT
                        ||| |||||||||| |||  |||||||
                        ATA TACTAGTTC TTG  ACCTTTA
                          T    G  GG      II
GAM51  CETN1         TATTATTGAACTAGAGATATGGAAAT 470    _ TCA _      II
                        TATTAT GA  AG GATATGGAAAT
                        |||||| ||  || |||||||||||
                        ATAATA CT  TC CTATACCTTTA
                          A  TGA T        II
GAM51  COL4A4        ATTATT-TAAAGTATATGGAAA   467 TATTATGATC _     T
                            AAGG ATATGGAAA
                            |||| |||||||||
                            TTTC TATACCTTT
                        AATAAA____  A     T
GAM51  DBT           ATTCTTACCCAGGATATGGAGAAT 465 TATTATG  A      AATI
                            ATC AGGATATGGA
                            ||| |||||||||||
                            TGG TCCTATACCT
                        AAGAA__  G     CTTA
GAM51  DDX6          TTTTGAAAAA--ATATGGAAAT   479 TATTA  TC
                            TGA AAGGATATGGAAA
                            ||| |||||||||||||
                            ACT TTTTTATACCTTT
                        A____  __
GAM51  DSG1          ATTTTGCTCGAGCTATATGGAAA  464 TATTA A A G_      TI
                            TG TC AG  ATATGGAAA
                            || || ||  |||||||||
                            AC AG TC  TATACCTTT
                        AAA__  G  C  GA       TI
GAM51  EDAR          ATGACCTCAAGGATAGGTAAA    461 TATTATGA     T _ T
                            TCAAGGATA GG AAA
                            ||||||||| || |||
```

```
                          AGTTCCTAT CC TTT
                  GG_____          _ A  T
GAM51  EDN3       TATTCTAGGCAAGGATATGAAA   473    ATGAT        AT
                  TATT   CAAGGATATGGAA
                  ||||   |||||||||||
                  ATAA   GTTCCTATACTTT
                  GATCC            ||
GAM51  FOXF1      TTAT-ATAAACATATGGAAAT   478  TATTATG C  G
                     AT AAG ATATGGAAAT
                     || ||| |||||||||
                     TA TTT TATACCTTTA
                  TA_____  T G
GAM51  HLF        ATG-TCAAGAGGGATATGGAAA   462  TATTATGATCAA      T
                        GGATATGGAAA
                        |||||||||||
                        CCTATACCTTT
                  GTTCTC_____       T
GAM51  LILRB4     TATTTTGTTCCTG--TATGGAAAT  476   A A AAGGA
                  TATT TG TC   TATGGAAAT
                  |||| || ||   |||||||||
                  ATAA AC AG   ATACCTTTA
                  A A GAC__
GAM51  LRAT       TATAATTAGAAATGATATGGAAA  474  TAT    CAAG___      TI
                  TATGAT    GATATGGAAA
                  ||||||    |||||||||||
                  ATATTA    CTATACCTTT
                  ___     ATCTTTA         ||
GAM51  MOCS2      ATGATCAAGGGTGTAGAAAT    463  TATTATGA   ATA
                      TCAAGG TGGAAA
                      |||||| ||||||
                      AGTTCC ATCTTT
                  _____     CAC
GAM51  PGAM1      TTATTAT-ACTGATATGGAAA   477  T    ATCAAG
                  ATTATG   GATATGGAAA
                  ||||||   |||||||||||
                  TAATAT   CTATACCTTT
                  _   GA____
GAM51  PSD        TAGTAAGTTTAAAG-TATGGAAAT  475  TATTATGATC  A      I
                     AAGG TATGGAAAT
                     |||| |||||||||
                     TTTC ATACCTTTA
                  ATCATTCAAA   _       I
GAM51  RP2        TATTATGATCAGGTAGATTTGGGAA  471          A__  A  AAATII
                  TATTATGATCA  GGAT TGG
                  |||||||||||  |||| |||
                  ATAATACTAGT  TCTA ACC
                     CCA  A  CTTIII
GAM51  SLC12A2    ATTAAGATTGAG-ATATGGAA    466  TATTAT CAA       A
                  GAT  GGATATGGAA
                  |||  |||||||||||
```

```
                      CTA  TCTATACCTT
                 AATT__  AC_       A
GAM52  ALK       TGAGCCTCCCGCTCTCCGCGCCG  516  C  G  _        GCI
                 TG GCCT CC CTTTCCGCGCCG
                 || |||| || ||||||||||||
                 AC CGGA GG GAGAGGCGCGGC
                      T   G  C        |||
GAM52  BN51T     GCCTTCGGTCTCCGCGCCGG     495  TGCGCCTGCCC
                        TTTCCGCGCCGG
                        ||||||||||||
                        AGAGGCGCGGCC
                 AAGCC_____
GAM52  BRF1      GCCT-CCCTTGCGGCGCGCCGGC  491  TGCGCCTG  TC__
                    CCCTT  CGCGCCGGC
                    |||||  |||||||||
                    GGGAA  GCGCGGCCG
                 A_____   CGCC
GAM52  BTEB1     GCCCCTGCCC----CGCGCCGGC  509  TG G    TTTC
                   C CCTGCCC  CGCGCCGG
                   | |||||||  |||||||||
                   G GGACGGG  GCGCGGCC
                    __ G      ____
GAM52  CYP2A6    CCTGCCCTTTCCCTGGCCCCG   482  TGCG  G_  TT G  GGC
                   CCT CCCT CC CGCC
                   ||| |||| || ||||
                   GGA GGGA GG GCGG
                 G___ AA  CC G  GTI
GAM52  EFNB2     TGCAGCCAGCCCTTTCCCCAGCC  513  _  T     G _  GGCI
                 TGC GCC GCCCTTTCC C GCC
                 ||| ||| |||||||||| | |||
                 ACG CGG CGGGAAAGG G CGG
                  T  T      G T  IIIC
GAM52  GCK       GCCTGCCCTTTTGGCCCAGG     494  TGCGCC    CC G
                   TGCCCTTT GC CCGG
                   |||||||| || ||||
                   ACGGGAAA CG GGTC
                  _____     AC  _
GAM52  GPR48     TGCGGCCGCC--TCCCGCGCCGGC 521  C   CT
                   TGCG CTGCC TTCCGCGCCGGC
                   |||| ||||| ||||||||||||
                   ACGC GGCGG AGGGCGCGGCCG
                      C  __
GAM52  GPX4      GCGCGTCGGCTTTCCGCGCC     503  T  CCTGCC      GG
                     GCG   CTTTCCGCGCC
                     |||   ||||||||||
                     CGC   GAAAGGCGCGG
                  G AGCC__       AI
GAM52  GSR       CGCCAGCTCGGTCCCGCGCCGGC  487  TGCG T CCT_       I
                   CC GC  TTCCGCGCCGGC
                   || ||  ||||||||||||
```

```
                         GG CG   AGGGCGCGGCCG
                         ____ T AGCC          C
GAM52  HMX1          GCGGCGGCC---TCCGCGCCGG   508 T_  CCT  CTT
                         GCG  GCC  TCCGCGCCGG
                         |||  |||  ||||||||||
                         CGC  CGG  AGGCGCGGCC
                         GC  ___  ___
GAM52  IRS1          GCGTCTGGC-TCTGCGCGCCGGC   512 TG C  CC   C
                         CG CTG  CTTT CGCGCCGGC
                         || ||| |||| ||||||||||
                         GC GAC  GAGA GCGCGGCCG
                         __ A  C_   C
GAM52  JUND          CGCCTCCCCCG-CCGCGCCGGC   490 TGCG  G   TT
                         CCT CCCT  CCGCGCCGGC
                         ||| ||||  ||||||||||
                         GGA GGGG  GGCGCGGCCG
                         ____  _   GC
GAM52  KCNS3        GCGCCTGCC---GCCGCGGCGGC  511 TG     CTTT   C
                         CGCCTGCC  CCGCG CGG
                         ||||||||  ||||| |||
                         GCGGACGG   GGCGC GCC
                         __    C___   C
GAM52  LAMC1        GCCTGCACT--CCGCGCCG     493     CTGCCCTT
                         TGCGC     TCCGCGCCG
                         |||||     |||||||||
                         ACGTG     AGGCGCGGC
                                   _____
GAM52  LTF         TGCGCCTGCCCT----GCGCC     519          TTCC   G
                         TGCGCCTGCCCT  GCGCC
                         ||||||||||||  |||||
                         ACGCGGACGGGA   CGCGG
                              ____   I
GAM52  MAFK        CGCGCTGTCCT---CGCGCCGGC   485 TG  C C  TTC
                         CGC TG CCT  CGCGCCGG
                         ||| || |||  |||||||||
                         GCG AC GGA   GCGCGGCC
                         __  _ A  ___
GAM52  MAN2A2       GCGCCCGGCCT--CCGCGCCG    504 TG   C TT    G
                         CGCCTG CC TCCGCGCCG
                         |||||| || |||||||||
                         GCGGGC GG AGGCGCGGC
                         __    C __     G
GAM52  MAPK12      GCGCCTCGGGCCGGCTCCGCGCCG 497 TG  ___ CT     GCI
                         CGCCT GCC TTCCGCGCCG
                         ||||| ||| |||||||||||
                         GCGGA  CGG GAGGCGCGGC
                         __   GCC  CC      GII
GAM52  MTCP1        CGCCTGCCCCAAACCGCGCGGGC  486 TGCG    TT_   C I
                         CCTGCCCT  CCGCGC GGC
                         ||||||||  |||||| |||
```

```
                    GGACGGGG  GGCGCG CCG
                           TTT    C  C
GAM52  MVK              CGCC-GCCCCT-CCGCGCCG      489 TGCGC     T
                       CTGCCCTT CCGCGCCG
                       |||||||| ||||||||
                       GGCGGGGA GGCGCGGC

                       _____     _
GAM52  NCKAP1        GCGCC--CCAATCCCGCGCCGGC  510 TGCGCCT    __
                       GCCCT TTCCGCGCCGGC
                       ||||| |||||||||||
                       CGGGG AGGGCGCGGCCG
                           G_____      TT
GAM52  NFRKB         GCGCCCGGCTCCCCTTCCGCGCC  498 TG    ___        GGCI
                       CGCCTG CCCTTTCCGCGCC
                       |||||| |||||||||||||
                       GCGGGC GGGGAAGGCGCGG
                         __    CGA          GIII
GAM52  NFRKB         CGGCTCCCCTT-CCGCGCCCGGC  488 TGCGC G        _
                       CT CCCTTTCCGCGCC GGC
                       || ||||||||||||| |||
                       GA GGGGAAGGCGCGG CCG
                         C____  _          G
GAM52  OIP2          TGCGCCTGCGCCGCTCCTCTCCTGC 515      _ T  GCG G II
                       TGCGCCTGC CC TTCC  CC GC
                       ||||||||| || |||| || ||
                       ACGCGGACG GG GAGG  GG CG
                          C C  AGA A II
GAM52  PAX8          GCGCCTGCCGCTGCCCTGGCCGGC  500 TG      _ T GC   I
                       CGCCTGCC CT TCC  GCCGGC
                       |||||||| || ||| ||||||
                       GCGGACGG GA GGG  CGGCCG
                         __     C C AC   G
GAM52  PCM1          GCCCGCACGACCCGCGCCGGC     496 T  CT  TTTCC
                       GCGC GCCC   GCGCCGGC
                       |||| ||||   ||||||||
                       CGTG TGGG   CGCGGCCG
                         G  C_  _____
GAM52  PFKFB2        GCGCCTGCCCTGTAACGCGACCG  501 TG     TTC_ _ CI
                       CGCCTGCCCT  CGCG CCGG
                       ||||||||||  |||| ||||
                       GCGGACGGGA  GCGC GGCT
                         __        CATT  T  II
GAM52  POU3F1        GCGCCCGCGCCCTGCAGCGCGCCGGC 499 TG    _ TC__     II
                       CGCCTGC CCTT  CGCGCCGGC
                       ||||||| ||||  |||||||||
                       GCGGGCG GGGA  GCGCGGCCG
                         __     C  CGTC    CI
GAM52  PPP2R2B       TGCGCCTGCC---TCCGCTGCC    518     CTT  _ GG
                       TGCGCCTGCC  TCCGC GCC
                       ||||||||||  ||||| |||
```

```
                    ACGCGGACGG  AGGCG CGG
                       ___       A   II
GAM52  PXN          GCCTGCCCTTCCCTGCCCC    492 TGCGCC      _ G GG
                    TGCCCTTTCC GC CC
                    |||||||||| || ||
                    ACGGGAAGGG CG GG
                       _____     A  G GG
GAM52  S100A10      TGAGCCTGCCC-TTCCTCTCGGG  520  C      T GCGC  C
                    TG GCCTGCCCTT CC   CGG
                    || |||||||||| ||   |||
                    AC CGGACGGGAA GG   GCC
                      T    _ AGA_  C
GAM52  SAS          TGCGCCTGCACCGTCCCTCCCTGC 514      _ T  GCG G II
                    TGCGCCTGC CC TTCC  CC GC
                    ||||||||| || ||||   || ||
                    ACGCGGACG GG AGGG  GG CG
                        T C  AGG A  II
GAM52  SDC1         GCGCCTGCCC--AGCGCGCCG    507 TG     TTTC    G
                    CGCCTGCCC  CGCGCCG
                    |||||||||  |||||||
                    GCGGACGGG  GCGCGGC
                       __     TC__   G
GAM52  SDC2         TGCGCCTGC---TCCCGCCGCCCGC 517      CCT   _ G
                    TGCGCCTGC  TTCCGC GCC GC
                    |||||||||  |||||| ||| ||
                    ACGCGGACG  AGGGCG CGG CG
                       ___      G G
GAM52  SORCS2       GCGCCTG-CCGGTCCTCGCCG    506 TG    CTT G  G
                    CGCCTGCC  TCC CGCCG
                    ||||||||  ||| |||||
                    GCGGACGG  AGG GCGGC
                       __     CC_  A   G
GAM52  TESK1        CCCGCCCCCGCCGCGCCGGC     484 TGCGCCTG  TT
                    CCCT CCGCGCCGG
                    |||| |||||||||
                    GGGG GGCGCGGCC
                       _____      GC
GAM52  TIF1         CCTGCCCTTGCCGCCGCCGG     483 TGCGCCTG  T  _
                    CCCTT CCGC GCCGG
                    ||||| |||| |||||
                    GGGAA GGCG CGGCC
                       _____    C  G
GAM52  WDR1         GCGCCTGCCC--TGCGCGC      502 TG     TTC   CG
                    CGCCTGCCCT CGCGC
                    |||||||||| |||||
                    GCGGACGGGA GCGCG
                       __       C__  AI
GAM52  WIG1         GCGCCGGCAGTCTCCGCGCCG    505 TG  T CC       GC
                    CGCC GC TTTCCGCGCCG
                    |||| || |||||||||||
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                          GCGG CG  AGAGGCGCGGC
                          __   C TC       GI
GAM53  AK3        AAGAC--AACCCCTCCCCT    525 GAAA  TG        G
                          GAC AGCCCCTCCCCT
                          III IIIIIIIIIII
                          CTG TTGGGGAGGGGA
                          ____  __        G
GAM53  CHIC2      CTGAGCCTCCGAGCTCCCCTGCC  528 GAAAGA    CCC      I
                          CTGAGC  TCCCCTGCC
                          IIIIII  IIIIIIIII
                          GGCTCG  AGGGGACGG
                      GA____    ___       G
GAM53  MAB21L1    GAAAGACTGTCCTCCCCCCTCTGC  529      AG _   _  CI
                          GAAAGACTG CC CCTCCC CTGC
                          IIIIIIIII II IIIIII IIII
                          CTTTCTGAC GG GGGGGG GACG
                           A_  A   A  II
GAM53  MHC2TA     AGTCTGGCAGCCCCTCCTCGTGCC  526 GAAAGA __     CC_  I
                          CTG AGCCCCTCC TGCC
                          III IIIIIIIII IIII
                          GAC TCGGGGAGG ACGG
                          _____  CG      AGC  G
GAM53  RAB2L      GACCGAGTCCCCTCCCCGGC    530 GAAAGACT _     T
                          GAG CCCCTCCCC GC
                          III IIIIIIIII II
                          CTC GGGGAGGGG CG
                          _____  A      C
GAM53  RAD51L3    AGAC---GCCCCTCCCCTACC    527 GAAAGACTGA
                          GCCCCTCCCCTG
                          IIIIIIIIIIII
                          CGGGGAGGGGAT
                      G_____
GAM53  SOX15      AAAGACTGA-CTCCGCCCCTG    524 GA      G C T    C
                          AAGACTGA C CC CCCCTG
                          IIIIIIII I II IIIIII
                          TTCTGACT G GG GGGGAC
                          __     _A C    A
GAM54  APPBP2     TAAACTCAGGTTTCTAAATCA    538 TAAA___      A TGACGG
                          AGGTTTCTAAA CA
                          IIIIIIIIIII II
                          TCCAAAGATTT GT
                      ATTTGAG       A IIIGGC
GAM54  BAZ1A      TAAAAGGTT--TAAAACATTAAGG  544      TC    GAC
                          TAAAAGGTT TAAAACAT  GG
                          IIIIIIIII IIIIIII  II
                          ATTTTCCAA ATTTTGTA  CC
                          __      ATT
GAM54  DLEU2      TAAAAGGTTT---AAACAT      541      CTA    GA
                          TAAAAGGTTT AAACAT
                          IIIIIIIIII IIIIII
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                          ATTTTCCAAA  TTTGTA
                            ___      II
GAM54   EGLN3          TAAAGGGATTTTTAAAACATGA  539 TA  __  C      CGG
                          AAAGG  TTT TAAAACATGA
                          IIIII  III IIIIIIIIII
                          TTTCC  AAA ATTTTGTACT
                          A_  CT  A       III
GAM54   GNB1           AAAATCTTGCTACAAACATGAC  534 TAAAAG_ TCTA      GG
                            GTT   AAACATGAC
                            III   IIIIIIIII
                            CGA   TTTGTACTG
                          TTTAGAA  TG__      AI
GAM54   HLA-DOB        TAAAAGGTTTTTAAAAACAGTGA  540       CT_  _ CGGI
                          TAAAAGGTTT  AAAACA TGA
                          IIIIIIIIII  IIIIII III
                          ATTTTCCAAA  TTTTGT ACT
                             AAT    C  IIIG
GAM54   MBL2           AAAAATTTCTTAAACATGAC     536 TAAA      A
                          AGGTTTCT AAACATGACG
                          IIIIIIII IIIIIIIIII
                          TTTAAAGA TTTGTACTGT
                            ____        A
GAM54   PPARBP         TAAAATGAGTTTAAAACATG     543     __  TC      ACG
                          TAAAA GGTT TAAAACATG
                          IIIII IIII IIIIIIIII
                          ATTTT TCAA ATTTTGTAC
                          AC  __        III
GAM54   ZNF22          AAATGTATCCTCAAAACATGATGG  535 TAAAAG  TC     C I
                          GTT TAAAACATGA GG
                          III IIIIIIIIII II
                          TAG GTTTTGTACT CC
                          TACA__  GA      A A
GAM54   ZNF22          AAAATGTATCTACAAAACATGATGG  533 TAAAAG T  __   C II
                          GT TCTA AAACATGA GG
                          II IIII IIIIIIII II
                          CA AGAT TTTGTACT CC
                          TTTA__  T  GT     A AI
GAM54   ZNF239         TAACTGGTTCCTAAAACAT      542 TAAAA       GACG
                          GGTTTCTAAAACAT
                          IIIIIIIIIIIIII
                          CCAAGGATTTTGTA
                          ATTGA          IIIG
GAM54   ZNF6           AGGACTCATGAAACATGAC      537 TAAAAGGTT TA_      G
                          TC  AAACATGAC
                          II  IIIIIIIII
                          AG  TTTGTACTG
                          G_____  TAC      A
GAM55   ANGPT1         ATACACATG-TTAAATTGC      549 TACCATAC   ATG
                          ACATG  AAGTTG
                          IIIII  IIIIII
```

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                         TGTAC  TTTAAC
                         _____        AA_
GAM55  GALC        CATACAACATGATGAACATGCT  550  TACCAT  _      GT
                         ACA CATGATGAA TGCT
                         ||| ||||||||| ||||
                         TGT GTACTACTT ACGA
                         _____    T     GT
GAM55  GALNS         CCATACACATACTGATCTTG   552  TACC     A  AG  C
                          ATACACATG TGA  TTG
                          ||||||||| |||  |||
                          TATGTGTAT ACT  AAC
                         ____         G  AG  A
GAM55  GJB3        TACTATAC---TG-TGAAGTTGC  555   C   ACA  A
                          TAC ATAC  TG TGAAGTTGC
                          ||| ||||  || |||||||||
                          ATG TATG  AC ACTTCAACG
                           A   ___  _
GAM55  HNRPA1        CCATACACATGA-GTATTTG   553  TACC        TGAAG  C
                          ATACACATGA    TTG
                          ||||||||||    |||
                          TATGTGTACT    AAC
                         ____          CATA_  A
GAM55  ITGA6        CCA-ACACATGATGTAAGT    551  TACCAT       _
                          ACACATGATG AAGTTG
                          |||||||||| ||||||
                          TGTGTACTAC TTCAGT
                        T_____          A
GAM55  LPIN2       TACCATACATATGCAAAGAAGT  554       C  AT__   TGCT
                          TACCATACA ATG   GAAGT
                          ||||||||| |||   |||||
                          ATGGTATGT TAC   CTTCA
                           A  GTTT   IIIT
GAM55  PRKG2       ACCATGCTTAT-ATGAAGTTGCT  548  TA   ACACATG
                          CCAT    ATGAAGTTGCT
                          ||||    |||||||||||
                          GGTA    TACTTCAACGA
                         __  CGAATA_
GAM55  RET        ACAAT-CA-ATGATGAAGTT    547  TACCATA  C
                          CA ATGATGAAGTTG
                          || ||||||||||||
                          GT TACTACTTCAAT
                        GTTA___  _
GAM56  CA3        GATCGTCGTAGTTGTGCTTGGC  558  ATG        GGI
                          GTCGTAGTTGTGT
                          |||||||||||||
                          CAGCATCAACACG
                        G__        AAC
GAM56  CA3        GATCGTCGTAGTTGTGCTTGGC  558  TCAGATG       __
                          GTCGTAGTTGTGT GGCT
                          ||||||||||||| ||||
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                              CAGCATCAACACG  CCGG
                              G_____           AA
GAM56  LGI1        TCAGATGGT-G-A-TTGTCTTGCT  560      C A  G  GI
                              TCAGATGGT GT GTT TGT
                              ||||||||| || ||| |||
                              AGTCTACCA TA CAG ACG
                                      C  A  A  AI
GAM56  LGI1        TCAGATGGT-G-A-TTGTCTTGCT  560      CGTA   GTG
                              TCAGATGGT  GTTGT  GCT
                              |||||||||  |||||  |||
                              AGTCTACCA  TAACA  CGA
                                      C___    GAA
GAM56  SLC6A1        GATGGTCGTCG-GGGGTGG       559       AGTT_  TGI
                              GATGGTCGT    GTG
                              |||||||||    |||
                              CTACCAGCA    CAC
                                      GCCCC  CII
GAM56  SLC6A1        GATGGTCGTCG-GGGGTGG       559 TCAGAT    AGTT_  T
                              GGTCGT    GTG GG
                              ||||||    ||| ||
                              CCAGCA    CAC CC
                              _____        GCCCC  _
GAM57  DCC        GTTTATGGGTAATTGGTATGCTGC  566       ATC_____     IIIG
                              GTTTATG     GTATGCTG
                              |||||||     ||||||||
                              CAAATAC     CATACGAC
                              CCATTAAC       GIII
GAM57  DCC        GTTTATGGGTAATTGGTATGCTGC  566 TGACGTTTATGATC      TI
                              GTATGCTGC
                              |||||||||
                              CATACGACG
                              TACCCATTAAC___      TT
GAM57  FHL1      TTTTTTTTCATATGCTGCT      572 TTTATGA        II
                              TCGTATGCTGC
                              |||||||||||
                              AGTATACGACG
                              AAAAAAA      AI
GAM57  FRAT2       CGTTTATGACTGT-TTCTG       564       C ATGCTI
                              CGTTTATGAT GT
                              |||||||||| ||
                              GCAAATACTG CA
                              A  AAGACI
GAM57  FUS1      TGACTGGTATATGCCCTGCTATGCTGCT567 GAC  T  AT _ _     I
                              GT TATG  C GT ATGCTGC
                              || |||| | || |||||||
                              CA ATAC  G CG TACGACG
                              C__ T  GG A  A     I
GAM57  FUS1      TGACTGGTATATGCCCTGCTATGCTGCT567     __ T  AT _ _     III
                              TGAC  GT TATG  C GT ATGCTGCT
                              |||| || |||| | || |||||||||
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                        ACTG CA ATAC G CG TACGACGA
                          AC T  GG A A        III
GAM57  GABRA5           TTTATGATC-TCTGTTTCT     571        GTA CTGCI
                        TTTATGATC  TG
                        ||||||||| ||
                        AAATACTAG  AC
                          AG_ AAAGA
GAM57  IL21R            TGACGTTTATTGAGGGTCTGCT   568         GATCGTATG
                        TGACGTTTAT      CTGCT
                        ||||||||||      |||||
                        ACTGCAAATA      GACGA
                          ACTCCCA__
GAM57  IL21R            TGACGTTTATTGAGGGTCTGCT   568 G    _ TC A  I
                        ACGTTTAT GA GT TGC
                        |||||||| || || |||
                        TGCAAATA CT CA ACG
                          _    A CC G  I
GAM57  MLLT4            GACGTTTATTAAC-TCTGC      565        GA__ GTATGI
                        GACGTTTAT  TC
                        |||||||||  ||
                        CTGCAAATA  AG
                          ATTG ACGIII
GAM57  MLLT4            GACGTTTATTAAC-TCTGC      565 TG       GATCGTATG
                        ACGTTTAT     CTG
                        ||||||||     |||
                        TGCAAATA     GAC
                          __  ATTGA____
GAM57  PTHLH            CGTTTATGA-CATGATGCTG     563       T _  II
                        CGTTTATGA CGT ATGCT
                        ||||||||| ||| |||||
                        GCAAATACT GTA TACGA
                          _ C  CI
GAM57  PTHLH            CGTTTATGA-CATGATGCTG     563 TGACGT   T _   C
                        TTATGA CGT ATGCTG
                        |||||| ||| ||||||
                        AATACT GTA TACGAC
                          _____    _ C   A
GAM57  SLC4A10          TTTATGATCCAAGTATACT      570        ___    III
                        TTTATGATC  GTATGC
                        |||||||||  ||||||
                        AAATACTAG  CATATG
                          GTT   AII
GAM57  VENTX2           TGACGTTTAAAAGCACATGC     569        T T   TGC
                        TGACGTTTA GA CGTATGC
                        ||||||||| || |||||||
                        ACTGCAAAT TT GTGTACG
                          T C   III
GAM57  VENTX2           TGACGTTTAAAAGCACATGC     569        T T   I
                        GACGTTTA GA CGTATG
                        |||||||| || ||||||
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                      CTGCAAAT TT GTGTAC
                         T C    I
GAM58 BAK1     AGGTCTCAGTGGAGGACGGGATCA 576 TGAG    AT____ A  ACI
                      GTCTCAG   GCG GATCA
                      ||||||   ||| |||||
                      CAGAGTC   TGC CTAGT
                         ____    ACCTCC  C  CGI
GAM58 CRY2     AGGTCTCAGCTGAAAG-TCA    580 _   A C ATCI
                      GGTCTCAG TG GAG
                      |||||||| || |||
                      CCAGAGTC AC TTC
                         T   G T AGII
GAM58 CRY2     AGGTCTCAGCTGAAAG-TCA    580 TGAG   A C A A
                      GTCTCAG TG GAG TCA
                      ||||||| || ||| |||
                      CAGAGTC AC TTC AGT
                         ____     G T _ G
GAM58 EDG8     GAGGTCTCAGCT-C-ACATCA  584       AT_ AGATI
                      GAGGTCTCAG  GCG
                      ||||||||||  |||
                      CTCCAGAGTC  TGT
                         GAG  AGTII
GAM58 EDG8     GAGGTCTCAGCT-C-ACATCA  584 TG    ATG AG  A
                      AGGTCTCAG  CG ATCA
                      |||||||||  || ||||
                      TCCAGAGTC  GT TAGT
                         __    GA_ G_  G
GAM58 F13A1    TGAGGTCTCAACATGGGTGAT   587        _ CGA CAAC
                      TGAGGTCTCAG ATG  GAT
                      ||||||||||| |||  |||
                      ACTCCAGAGTT TAC  CTA
                         G  CCA  IIIC
GAM58 F13A1    TGAGGTCTCAACATGGGTGAT   587 G      _ CGAGAI
                      AGGTCTCAG ATG
                      ||||||||| |||
                      TCCAGAGTT TAC
                      _    G  CCACTI
GAM58 FLRT2    AGGTCTCAGAGGATGTGTGAT    577       TGCGAGAIII
                      AGGTCTCAGA
                      ||||||||||
                      TCCAGAGTCT
                         CCTACACACT
GAM58 FLRT2    AGGTCTCAGAGGATGTGTGAT    577 T_____ TCTCA_  GAGATCAAC
                      GAGG    GATGC
                      ||||    |||||
                      CTCC    CTACG
                    CAGAGT  TACACA   IIICAACTA
GAM58 HIVEP3   AGTTCTGGGTTG-GAGATCAAC  582 GG_ CAGA C   I
                      TCT  TG GAGATCAA
                      |||   || |||||||||
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                                        AGA    AC CTCTAGTT
                                        TCA    CCCA  _      I
GAM58  IL1RAPL2        AGGTCTCAGATGCGTAGTTC     579           _ ATII
                      AGGTCTCAGATGCG AG
                      IIIIIIIIIIIII II
                      TCCAGAGTCTACGC TC
                              A  AAGI
GAM58  IL1RAPL2        AGGTCTCAGATGCGTAGTTC     579  TGAG        _ A AA
                        GTCTCAGATGCG AG TC
                        IIIIIIIIIIII II II
                        CAGAGTCTACGC TC AG
                        ____           A  A GT
GAM58  ISLR          GTCTCAGATGAG-GA-CAA        585          CGA  CAI
                     GTCTCAGATG  GAT
                     IIIIIIIIII  III
                     CAGAGTCTAC  CTG
                          TC_  TTI
GAM58  MFI2          GAGG-CTGAGATGCGAGGATCA     583    T C      _  I
                      AGG CT AGATGCGAG ATC
                      III II IIIIIIIII III
                      TCC GA TCTACGCTC TAG
                       _  C      C  I
GAM58  MFI2          GAGG-CTGAGATGCGAGGATCA     583  TG T C      _  AC
                         AGG CT AGATGCGAG ATCA
                         III II IIIIIIIII IIII
                         TCC GA TCTACGCTC TAGT
                         __  _ C      C  CI
GAM58  NAP1L3          AGGTCTCAGTT--GA-ATCAA    581 _      A CGA
                        GGTCTCAG TG  GATCA
                        IIIIIIII II  IIIII
                        CCAGAGTC AC  TTAGT
                         T     A ___
GAM58  NAP1L3          AGGTCTCAGTT--GA-ATCAA    581  TGAG    A CGA
                        GTCTCAG TG  GATCA
                        IIIIIII II  IIIII
                        CAGAGTC AC  TTAGT
                        ____      A ___
GAM58  RBP4          AGTTCTCAGATGAAACTAGAT      578  G      C GAIII
                      AG TCTCAGATG GA
                      II IIIIIIIII II
                      TC AGAGTCTAC TT
                       A    T GATCT
GAM58  RBP4          AGTTCTCAGATGAAACTAGAT      578  TGAGG      CG___  CAAC
                       TCTCAGATG   AGAT
                       IIIIIIIII   IIII
                       AGAGTCTAC   TCTA
                       A____       TTTGA  AGII
GAM58  TFEB          TCTCAGATGAG-GATCCAC        586          CGA  AAI
                     TCTCAGATG  GATC
                     IIIIIIIII  IIII
```

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                              AGAGTCTAC  CTAG
                              TC_   GTG
GAM58  TFEB        TCTCAGATGAG-GATCCAC      586 __    TC  G GCGAGATCA
                              TGAGG TCA AT
                              |||||  ||| ||
                              ACTCC  GGT TG
                       CT    TA  G  ACAIIICAA
GAM58  TPMT        AGGTCTCAGAGAAGCAAGAATCA  575 GGT   T__    TCI
                          CTCAGA  GCGAGA
                          |||||| ||||||
                          GAGTCT  CGTTCT
                       ___     CTT   TAG
GAM58  TPMT        AGGTCTCAGAGAAGCAAGAATCA  575 TGAG     T__   _ ACI
                           GTCTCAGA  GCGAGA TCA
                           ||||||||  |||||| |||
                           CAGAGTCT  CGTTCT AGT
                       ____      CTT   T GAI
GAM59  ATP1A2        TCACAGGTTCAAGCAATTCTCC  601  A  TC      AG
                           TCA AGGTTT  GCAATTCTCC
                           ||| |||||| ||||||||||
                           AGT TCCAAG  CGTTAAGAGG
                            G    TT      II
GAM59  ATP1A2        TCACAGGTTCAAGCAATTCTCC  601 CAA   TC    I
                           AGGTTT  GCAATTCTC
                           |||||| |||||||||
                           TCCAAG  CGTTAAGAG
                            GTG    TT     I
GAM59  AVPR2        CACAGGCTCTGGCCAATTCTCCA  596 AA    C _    I
                           AGGTTTT GC AATTCTCC
                           ||||||| || |||||||||
                           TCCGAGA CG TTAAGAGG
                            G_    C G    I
GAM59  AVPR2        CACAGGCTCTGGCCAATTCTCCA  596 TCAA    C _    GI
                           AGGTTTT GC AATTCTCCA
                           ||||||| || ||||||||||
                           TCCGAGA CG TTAAGAGGT
                        TG__    C G    GI
GAM59  C5R1        TCCAAGGTTCGAGCAATTCTCC   603  A  TC     AG
                           TC AAGGTTT  GCAATTCTCC
                           || |||||| ||||||||||
                           AG TTCCAAG  CGTTAAGAGG
                            G   CT     II
GAM59  C5R1        TCCAAGGTTCGAGCAATTCTCC   603 CA    TC    I
                           AAGGTTT  GCAATTCTC
                           ||||||| |||||||||
                           TTCCAAG  CGTTAAGAG
                            GG    CT     I
GAM59  EGLN3        AGGTTGTGATAATTCTCCAG    593     TTCGC     I
                           GGTT   AATTCTCCA
                           ||||   |||||||||
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                      CCAA    TTAAGAGGT
                      CACTA        I
GAM59  EGLN3     AGGTTGTGATAATTCTCCAG    593  TCAAAGGTTTTCGC
                          AATTCTCCA
                          IIIIIIIII
                          TTAAGAGGT
                      ACACTA_____
GAM59  FBXW1B    TCAAAGGTTGTCTGCATATTC    600      T _ _  TCCAG
                      TCAAAGGTT TC GCA ATTC
                      IIIIIIIIII II III IIII
                      AGTTTCCAA AG CGT TAAG
                        C  A  A  IIIGA
GAM59  FBXW1B    TCAAAGGTTGTCTGCATATTC    600      T _ ATTIII
                      TCAAAGGTT TC GCA
                      IIIIIIIIII II III
                      AGTTTCCAA AG CGT
                        C  A  ATAAGI
GAM59  FBXW7     CAAAGGTTTTCAC-ATTCTGCAG   599 _       A  C I
                      AAAGGTTTTCGCA TTCT CA
                      IIIIIIIIIIIII IIII II
                      TTTCCAAAAGTGT AAGA GT
                        G        _  C I
GAM59  FBXW7     CAAAGGTTTTCAC-ATTCTGCAG   599 TC      A  C
                        AAAGGTTTTCGCA TTCT CAG
                        IIIIIIIIIIIII IIII III
                        TTTCCAAAAGTGT AAGA GTC
                        __       _  C
GAM59  GOCAP1    CATATGTATTTC-CAATTCTCC   595 AAAG _ G      I
                        GT TTTC CAATTCTC
                        II IIII IIIIIIIII
                        CA AAAG GTTAAGAG
                      TATA  T  _     I
GAM59  GOCAP1    CATATGTATTTC-CAATTCTCC   595 TCAAAG _ G     AG
                        GT TTTC CAATTCTCC
                        II IIII IIIIIIIII
                        CA AAAG GTTAAGAGG
                      TATA__ T  _    AI
GAM59  IGFBP3    AAAGGTTTTC-CTATTCTC     591      GCA  I
                        AAAGGTTTTC ATTCT
                        IIIIIIIIII IIIII
                        TTTCCAAAAG TAAGA
                          GA_  G
GAM59  IGFBP3    AAAGGTTTTC-CTATTCTC     591 TCAA    GCA  C
                        AGGTTTTC ATTCTC
                        IIIIIIII IIIIII
                        TCCAAAAG TAAGAG
                        ____     GA_  C
GAM59  MEIS2    CAAAGAGACTTCTCCCAATTCTCCA 594 AA _  G       I
                        AGG TTTTC CAATTCTCC
                        III IIIII IIIIIIIII
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                           TCT AAGAG GTTAAGAGG
                           C_   G   G        I
GAM59   MEIS2      CAAAGAGACTTCTCCCAATTCTCCA  594  TCAA   _    G        II
                           AGG TTTTC CAATTCTCCAG
                           ||| ||||| |||||||||||
                           TCT AAGAG GTTAAGAGGTT
                           TTTC  G    G       II
GAM59   MYF6       CAACAGATTTCGCAATTTTC      598  CAA    T     CI
                           AGGTTT CGCAATT
                           |||||| |||||||
                           TCTAAA GCGTTAA
                           TG_    _    AA
GAM59   MYF6       CAACAGATTTCGCAATTTTC      598  TCAA    T     C  CA
                           AGGTTT CGCAATT TC
                           |||||| ||||||| ||
                           TCTAAA GCGTTAA AG
                           TTG_    _     A CI
GAM59   NKX3A      AAGATTTCCACGCAATTCTCCA    592  AGG  TT         I
                           TT CGCAATTCTCC
                           || |||||||||||
                           AG GCGTTAAGAGG
                           TAA  GT         I
GAM59   NKX3A      AAGATTTCCACGCAATTCTCCA    592  TCAAAGG  TT
                           TT CGCAATTCTCCAG
                           || ||||||||||||||
                           AG GCGTTAAGAGGTT
                           TAA____  GT
GAM59   OPA3       TCATGGGTTCAAGCAATTCTCC    602   AA   TC         AG
                           TCA GGTTT GCAATTCTCC
                           ||| ||||| ||||||||||
                           AGT CCAAG CGTTAAGAGG
                           AC    TT        II
GAM59   OPA3       TCATGGGTTCAAGCAATTCTCC    602  CAAA    TC       I
                           GGTTT GCAATTCTC
                           ||||| |||||||||
                           CCAAG CGTTAAGAG
                           GTAC    TT       I
GAM59   SVIL       AAAGGTTGATTCGCATAGATTCTCCAG590  AAGGTT    ___      I
                           TTCGCA ATTCTCCA
                           |||||| ||||||||
                           AAGCGT TAAGAGGT
                           ACT___    ATC     I
GAM59   SVIL       AAAGGTTGATTCGCATAGATTCTCCAG590  TCAA    __   ___      III
                           AGGTT TTCGCA ATTCTCCAG
                           ||||| |||||| |||||||||
                           TCCAA AAGCGT TAAGAGGTC
                           ____    CT    ATC    TCI
GAM59   ZNF141     CAAAGGTTTGC-CACATTCT      597         _     ATTCII
                           CAAAGGTTT TCGCA
                           ||||||||| |||||
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                    GTTTCCAAA GGTGT
                      C   AAGAII
GAM59  ZNF141      CAAAGGTTTGC-CACATTCT    597  TC      _    A   CCA
                    AAAGGTTT TCGCA TTCT
                    |||||||| ||||| ||||
                    TTTCCAAA GGTGT AAGA
                      __       C   _  AII
GAM60  ABL1        TGACAC--CTGACCCCTGA    612      GT       GAA
                    TGACAC CTGACCCCTGA
                    |||||| ||||||||||
                    ACTGTG GACTGGGGACT
                      __          III
GAM60  CERD4       GACCAGCCTGTCC-CTGAGAAG   611 TGA C   AC
                    CA GTCTG  CCCTGAGAAGG
                    || |||||  |||||||||||
                    GT CGGAC  GGGACTCTTCT
                    TG_  _    A_
GAM60  EPO         GACAGTTCCTCTGGCCCCTGAGA 609 TGACACG_ A     AGGI
                       TCTG CCCCTGAGA
                       |||| |||||||||
                       AGAC GGGGACTCT
                    TGTCAAGG   C      AIII
GAM60  GAS7        TGACCGGTAAGACCCCTGAAAA    614    A TCT_        GG
                    TGAC CG  GACCCCTGAGAA
                    |||| ||  |||||||||||
                    ACTG GC  CTGGGGACTTTT
                     _  CATT          II
GAM60  GNLY        TGACACTTTATTCCCCTGAGAGGG  616     GTCTGA    A I
                    TGACAC    CCCCTGAGA GG
                    ||||||    |||||||||| ||
                    ACTGTG    GGGGACTCT CC
                     AAATAA      C I
GAM60  HPCAL1      CAGGTCTGACCCCAGCTAAGG     608 TGACAC      TGAG
                      GTCTGACCCC  AAGG
                      ||||||||||  ||||
                      CAGACTGGGG  TTCC
                    _____       TCGA
GAM60  LTBP2       TGCCACA-CTGACCCCTGA    613 TGA   T      GAA
                     CACG CTGACCCCTGA
                     |||| |||||||||||
                     GTGT GACTGGGGACT
                    ACG  _          III
GAM60  MAPK14      GACACTTCTCCACCCCTGAG     610 TG  G  G_     AAG
                    ACAC TCT ACCCCTGAG
                    |||| ||| |||||||||
                    TGTG AGA TGGGGACTC
                     __  A  GG     CII
GAM60  PCDHB16     TGACAC--CTAACC-CTGAGAAG   615     GT   C
                    TGACAC CTGACCC TGAGAAG
                    |||||| ||||||| |||||||
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                                ACTGTG GATTGGG ACTCTTC

                                       __       _
GAM60  RCP          CAAGTCCTTGACCCCTGGAGCAGG  607 TGACAC  __     _ A  I
                       GTCT  GACCCCTG AG AGG
                       ||||  |||||||| || |||
                       CAGG  CTGGGGAC TC TCC
                       _____        AA    C  G  A
GAM60  TCF1         ACAGGCCTGTGTCCTGAGAAG     606 TGACAC   ACC      G
                       GTCTG CCTGAGAAG
                       ||||| |||||||||
                       CGGAC GGACTCTTC
                    TC____      ACA     A
GAM61  BARX2          TTCCCTCAAAAGGGTTTTA      625   AA  _    ATGTA
                       TTCC CAAA GGGTTTTA
                       |||| |||| |||||||||
                       AAGG GTTT CCCAAAAT
                        GA   T       IIIGA
GAM61  C21orf2      TTCCAACAAAGCGCTTTACTG      627        G  A TAG
                       TTCCAACAAAG GTTTTA TG
                       ||||||||||| |||||| ||
                       AAGGTTGTTTC CGAAAT AC
                          G   G III
GAM61  COL4A4         TTCCAACAAATCTTTTAAATTTAG 629        GGG   TG_ I
                       TTCCAACAAA TTTTAA TAG
                       |||||||||| |||||| |||
                       AAGGTTGTTT AAAATT ATC
                         AG_   TAA  I
GAM61  DMD          TCCACCAAGAAGGGTTTTTTTGTA   623 TT_  CA     AA  I
                       CCAA AAGGGTTTT TGTAG
                       |||| ||||||||| |||||
                        GGTT TTCCCAAAA ACATT
                        GGT  C_     AA  I
GAM61  DNTT         TCCTACACGAAGGGTTTTGATGT    622 TT A __     A AGI
                       CC ACA AAGGGTTTT ATGT
                       || ||| ||||||||| ||||
                       GG TGT TTCCCAAAA TACA
                       __ A GC      C  GII
GAM61  EGLN1        TTCCAACAATTTCTTTTAA        626       AGGG    TGTA
                       TTCCAACAA TTTTAA
                       ||||||||| ||||||
                       AAGGTTGTT AAAATT
                        AAAG   IIIG
GAM61  HTR2A        CCAAGCAGAATGGTTTTAAT       621 TTCCAACAAAG       TA
                          GGTTTTAATG
                          ||||||||||
                          CCAAAATTAT
                       TTCGTCTTA__        TI
GAM61  SH3BP5       TTCTAGAAAATGGTTTTAATG      628 TTCCAACAAAG       TAG
                          GGTTTTAATG
                          ||||||||||
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                            CCAAAATTAC
                         AAGATCTTTTA          III
GAM61  SPTBN4       TTCAAAGCCAAAGGG-TTTATTATAG 624  TTCCAA__        TAA    II
                         CAAAGGGTTT  TGTAG
                         IIIIIIIIII  IIIII
                         GTTTCCCAAA  ATATC
                         AAGTTTCG        TA_    II
GAM61  TBXAS1       CAACAAAGGGTTTCAGTGTA   620  TTCCAA        A
                         CAAAGGGTTTTA TGTA
                         IIIIIIIIIIII IIII
                         GTTTCCCAAAGT ACAT
                         _____            C
GAM61  ZNF189       AACAAAACAGGTTTTAATG      619  TTCCAACAAA        TA
                         GGGTTTTAATG
                         IIIIIIIIIII
                         TCCAAAATTAC
                      TTTG_____        CA
GAM62  ADAM28       TAAAACCAACCTCAAAT-CTTA   649     GT      T CTTACA
                      TAAA  CAACCTCAA TC
                      IIII  IIIIIIIII II
                      ATTT  GTTGGAGTT AG
                         TG       T AATIII
GAM62  ADAM28       TAAAACCAACCTCAAAT-CTTA   649 _  GT      T CTTI
                         AAA  CAACCTCAA TC
                         III  IIIIIIIII II
                         TTT  GTTGGAGTT AG
                      A  TG       T AAII
GAM62  BACH2        AAAGTCAACCATCTATTCC      633         _  A  II
                         AAAGTCAACC TC ATTC
                         IIIIIIIIII II IIII
                         TTTCAGTTGG AG TAAG
                            T A  GI
GAM62  BACH2        AAAGTCAACCATCTATTCC      633 TA      _  A   TAC
                         AAGTCAACC TC ATTCCT
                         IIIIIIIII II IIIIII
                         TTCAGTTGG AG TAAGGG
                         __       T A   III
GAM62  BNC         TAAAGTCAA-ATCAAATACTT     646       CC  TTC  AC
                         TAAAGTCAA TCAA  CTT
                         IIIIIIIII IIII  III
                         ATTTCAGTT AGTT  GAA
                            T_  TAT  II
GAM62  BNC         TAAAGTCAA-ATCAAATACTT     646 _       CC  TTCCTI
                         AAAGTCAA TCAA
                         IIIIIIII IIII
                         TTTCAGTT AGTT
                         A   T_  TATGAI
GAM62  C18orf1     TAAAGTTTAAGCCTCAATTC      643      CAA__       CTTAC
                         TAAAGT  CCTCAATTC
                         IIIIII  IIIIIIIII
```

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                          ATTTCA  GGAGTTAAG
                          AATTC     IIIAC
GAM62  C18orf1     TAAAGTTTAAGCCTCAATTC  643    CAA__      III
                          TAAAGT  CCTCAATT
                          IIIIII  IIIIIIII
                          ATTTCA  GGAGTTAA
                          AATTC     GII
GAM62  CDH1        AAAGTGAGACAAAATTCCTTA  636 TAA__ T CCTC      CA
                          AG CAA  AATTCCTTA
                          II III  IIIIIIIII
                          TC GTT  TTAAGGAAT
                          TTCAC T ____      TI
GAM62  CHC1L       AATGTGAACCTCAA-TAATTACA  638 AA_ C    TCC  I
                          GT AACCTCAAT  TTAC
                          II IIIIIIIII  IIII
                          CA TTGGAGTTA  AATG
                          TTA C     TT_  I
GAM62  CHC1L       AATGTGAACCTCAA-TAATTACA  638 TAAA C    TCC
                          GT AACCTCAAT  TTACA
                          II IIIIIIIII  IIIII
                          CA TTGGAGTTA  AATGT
                          TA__ C    TT_
GAM62  CRACC       AAAGTCAACGTTCTTCATTC  632        CTCAATTIII
                          AAAGTCAAC
                          IIIIIIIII
                          TTTCAGTTG
                            CAAGAAGTAA
GAM62  CRACC       AAAGTCAACGTTCTTCATTC  632 TA      ___ CA  CTTAC
                          AAGTCAAC CT ATTC
                          IIIIIIII II IIII
                          TTCAGTTG GA TAAG
                          __    CAA AG  AIIIA
GAM62  CYP26A1     TAAAGTCAACACAACACTCCTTA  644       CTCA_      CAI
                          TAAAGTCAAC    ATTCCTTA
                          IIIIIIIIII    IIIIIIII
                          ATTTCAGTTG    TGAGGAAT
                          TGTTG      III
GAM62  CYP26A1     TAAAGTCAACACAACACTCCTTA  644 A      CTCA_    I
                          AAGTCAAC    ATTCCTT
                          IIIIIIII    IIIIIII
                          TTCAGTTG    TGAGGAA
                          _    TGTTG     I
GAM62  FGFR2       TATAGAGAACCTCAATCTCTT  648 AA TC    TC I
                          AG AACCTCAAT CT
                          II IIIIIIIII II
                          TC TTGGAGTTA GA
                          TA TC     GA I
GAM62  FGFR2       TATAGAGAACCTCAATCTCTT  648 TAA TC    TC ACA
                          AG AACCTCAAT CTT
                          II IIIIIIIII III
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                          TC  TTGGAGTTA  GAA
                         ATA  TC        GA  III
GAM62   GRB14          TAAAGTCAATC-CAAGTCTTT    647          C T  T CTTAC
                        TAAAGTCAA C CAA TC
                        |||||||| | ||| ||
                        ATTTCAGTT G GTT AG
                           A _    C  AAAII
GAM62   GRB14          TAAAGTCAATC-CAAGTCTTT    647 _       C T  T CTI
                         AAAGTCAA C CAA TC
                         |||||||| | ||| ||
                         TTTCAGTT G GTT AG
                          A    A _  C  AAI
GAM62   IPP          AACCTCCTATTAATTCCTTAC      639          _____        IIIG
                        AACCTC   AATTCCTTA
                        ||||||   |||||||||
                        TTGGAG   TTAAGGAAT
                          GATAA       GIII
GAM62   IPP          AACCTCCTATTAATTCCTTAC      639 TAAAGTCAACCTC       A
                              AATTCCTTAC
                              ||||||||||
                              TTAAGGAATG
                         ATAA_____          A
GAM62   KCND2         AAGCTAAGCTTTATTCCTTACA    640   TC C CA       I
                        AG  AA CT ATTCCTTAC
                        || || || |||||||||
                        TC  TT GA TAAGGAATG
                         GA  C  AA        I
GAM62   KCND2         AAGCTAAGCTTTATTCCTTACA    640 TAAA TC C CA
                         G  AA CT ATTCCTTACA
                         | || || ||||||||||
                         C  TT GA TAAGGAATGT
                        ____GA  C  AA
GAM62   MYBL1          TAAAGTCAAAAT-TATTCTTTAC    650       CCTCA  C  A
                        TAAAGTCAA    ATTC TTAC
                        |||||||||    |||| ||||
                        ATTTCAGTT    TAAG AATG
                          TTAA_  A  I
GAM62   NEBL           TAAAGTCAACATTTTTTCC       645        CTCAA  TTAC
                        TAAAGTCAAC    TTCC
                        ||||||||||    ||||
                        ATTTCAGTTG    AAGG
                          TAAAA   IIIA
GAM62   NEBL           TAAAGTCAACATTTTTTCC       645        CTCAATTCII
                        TAAAGTCAAC
                        ||||||||||
                        ATTTCAGTTG
                          TAAAAAAGGI
GAM62   PSEN1        AAAGTCA-CCTCAATTCTCTCAC     635        A       _  I
                        AAGTCA CCTCAATTC CTTA
                        |||||| ||||||||| ||||
```

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                              TTCAGT GGAGTTAAG GAGT
                                _        A    I
GAM62  PSEN1      AAAGTCA-CCTCAATTCTCTCAC  635 TA   A      _    A
                  AAGTCA CCTCAATTC CTTAC
                  |||||| ||||||||| |||||
                  TTCAGT GGAGTTAAG GAGTG
                        __     _   A    G
GAM62  SGCG       TCAACCTCAAATTCCCTTCA  651        _    ACII
                  TCAACCTCAA TTCCTT
                  |||||||||| ||||||
                  AGTTGGAGTT AAGGGA
                         T    AGTI
GAM62  SVIL       AAAATCACACTGCAATTCCTTA  634 A    AC  _       I
                  AGTCA CT CAATTCCTT
                  ||||| || |||||||||
                  TTAGT GA GTTAAGGAA
                   _    GT  C       I
GAM62  SVIL       AAAATCACACTGCAATTCCTTA  634 TA   AC  _       CA
                  AAGTCA CT CAATTCCTTA
                  |||||| || ||||||||||
                  TTTAGT GA GTTAAGGAAT
                     __  GT  C       AI
GAM62  TAF1C      AGTCA-CATGCAATTCCTTTCA  641    ACCT      ACI
                  GTCA   CAATTCCTT
                  ||||   |||||||||
                  CAGT   GTTAAGGAA
                   GTAC       AGI
GAM62  TAF1C      AGTCA-CATGCAATTCCTTTCA  641 TAAAGTCAACCT      ACA
                       CAATTCCTT
                       |||||||||
                       GTTAAGGAA
                  GTGTAC_____      AGT
GAM62  TMOD       AGTCAACCT-AAAACCTTA  642        C TT  I
                  AGTCAACCT AA CCTT
                  ||||||||| || ||||
                  TCAGTTGGA TT GGAA
                   _    TT   T
GAM62  TMOD       AGTCAACCT-AAAACCTTA  642 TAAAGT   C TT
                  CAACCT AA CCTTA
                  |||||| || |||||
                  GTTGGA TT GGAAT
                  _____   _ TT
GAM62  ZNF200     AAAGTAAAC---AATTCCTTTCA  637    CAACCT     AI
                  AAAGT   CAATTCCTT
                  |||||   |||||||||
                  TTTCA   GTTAAGGAA
                   TTT___      AG
GAM62  ZNF200     AAAGTAAAC---AATTCCTTTCA  637 TA   CAACCT      AC
                  AAGT   CAATTCCTT
                  ||||   |||||||||
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                         TTCA      GTTAAGGAA
                   __      TTT___        AG
GAM63  ADAT1     TGAGAACAA-GTCCAGGGCAG    670 _       GT  C  CAI
                      GAGAACAAG  CA GGT
                      ||||||||| || |||
                      CTCTTGTTC  GT CCG
                      A       AG  C  TII
GAM63  ATP2B2    AGCACACCCTCACTGGTCAGCTG   658 GA  AGG   _      I
                      ACA   TCAC GGTCAGCT
                      ||| |||| |||||||||
                      TGT  AGTG CCAGTCGA
                      G_  GGG   A     I
GAM63  CX3CR1    TGTGAACAAGGTCTGGACGG      668 TGA        ACGIII
                      GAACAAGGTC
                      ||||||||||
                      CTTGTTCCAG
                      ACA       ACCTGC
GAM63  FY       GAGAACAAGGTCTCTG-CAG     662 G        ACG CI
                      AGAACAAGGTC  GT
                      |||||||||| ||
                      TCTTGTTCCAG  CG
                      _       AGA  TC
GAM63  GLTSCR1   ACACAGGTCACGG--AGCTG     655  _      TC  I
                      ACA AGGTCACGG AGCT
                      ||| ||||||||| ||||
                      TGT TCCAGTGCC TCGA
                      G     __     C
GAM63  H3F3B     TGAGAACAAGTGCA--GTCAG     671 _      GTCA   I
                      GAGAACAAG  CGGTCA
                      |||||||||  ||||||
                      CTCTTGTTC  GTCAGT
                      A    AC__     I
GAM63  HUNK      TGAGGAAGACAGTCACGGTC      665    AACAA_      II
                      TGAG    GGTCACGGT
                      ||||    |||||||||
                      ACTC    TCAGTGCCA
                      CTTCTG      GI
GAM63  IFITM2    TGGGATACA-GGTCACGGGCAG    666 __ GA  A      T I
                      GA ACA GGTCACGG CA
                      || ||| ||||||||| ||
                      CT TGT CCAGTGCC GT
                      CC A_ _      C I
GAM63  IL1F8     GAGAACAAGAT-A-GATCAGATG   663        CAC   CI
                      GAGAACAAGGT  GGTCAG
                      ||||||||||  ||||||
                      CTCTTGTTCTA  CTAGTC
                          T__    TA
GAM63  KIF3B     GAAGCAAGGTCACTGGTCA      660 _      _   III
                      GAA CAAGGTCAC GGTC
                      ||| |||||||||| ||||
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                          CTT GTTCCAGTG CCAG
                           C      A    TII
GAM63  KLK5      AACTAGAGAGACACGGTCAGC   654 AACAA___  T      III
                          GG CACGGTCAG
                          || |||||||||
                          TC GTGCCAGTC
                      TTGATCTC  T      GII
GAM63  LNK       GAGAACAAGTTTCCACTGCCAGCT 661 AG    G__   G     I
                        AACAAG  TCAC GTCAGC
                        ||||||  |||| ||||||
                        TTGTTC  GGTG CGGTCG
                     __       AAA  A    I
GAM63  PNUTL1    TGAGAATAAATT-AGGGTCAGCTG 672 _   C  GTCAC      I
                        GAGAA AAG   GGTCAGCT
                        ||||| |||   ||||||||
                        CTCTT TTT   CCAGTCGA
                     A    A  AATC_      I
GAM63  PODXL     AGAACAAGGGGTTCAAGGT      657        ___  C  III
                        AGAACAAGG TCA GG
                        ||||||||| ||| ||
                        TCTTGTTCC AGT CC
                     CCA   T  AII
GAM63  PSG11     AGAGCACGG-CT-GGTCAGCTG   659 _ A A  CAC      I
                        GA CA GGT  GGTCAGCT
                        || || |||  ||||||||
                        CT GT CCG  CCAGTCGA
                     T  C  G  A__      I
GAM63  SCA1      TGAGAACAAAGTCTATGTGGCAGC 669 GA      AC___  T I
                        GAACAAGGTC   GG CAG
                        ||||||||||   || |||
                        CTTGTTTCAG   CC GTC
                     __       ATACA _   I
GAM63  SLC13A1   ACAAGGTCAGTAACAGCTG      656       CGGT   II
                        ACAAGGTCA  CAGCT
                        |||||||||  |||||
                        TGTTCCAGT  GTCGA
                     CATT    CI
GAM63  SORCS1    TGAGAACAACTGGCCAAGGTC    667         __  C  III
                        TGAGAACAA GGTCA GGT
                        ||||||||| ||||| |||
                        ACTCTTGTT CCGGT CCA
                     GA    T  GII
GAM63  STX1A     GAGGACAGGG-CA-GGTCAGCTG  664  A A T C      I
                        GAG ACA GG CA GGTCAGC
                        ||| ||| || || ||||||||
                        CTC TGT CC GT CCAGTCG
                     C  C _ _    A
GAM64  ACVR1     TGCTCCAGGCTG---TAGTCC    687 TT G     CAT
                        GC CCAGGCTGT AGTCC
                        || |||||||| |||||
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                         CG GGTCCGACA  TCAGG
                         __    A        ___
GAM64  ADORA1        CGCGCGGCAGCTCATAGTCCT    676 TTGCGCCA  T _
                         GGC G TCATAGTCCTT
                         ||| | ||||||||||
                         CCG C AGTATCAGGAG
                         CG_____  T G
GAM64  AICDA         TTG-GCCAGGCTGGTCTCAAACTCCT 692   C     ___  TAG  TII
                         TTG GCCAGGCTG  TCA  TCCT
                         ||| |||||||||  |||  ||||
                         AAC CGGTCCGAC  AGT  AGGA
                         _       CAG  TTG   |||
GAM64  ANKH          TTG-GCCAGGCTGGTCTCAAACTCCT 692   C     ___  TAG  TII
                         TTG GCCAGGCTG  TCA  TCCT
                         ||| |||||||||  |||  ||||
                         AAC CGGTCCGAC  AGT  AGGA
                         _       CAG  TTG   |||
GAM64  ASL           TTGC-CCAGGCTGTGTCAAACTCCT 690   G    __  TAG   TI
                         TTGC CCAGGCT GTCA  TCCT
                         |||| ||||||| ||||  ||||
                         AACG GGTCCGA CAGT  AGGA
                         _       CA  TTG   II
GAM64  AVP           CGCCAGGCTGTCATGGCC      677 TTGCGC      A_  CT
                         CAGGCTGTCAT GTC
                         ||||||||||| |||
                         GTCCGACAGTA CGG
                         _____         CC  CG
GAM64  B4GALT2       GCCAGGCTGTGGTCAGTCCT    680 TTGCGCCA    CA_
                         GGCTGT  TAGTCCT
                         ||||||  |||||||
                         CCGACA  GTCAGGA
                         _____        CCA
GAM64  CACNA1C       GGCGGCTCGCGCACCCAGGC    685 ACACG GG   GT
                         GC CGCG CACCCAGG
                         || |||| |||||||||
                         CG GCGC GTGGGTCC
                         _____  A_   __
GAM64  CD28          TGCGCCAGG-TCCCATAGTACT   688 TT     CTG    C
                         GCGCCAGG  TCATAGT CTT
                         ||||||||  ||||||| |||
                         CGCGGTCC  GGTATCA GAG
                         __      AG_     T
GAM64  CD68          TTG-GCCAGGCTGGTCTCAAACTCCT 692   C     ___  TAG  TII
                         TTG GCCAGGCTG  TCA  TCCT
                         ||| |||||||||  |||  ||||
                         AAC CGGTCCGAC  AGT  AGGA
                         _       CAG  TTG   |||
GAM64  CRY2          GGCTGCTTGGGCACCCAGGC    686 ACACGGCG GC  T
                         GC GG CACCCAGG
                         || || |||||||||
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                          CG  CC GTGGGTCC
                          _____  AA  C
GAM64  CYP4F3        TTG-GCCAGGCTGGTCTCAAACTCCT 692   C      ___  TAG   TII
                     TTG GCCAGGCTG  TCA  TCCT
                     ||| |||||||||  |||  ||||
                     AAC CGGTCCGAC  AGT  AGGA
                           _    CAG  TTG  III
GAM64  EPHA8         CGG-GGTGGGCTCACCCAGGC    679  ACAC C C  GG
                          GG GG GC  TCACCCAGG
                          || || ||  |||||||||
                          CC CC CG  AGTGGGTCC
                          ___  A  _  __
GAM64  FBXL7        TTG-GCCAAG--GTCATAGTCATT  696   C    CT      CTT
                     TTG GCCAGG GTCATAGTC
                     ||| |||||| |||||||||
                     AAC CGGTTC CAGTATCAG
                          _   __      TAA
GAM64  GPR4         GCCAGGCTGCCTCAGTCATT    682 TTGCGCCA     A   CT
                          GGCTGTC TAGTC
                          ||||||| |||||
                          CCGACGG GTCAG
                          _____    A  TA
GAM64  HCN2         CACGGCGGCG-GGAC-CCCAG   675 AC      C TCA   G
                          ACGGCGGCG GG  CCCAG
                          ||||||||| ||  |||||
                          TGCCGCCGC CC  GGGTC
                          __        _  TG_  G
GAM64  HEM1        TGCTCGAGTCAG-CATAGTCCT    689 TT GCC GCT T
                          GC  AG  G CATAGTCCTT
                          ||  ||  | |||||||||||
                          CG  TC  C GTATCAGGAG
                          __ AGC  AGT _
GAM64  IL17R       TTG-GCCAGGCTGGCTCAAACTCCT 694   C      __  TAG  TI
                     TTG GCCAGGCTG  TCA  TCCT
                     ||| |||||||||  |||  ||||
                     AAC CGGTCCGAC  AGT  AGGA
                           _    CG  TTG  II
GAM64  KIF3B       TTG-GCCAGGCTGGTCTCGAAGTCCT 693   C     _ AT__   TII
                     TTG GCCAGGCTG TC   AGTCCT
                     ||| ||||||||| ||   ||||||
                     AAC CGGTCCGAC AG   TCAGGA
                           _    C AGCT    III
GAM64  KNSL1       TTG-GCCAGGCTGGTCTCAAACTCCT 692   C      ___  TAG   TII
                     TTG GCCAGGCTG  TCA  TCCT
                     ||| |||||||||  |||  ||||
                     AAC CGGTCCGAC  AGT  AGGA
                           _    CAG  TTG  III
GAM64  LAMP2       TTG-GCCAGGCTGGTCTCAAACTCCT 692   C      ___  TAG   TII
                     TTG GCCAGGCTG  TCA  TCCT
                     ||| |||||||||  |||  ||||
```

```
                              AAC CGGTCCGAC  AGT  AGGA
                               _     CAG  TTG    III
GAM64  MDFI         GCGCCAGGCTGGCTTAGCCC     683 TTGC      TCA
                              GCCAGGCTG  TAGTCCT
                              IIIIIIIII  IIIIIII
                              CGGTCCGAC  ATCGGGG
                              ____          CGA
GAM64  NPHP1        TTG-GCCAGGCTGGTCTCAAACTCCT 692   C       ___  TAG  TII
                              TTG GCCAGGCTG  TCA  TCCT
                              III IIIIIIIII  III  IIII
                              AAC CGGTCCGAC  AGT  AGGA
                               _     CAG  TTG    III
GAM64  PAICS        TTG-GCCAGGCTGGTCTCAAACTCCT 692   C       ___  TAG  TII
                              TTG GCCAGGCTG  TCA  TCCT
                              III IIIIIIIII  III  IIII
                              AAC CGGTCCGAC  AGT  AGGA
                               _     CAG  TTG    III
GAM64  POLH         TTG-GCCAGGCTGGTCTCAAACTCCT 692   C       ___  TAG  TII
                              TTG GCCAGGCTG  TCA  TCCT
                              III IIIIIIIII  III  IIII
                              AAC CGGTCCGAC  AGT  AGGA
                               _     CAG  TTG    III
GAM64  PRKY         TTG-GCCAGGCTGGTCTCAAACTCCT 692   C       ___  TAG  TII
                              TTG GCCAGGCTG  TCA  TCCT
                              III IIIIIIIII  III  IIII
                              AAC CGGTCCGAC  AGT  AGGA
                               _     CAG  TTG    III
GAM64  PTGIS        GGCGGCAGTGGGGGTCACCCAGGC  684 ACA  C CGC          I
                              CGG GG  GGTCACCCAGGC
                              III II  IIIIIIIIIII
                              GTC CC  CCAGTGGGTCCG
                              C__   A C__         C
GAM64  SWAP70       TTG-GCCAGGCTGCTCTTGAACTCCT 695   C       CATAG___   TII
                              TTG GCCAGGCTGT     TCCT
                              III IIIIIIIII      IIII
                              AAC CGGTCCGACG      AGGA
                               _      AGAACTTG   III
GAM64  TGFA         GCCAGGCTGTTCTA-TCCT     681 TTGCGCCA    CA G
                              GGCTGT  TA TCC
                              IIIIII  II III
                              CCGACA  AT AGG
                              _____      AG  _
GAM64  TPST2        CGCCAGGCTCACATCTCCCTT    678 TTGCGC   GT AG
                              CAGGCT  CAT  TCCTT
                              IIIIII  III  IIIII
                              GTCCGA  GTA  GGGAA
                              _____      GT  GA
GAM64  VHL          TTG-GCCAGGCTGGTCTCAAACTCCT 692   C       ___  TAG  TII
                              TTG GCCAGGCTG  TCA  TCCT
                              III IIIIIIIII  III  IIII
```

```
                        AAC CGGTCCGAC  AGT  AGGA
                         _      CAG  TTG   III
GAM64  XT3          TTG-GCCAGGCTGGCCTCAAACTCCT 691   C      ___  TAG  TII
                    TTG GCCAGGCTG  TCA  TCCT
                    III IIIIIIIII  III  IIII
                        AAC CGGTCCGAC  AGT  AGGA
                         _      CGG  TTG   III
GAM65  ADAM19          ACAACCCAGGTCTCTTTCTG     700          CTTTI
                      CAGCTCAGGTCTCT
                      IIIIIIIIIIIII
                      GTTGGGTCCAGAGA
                        AAGAI
GAM65  ADAM19          ACAACCCAGGTCTCTTTCTG     700 TCAC       C   C
                       AGCTCAGGTCTCT TTTG
                       IIIIIIIIIIIII IIII
                       TTGGGTCCAGAGA AGAC
                        ____          A  C
GAM65  DGKI        GCTCATGTC-CTCTTTGCC     716    G  T     I
                   GCTCA GTC CTCTTTGC
                   IIIII III IIIIIIII
                   CGAGT CAG GAGAAACG
                     A  _      G
GAM65  DUSP6         CAGAGCTGAAATCTCTTTG   709 AC  C        I
                     AGCT AGGTCTCTCTTT
                     IIII IIIIIIIIIIII
                     TCGA TTTAGAGAGAAA
                     TC  C       I
GAM65  DUSP6         CAGAGCTGAAATCTCTTTG   709  TCAC  C        CC
                     AGCT AGGTCTCTCTTTG
                     IIII IIIIIIIIIIIII
                     TCGA TTTAGAGAGAAAC
                     TC__  C       CI
GAM65  EDAR       TCACAGCTCCAGAGCCCTCGTTG   717       _ GT   T CCI
                  TCACAGCTC AG  CTCTC TTG
                  IIIIIIIII II  IIIII III
                  AGTGTCGAG TC  GGGAG AAC
                    G TC   C III
GAM65  EDAR       TCACAGCTCCAGAGCCCTCGTTG   717       _ GT   TTTI
                  ACAGCTC AG  CTCTC
                  IIIIIII II  IIIII
                  TGTCGAG TC  GGGAG
                    G TC   CAII
GAM65  FMR2       CACAGCTCAAGTCTGGCTGTTT    707 AC       CT TI
                  AGCTCAGGTCT CT
                  IIIIIIIIIII II
                  TCGAGTTCAGA GA
                    __       CC CA
GAM65  FMR2       CACAGCTCAAGTCTGGCTGTTT    707 TC        CT TTGCC
                  ACAGCTCAGGTCT CT
                  IIIIIIIIIIII II
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                              TGTCGAGTTCAGA GA
                              __       CC  CAAAA
GAM65  HD          CACAGCTCAGTGACACTCTT    705          GT___   CTII
                       CACAGCTCAG    CTCT
                       |||||||||    ||||
                       GTGTCGAGTC    GAGA
                          ACTGT   AIII
GAM65  HD          CACAGCTCAGTGACACTCTT    705 TC      GTCT_   TGC
                        ACAGCTCAG    CTCTT
                        |||||||||    |||||
                        TGTCGAGTC    GAGAA
                          __       ACTGT    TII
GAM65  LTBP2      ACAGCTCAGCCCCCTCATTACC    702 TCAC      G     T
                        AGCTCAG TCTCTC TTGCC
                        ||||||| |||||| |||||
                        TCGAGTC GGGGAG AATGG
                          ____      G     T
GAM65  LTBP2      ACAGCTCAGCCCCCTCATTACC    702           G     T   I
                        CAGCTCAG TCTCTC TTGC
                        |||||||| |||||| ||||
                        GTCGAGTC GGGGAG AATG
                          G       T    I
GAM65  MEF2C       ACAGCT--GCTCTCTCTTT    699       CAGG      I
                        ACAGCT   TCTCTCTT
                        ||||||   ||||||||
                        TGTCGA   AGAGAGAA
                          CG__       A
GAM65  MEF2C       ACAGCT--GCTCTCTCTTT    699 TCAC  CAGG      G
                         AGCT   TCTCTCTTT
                         ||||   |||||||||
                         TCGA   AGAGAGAAA
                          ____   CG__      G
GAM65  NCOA6     TCACAGCTCAAAATTGCTCTTTG    718         TCT_    CCI
                       TCACAGCTCAGG   CTCTTTG
                       ||||||||||||   |||||||
                       AGTGTCGAGTTT   GAGAAAC
                          TAAC    III
GAM65  NCOA6     TCACAGCTCAAAATTGCTCTTTG    718 C        TCT_    I
                        ACAGCTCAGG   CTCTTT
                        ||||||||||   ||||||
                        TGTCGAGTTT   GAGAAA
                          _       TAAC    I
GAM65  PDGFB       GCTCCGGTTTTCTCTTTGC    715     A C_       II
                        GCTC GGT  TCTCTTTG
                        |||| |||  ||||||||
                        CGAG CCA  AGAGAAAC
                          G  AA     GI
GAM65  PRNP      CATCTCAGGTCTACTCTATG    712 CAG        _  TTII
                        CTCAGGTCT CTCT
                        ||||||||| ||||
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```
                        GAGTCCAGA GAGA
                        GTA    T  TACI
GAM65  PRNP        CATCTCAGGTCTACTCTATG   712  TCACAG      _   T  C
                        CTCAGGTCT CTCT TG
                        ||||||||| |||| ||
                        GAGTCCAGA GAGA AC
                        _____      T   T  A
GAM65  RCN1        CACAGCTCAGAGTATCACCTTG  706  A      _  C  T   I
                        CAGCTCAG GT TC CTTT
                        |||||||| || || ||||
                        GTCGAGTC CA AG GGAA
                        _        T  T  T   I
GAM65  RCN1        CACAGCTCAGAGTATCACCTTG  706  TC     _  C  T   CC
                        ACAGCTCAG GT TC CTTTG
                        ||||||||| || || |||||
                        TGTCGAGTC CA AG GGAAC
                        __        T  T  T  AI
GAM65  SERPINA5      CTCTGGACCTCTCTTTGCC     713   A _        II
                        CTC GG TCTCTCTTTGC
                        ||| || ||||||||||
                        GAG CC GGAGAGAAACG
                        A  T        GI
GAM65  SGT        CAGGTCCGAGGTCTCTCTCTTCC  711  AG  C       GI
                        CT AGGTCTCTCTTT
                        || |||||||||||
                        GG TCCAGAGAGAGA
                        A_  C        AG
GAM65  SGT        CAGGTCCGAGGTCTCTCTCTTCC  711  TCACAG  C      G  I
                        CT AGGTCTCTCTTT CC
                        || ||||||||||| ||
                        GG TCCAGAGAGAGA GG
                        CA____  C      A G
GAM65  SLC22A3       CTCTTGTCTCTCTTTAGCC    714   AG       CII
                        CTC GTCTCTCTTTG
                        ||| |||||||||||
                        GAG CAGAGAGAAAT
                        AA        CGG
GAM65  SLC9A3R2      TCACATCTCTGGGTCTCTCT   719   G  A_     TTGC
                        TCACA CTC GGTCTCTCT
                        ||||| ||| ||||||||||
                        AGTGT GAG CCAGAGAGA
                        A  AC        IIIC
GAM65  SLC9A3R2      TCACATCTCTGGGTCTCTCT   719   G  A_      II
                        TCACA CTC GGTCTCTC
                        ||||| ||| |||||||||
                        AGTGT GAG CCAGAGAG
                        A  AC    AI
GAM65  TBX6      CACACCT--GGTCTCTCTT     708   G  CA      I
                        CACA CT GGTCTCTCT
                        |||| || |||||||||
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                           GTGT GA  CCAGAGAGA
                             G  __      A
GAM65  TBX6          CACACCT--GGTCTCTCTT      708 TC  G CA      G
                         ACA CT  GGTCTCTCTTT
                         III II  IIIIIIIIIII
                         TGT GA  CCAGAGAGAAG
                          __   G  __      I
GAM65  TRPM1         CACAGCTCAGG-CTCTTTCAGCC  710 _      T  C T I
                       ACAGCTCAGG CTCT TT GC
                       IIIIIIIIII IIII II II
                       TGTCGAGTCC GAGA AG CG
                            G    _  A T I
GAM65  TRPM1         CACAGCTCAGG-CTCTTTCAGCC  710 TC      T  C T
                       ACAGCTCAGG CTCT TT GCC
                       IIIIIIIIII IIII II III
                       TGTCGAGTCC GAGA AG CGG
                         __      _  A T
GAM65  WBSCR5        AGCACAGTGGTCCCTCTTTGCC   703 GCTCA          I
                           GGTCTCTCTTTGC
                           IIIIIIIIIIIII
                           CCAGGGAGAAACG
                        TGTCA           I
GAM65  WBSCR5        AGCACAGTGGTCCCTCTTTGCC   703 TCACAGCTCA
                             GGTCTCTCTTTGCC
                             IIIIIIIIIIIIII
                             CCAGGGAGAAACGG
                        GTCA_____
GAM65  XRCC3         TCA-ACCTCGGATC-CTCTTTGCC  720 CA   CA TC       I
                       CAGCT GG  TCTCTTTGC
                       IIIII II  IIIIIIIII
                       GTTGG CC  GGAGAAACG
                        A_   AG TA      I
GAM65  XRCC3         TCA-ACCTCGGATC-CTCTTTGCC  720 TCA   CA TC
                       CAGCT GG  TCTCTTTGCC
                       IIIII II  IIIIIIIIII
                       GTTGG CC  GGAGAAACGG
                        A__   AG TA
GAM65  ZNF134        ACAGCTCA-GACCCTCTTGGC    701 _     T    TGI
                        CAGCTCAGG CTCTCTT
                        IIIIIIIII IIIIIII
                        GTCGAGTCT GGGAGAA
                        T    _    CCI
GAM65  ZNF134        ACAGCTCA-GACCCTCTTGGC    701 TCAC    T    T
                        AGCTCAGG CTCTCTT GC
                        IIIIIIII IIIIIII II
                        TCGAGTCT GGGAGAA CG
                        ____      _    C
GAM65  ZNF174        CAGAGACTTAAGT-TCTCTTTGCC  704 ACA_  C  C      I
                        GCT AGGT TCTCTTTGC
                        III IIII IIIIIIIII
```

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                              TGA TTCA AGAGAAACG
                              TCTC  A   _       I
GAM65  ZNF174      CAGAGACTTAAGT-TCTCTTTGCC  704  TCACA  C   C        I
                              GCT AGGT TCTCTTTGCC
                              ||| |||| |||||||||||
                              TGA TTCA AGAGAAACGG
                              TCTC_ A  _        G
GAM66  ADORA1        AGACAAG--CAGACTCCCCT    724 _  T  TC       I
                              GAC AGT  GGACTCCCC
                              ||| ||| |||||||||
                              CTG TCG  TCTGAGGGG
                               T   T   __       I
GAM66  ADORA1        AGACAAG--CAGACTCCCCT    724 TGAGACTAGTT
                              CGGACTCCCCT
                              |||||||||||
                              GTCTGAGGGGA
                              TGTTC_____
GAM66  BARHL1     GAGACGGGGCTCCGCACTCCCCTTC 729 AGACTAG  G       I
                              TTCG ACTCCCCTT
                              |||| |||||||||
                              AGGC TGAGGGGAA
                              TGCCCCG  G      I
GAM66  BARHL1     GAGACGGGGCTCCGCACTCCCCTTC 729 TG  TA_ _ G       II
                              AGAC  GTTC G ACTCCCCTTC
                              ||||  |||| | |||||||||||
                              TCTG  CGAG C TGAGGGGAAG
                              __    CCC  G G      AI
GAM66  CABC1   TGAGA--AGTG-GAACTCCCCTTC  736     CT  TC
                              TGAGA AGT  GGACTCCCCTTC
                              ||||| ||| ||||||||||||
                              ACTCT TCA CTTGAGGGGAAG
                                __  C_
GAM66  CABC1   TGAGA--AGTG-GAACTCCCCTTC  736 _   CT  TC
                              GAGA AGT  GGACTCCCCTT
                              |||| ||| ||||||||||||
                              CTCT TCA CTTGAGGGGAA
                              A  __  C_
GAM66  CKTSF1B1   TGAGACTA--TCA-ACTCCCCTT  735      GT  G
                              TGAGACTA TCG ACTCCCCTT
                              |||||||| ||| |||||||||
                              ACTCTGAT AGT TGAGGGGAA
                                      __  _
GAM66  CKTSF1B1   TGAGACTA--TCA-ACTCCCCTT  735 _     GT  G
                              GAGACTA TCG ACTCCCCT
                              ||||||| ||| |||||||||
                              CTCTGAT AGT TGAGGGGA
                              A      __  _
GAM66  DNAJB1      AGACATTGTTCCAACTCCCCTTC  723 GACTA  G       I
                              GTTC GACTCCCCTT
                              |||| |||||||||||
```

```
                         CAAG TTGAGGGGAA
                        GTAAA    G         I
GAM66   DNAJB1      AGACATTTGTTCCAACTCCCCTTC  723  TGAGACTA   G         I
                            GTTC GACTCCCCTTC
                            |||| |||||||||||
                            CAAG TTGAGGGGAAG
                        TGTAAA__   G         G
GAM66   FOXD1       GAC-AGGGCGGACT-CCCTTC    728     T TT      CTI
                        GAC AG CGGACTCCC
                        ||| || |||||||||
                        CTG TC GCCTGAGGG
                         _  CC      AAG
GAM66   FOXD1       GAC-AGGGCGGACT-CCCTTC    728  TGAGACT TT      C
                          AG CGGACTCCC TT
                          || ||||||||| ||
                          TC GCCTGAGGG AG
                        _____  CC       A
GAM66   GLTSCR2       GAGACTAGTTC--TCTCCC     730        GGA   I
                        GAGACTAGTTC CTCC
                        ||||||||||| ||||
                        CTCTGATCAAG GAGG
                           A__   G
GAM66   GLTSCR2       GAGACTAGTTC--TCTCCC     730  TG      GGA   CT
                         AGACTAGTTC CTCCC
                         |||||||||| |||||
                         TCTGATCAAG GAGGG
                          __       A__  AI
GAM66   HSPA8        GAGACTAGTTCTCTCTCCC     731         GGA  II
                        GAGACTAGTTC CTCC
                        ||||||||||| ||||
                        CTCTGATCAAG GAGG
                          AGA   GI
GAM66   HSPA8        GAGACTAGTTCTCTCTCCC     731  TG     GGA   CTT
                         AGACTAGTTC CTCCC
                         |||||||||| |||||
                         TCTGATCAAG GAGGG
                          __      AGA   AII
GAM66   IKBKB       GAGAC-AG---GGACTCCCC     732  _   T TTC
                         AGAC AG  GGACTCCC
                         |||| ||  |||||||||
                         TCTG TC  CCTGAGGG
                          C     _  ___
GAM66   IKBKB       GAGAC-AG---GGACTCCCC     732  TG   T TTC
                         AGAC AG  GGACTCCCC
                         |||| ||  |||||||||
                         TCTG TC  CCTGAGGGG
                         __    _  ___
GAM66   NESG1       TGATGATTAG---GGACTCCCC   733  _  C TTC       TT
                         TGA GA TAG  GGACTCCCC
                         ||| || |||  |||||||||
```

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                        ACT CT ATC  CCTGAGGGG
                         A A  ___        II
GAM66  NESG1           TGATGATTAG---GGACTCCCC   733 _ _ C TTC     I
                         GA GA TAG  GGACTCCC
                         II II III  IIIIIIIII
                         CT CT ATC  CCTGAGGG
                         A A A  ___        I
GAM66  NTSR1           GACTGGGGCTGGACTCCCC    726  A__  C    II
                         GACT  GTT GGACTCCC
                         IIII  III IIIIIIIII
                         CTGA  CGA CCTGAGGG
                          CCC  _    GI
GAM66  NTSR1           GACTGGGGCTGGACTCCCC    726 TGAGACTA C     TT
                          GTT GGACTCCCC
                          III IIIIIIIIII
                          CGA CCTGAGGGG
                         ACCC____ _    CT
GAM66  NTSR1           GAATAGGCCTGACTCCCCT    727  C TT G     II
                         GA TAG C GACTCCCC
                         II III I IIIIIIIII
                         CT ATC G CTGAGGGG
                          T  CG A    AI
GAM66  NTSR1           GAATAGGCCTGACTCCCCT    727 TGAGAC TT G     T
                          TAG C GACTCCCCT
                          III I IIIIIIIII
                          ATC G CTGAGGGGA
                         _____ CG A     C
GAM66  RAB1A           GACTTCGCTCGGACTCCCC    725  A_         II
                         GACT GTTCGGACTCCC
                         IIII IIIIIIIIIIII
                         CTGA CGAGCCTGAGGG
                          AG       GI
GAM66  RAB1A           GACTTCGCTCGGACTCCCC    725 TGAGACTA
                         GTTCGGACTCCCCT
                         IIIIIIIIIIIII
                         CGAGCCTGAGGGGG
                         AAG_____
GAM66  WNT10B          TGAAACTA-TAGGGACTCCCC    734     GTTC     TT
                         TGAGACTA  GGACTCCCC
                         IIIIIIII  IIIIIIIII
                         ACTTTGAT  CCTGAGGGG
                          ATC_      II
GAM66  WNT10B          TGAAACTA-TAGGGACTCCCC    734 _      GTTC      I
                         GAGACTA  GGACTCCC
                         IIIIIII  IIIIIIII
                         CTTTGAT  CCTGAGGG
                          A  ATC_     I
GAM67  ARHGEF7          TTGGGTCAGGG-GTGC-CCAG    747 TATT     CT T
                         GGGTCAGGG TGC CCAG
                         IIIIIIIII III IIII
```

```
                        CCCAGTCCC ACG GGTC
                        ____         C_  _
GAM67  COL4A2     TGGG-CAGGGCTTGCCCTCCAG   744 TATTGGGT      __    A
                       CAGGGCTTGC TCCAG

                       |||||||||| |||||
                       GTCCGAACG AGGTC

                       C_____        GG   C
GAM67  DGCR2      TCAGGGCTTCAGGTTCCAGA     742 TA TG  __     TGCT
                       T GGT CAGGGCT   CCAG

                       | ||| ||||||| ||||
                       A CCA GTCTCGG  GGTC

                       A_ GT AG         ____
GAM67  GM2A       TTAGGTCAGGGCTGCTTGCCCCAG  746 TATT        ____    AI
                       GGGTCAGGGCT TGCTCCAG

                       |||||||||| ||||||||
                       TCCAGTCCCGA ACGGGGTC

                       ____         CGA    GG
GAM67  PES1       GGGTCAGGGCTGGCTGGAGA     741 TATTGGGT    T  CC
                       CAGGGCT GCT AG

                       ||||||| ||| ||
                       GTCCCGA CGA TC

                       _____       C  CC
GAM67  SLC2A8     TTGGAGTCACAGGCTTGCTCCA    745 TATT    _      GA
                       GGGTCA GGGCTTGCTCCA

                       |||||| |||||||||||
                       CTCAGT TCCGAACGAGGT

                       C___   G       AG
GAM67  TAP2       ATTGGGTCAGGGTGTGGACTCTAG  739 TA       CTT__  C AI
                       TTGGGTCAGGG   GCTC AG

                       |||||||||| |||| ||
                       AACCCAGTCCC  TGAG TC

                       __        ACACC   A CI
GAM67  TRH        TGGGTCAGGGCTCTGC-CCA      743 TATTGG    _ T  G
                       GTCAGGGCT TGC CCA

                       ||||||||| ||| |||
                       CAGTCCCGA ACG GGT

                       _____      G _ G
GAM67  WBP2       GGGTCAGGGGCCCTTGTTCC      740 TATT   AGGG  C AG
                       GGGTC  CTTG TCC

                       |||||  |||| |||
                       CCCGG  GAAC AGG

                       GTC_   ____   A  GC
GAM68  ADARB1     GCTGGGGACAACCGTGGACACCT   774       __  C__   IIIA
                       GCTGGGGAC CCG  GCACC

                       ||||||||| ||| |||||
                       CGACCCCTG GGC TGTGG

                       TT ACC   AIII
GAM68  ARHGAP6    GCCCGCCGTGGCTCCCCGCGCAC   767   G _ GA_      CTI
                       GCCCG CTG GG  CCCGCGCAC

                       ||||| ||| || |||||||||
```

```
                        CGGGC GGC CC  GGGCGCGTG
                          _  A  GAG        III
GAM68  ARHGAP6       GCCCGCCGTGGCTCCCCGCGCAC  767 C  G  _  GA_      I
                        CCG CTG GG  CCCGCGCA
                        III III II  IIIIIIII
                        GGC GGC CC  GGGCGCGT
                          _  _  A  GAG       I
GAM68  B3GNT3        GCCCAGAGGCTGGGGACCC  764  ___        GCGCACC
                        GCCC  GGCTGGGGACCC
                        IIII  IIIIIIIIIII
                        CGGG  CCGACCCCTGGG
                          TCT        IIITCCA
GAM68  B3GNT3        GCCCAGAGGCTGGGGACCC  764  ___         III
                        GCCC  GGCTGGGGACC
                        IIII  IIIIIIIIII
                        CGGG  CCGACCCCTGG
                          TCT        GII
GAM68  CSF3          CCCAGGTGGGGACCCTCAGGACC  753 C  C     G  CAI
                        GG TGGGGACCC CG
                        II IIIIIIIII II
                        CC ACCCCTGGG GT
                        T  _      A  CCT
GAM68  CSF3          CCCAGGTGGGGACCCTCAGGACC  753 GC   C    G  C_  TI
                        CCGG TGGGGACCC CG  ACC
                        IIII IIIIIIIII II  III
                        GGTC ACCCCTGGG GT  TGG
                        __   C     A  CC  TI
GAM68  DDAH2         CGGCTGGGGCCCCACCCCCC  762 GCCCGG    A  G  A
                          CTGGGG CCC CGC CC
                          IIIIII III III II
                          GACCCC GGG GTG GG
                          _____    _  _  G
GAM68  DDAH2         CGGCTGGGGCCCCACCCCCC  762        A  GCACI
                        GGCTGGGG CCCGC
                        IIIIIIII IIIII
                        CCGACCCC GGGTG
                          G    GGGGI
GAM68  EIF2B1        GCCC--CAGGGGACCCGAGC  772    GGCT      C  AC
                        GCCC  GGGGACCCG GC
                        IIII  IIIIIIIII II
                        CGGG  CCCCTGGGC CG
                          GT__      T  II
GAM68  EIF2B1        GCCC--CAGGGGACCCGAGC  772    GGCT      CI
                        GCCC  GGGGACCCG
                        IIII  IIIIIIIII
                        CGGG  CCCCTGGGC
                          GT__      TC
GAM68  EP300         GCCCGGCTGCTGGA-CCGCG  768         G_  _  CII
                        GCCCGGCTG GGACC CG
                        IIIIIIIII IIIII II
```

```
                              CGGGCCGAC  CCTGG GC
                                    GA   C  III
GAM68  EP300        GCCCGGCTGCTGGA-CCGCG      768        G_   C  CACC
                        GCCCGGCTG  GGACC GCG
                        ||||||||| ||||| |||
                        CGGGCCGAC  CCTGG CGC
                              GA    _   IIIT
GAM68  FANCG        GCCCA-CTGGGGACCCAGCTCA      770     G       C  ACCT
                        GCCCG CTGGGGACCCG GC
                        ||||| ||||||||||| ||
                        CGGGT GACCCCTGGGT CG
                              _          _ AGTI
GAM68  FANCG        GCCCA-CTGGGGACCCAGCTCA      770 C  G       _  GCI
                          CC GCTGGGGACCC GC
                          || ||||||||||| ||
                          GG TGACCCCTGGG CG
                          _  G       T AGI
GAM68  FZD1         CCCGGCTGGCGGCGCCGCGC      751        _ AC    II
                        CCCGGCTGG GG CCGCG
                        ||||||||| || |||||
                        GGGCCGACC CC GGCGC
                              G  GC   GI
GAM68  FZD1         CCCGGCTGGCGGCGCCGCGC      751 GC     _ AC    ACC
                        CCGGCTGG GG CCGCGC
                        |||||||| || ||||||
                        GGCCGACC CC GGCGCG
                          __     G  GC   AII
GAM68  HOXA3        CCCGGCTGGGCCGCGGGGCACCT  756        GAC  ___   I
                        CCGGCTGGG  CCGC  GCACC
                        |||||||||  ||||  |||||
                        GGCCGACCC  GGCG  CGTGG
                          ___     CCC    I
GAM68  HOXA3        CCCGGCTGGGCCGCGGGGCACCT  756 GC     GAC  ___    I
                        CCGGCTGGG  CCGC  GCACCT
                        |||||||||  ||||  ||||||
                        GGCCGACCC  GGCG  CGTGGA
                          __     ___   CCC    C
GAM68  IL17R        CCCGGCTGGGGACGCAGCG      752        C _  II
                        CCCGGCTGGGGAC C GC
                        ||||||||||||| | ||
                        GGGCCGACCCCTG G CG
                              C T  CI
GAM68  IL17R        CCCGGCTGGGGACGCAGCG      752 GC     C _  CACC
                        CCGGCTGGGGAC C GCG
                        ||||||||||||| | |||
                        GGCCGACCCCTG G CGC
                          __        C T  TIII
GAM68  IRS1         CCCGGCTGGAGTCCGGCACA      754        A C  I
                        CCGGCTGGGG CC GCGC
                        ||||||||||| || ||||
```

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                          GGCCGACCTC GG CGTG
                             A  C     I
GAM68  IRS1      CCCGGCTGGAGTCCGGCACA    754 GC      A C    CC
                      CCGGCTGGGG CC GCGCA
                      ||||||||| || |||||
                      GGCCGACCTC GG CGTGT
                       __         A  C    CI
GAM68  ITPKB     GCCCAGCGTTGGGGACCCTCCCTCC  766 C  __       GCGCACI
                      CGGC TGGGGACCC
                      |||| |||||||||
                      GTCG ACCCCTGGG
                       _   CA       AGGGAII
GAM68  ITPKB     GCCCAGCGTTGGGGACCCTCCCTCC  766       __      GCGCA  II
                      GCCCGGC TGGGGACCC   CCT
                      ||||||| |||||||||    |||
                      CGGGTCG ACCCCTGGG   GGA
                          CA     AG___  GG
GAM68  KCNK10      GCCCGGCT--GGA---GCGCACC  773        ACC    A
                      GCCCGGCTGGGG CGCGC
                      |||||||||||| |||||
                      CGGGCCGACCTC GCGTG
                              ___    G
GAM68  KCNK10      GCCCGGCT--GGA---GCGCACC  773        GACCC
                      GCCCGGCTGGG   GCGCAC
                      |||||||||||   ||||||
                      CGGGCCGACCT   CGCGTG
                       _____
GAM68  MN1         GCCGGAGTCTCCGCGCACC     775       AC_    II
                      GCTGGGG CCGCGCAC
                      ||||||| ||||||||
                      CGGCCTC GGCGCGTG
                         AGA      GI
GAM68  OAS3      GCTGGGGACTCCGC-CCCCT      776       _  GCA II
                      GCTGGGGAC CCGC  CC
                      ||||||||| ||||   ||
                      CGACCCCTG GGCG   GG
                       A  GG_  AI
GAM68  OTX1      GGCTGGGGA--CGCGCTCCT     781       CC   ACI
                      GGCTGGGGAC GCGC
                      |||||||||| ||||
                      CCGACCCCTG CGCG
                        __    AGG
GAM68  OVOL1       CTGGGGACCTGCAGCCCCT    763       C _ A II
                      CTGGGGACC GC GC CC
                      ||||||||| || || ||
                      GACCCCTGG CG CG GG
                        A T  G  AI
GAM68  OVOL1       CTGGGGACCTGCAGCCCCT     763 GCCCGG  G A  GC A
                      CTG GG CCC GC CC
                      ||| || ||| || ||
```

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                              GAC TC GGG  CG GG
                            TG____  G  G  A_  _
GAM68  PACE            CCGGCTGGG--CCAGCGCCCCT   758        GA  C   ACI
                            CCGGCTGGG  CC GCGC
                            ||||||||| || ||||
                            GGCCGACCC  GG CGCG
                               __  T   GGG
GAM68  PACE            CCGGCTGGG--CCAGCGCCCCT   758 GCCC     GA  C   A
                              GGCTGGG  CC GCGC CC
                              ||||||| || |||| ||
                              CCGACCC  GG CGCG GG
                              ____     __ T  G
GAM68  PCOLN3          GGC-GGGGACCCGCACTCC      780    T        ACI
                            GGC GGGGACCCGCGC
                            ||| |||||||||||
                            CCG CCCCTGGGCGTG
                            _        AGG
GAM68  PCOLN3          GGC-GGGGACCCGCACTCC      780 GCCCGGCTG       A
                              GGGACCCGCGC C
                              ||||||||||| |
                              CCCTGGGCGTG G
                            _____         A
GAM68  PFKFB3          GGCTGGGGATGCCCG-GCAC    778       __  _  AII
                            GGCTGGGGA CCCG CGC
                            ||||||||| |||| |||
                            CCGACCCCT GGGC GTG
                             AC  C  III
GAM68  PFKFB3          GGCTGGGGATGCCCG-GCAC    778 _____    T G  A CGCGCACC
                            GCCCGGC G GG CC
                            ||||||| | || ||
                            CGGGCCG T CC GG
                            CCCCTA    _ G _ IIITCCAC
GAM68  PRX            CGGCTGGGGCCTCCACAGCA     759        AC_   CIII
                            CGGCTGGGG  CCGCG
                            |||||||||  |||||
                            GCCGACCCC  GGTGT
                             GGA    CGTI
GAM68  PRX            CGGCTGGGGCCTCCACAGCA     759 GCCCGG    AC_  _  CC
                            CTGGGG  CCGC GCA
                            ||||||  |||| |||
                            GACCCC  GGTG CGT
                            _____    GGA  T  CC
GAM68  RPH3AL        GCCCTGGCTGGGGA----TGCACCT 765    _        CCC  AI
                            GCCC GGCTGGGGA  GCGC
                            |||| |||||||||  ||||
                            CGGG CCGACCCCT  CGTG
                             A    A__  GA
GAM68  RPH3AL        GCCCTGGCTGGGGA----TGCACCT 765    _        CCCGC
                            GCCC GGCTGGGGA   GCACCT
                            |||| |||||||||   ||||||
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                              CGGG CCGACCCCT   CGTGGA
                                A       A____
GAM68  SCNN1A         GCCTGGCTGGGGAGCCCGC     769   C     _    GCACC
                     GCC GGCTGGGGA CCCGC
                     ||| ||||||||| |||||
                     CGG CCGACCCCT GGGCG
                       A      C    |||TC
GAM68  SCNN1A         GCCTGGCTGGGGAGCCCGC     769   C     _    ||
                     GCC GGCTGGGGA CCCG
                     ||| ||||||||| ||||
                     CGG CCGACCCCT GGGC
                       A      C    G|
GAM68  SET7          CGGCTGGGGACACTGCCCAGCT   760       CC_ G CC|
                     GCTGGGGAC  GC CA
                     ||||||||| || ||
                     CGACCCCTG  CG GT
                        TGA  G C||
GAM68  SLC1A2        CGGCGCGCGACCCGCGCTCC     761   TGGG    AC|
                     GGC  GACCCGCGC
                     |||  |||||||||
                     CCG  CTGGGCGCG
                       CGCG    AG|
GAM68  SLC6A8        GCCCGGCTGG---CCCGCG      771       GGA
                     GCCCGGCTGG CCCGC
                     |||||||||| |||||
                     CGGGCCGACC GGGCG
                              ___
GAM68  SLC6A8        GCCCGGCTGG---CCCGCG      771       GGA    CA
                     GCCCGGCTGG CCCGCG
                     |||||||||| ||||||
                     CGGGCCGACC GGGCGC
                              ___    ||
GAM68  SLC6A8        GGCTGGGGACCACACGCAC      779         _   A|||
                     GGCTGGGGACC CGCGC
                     ||||||||||| |||||
                     CCGACCCCTGG GTGTG
                        T   CGTG
GAM68  SORL1         CCGGCTGGGCCGGGACCGCGCGCGCC 757 _ CC   G _  A T||
                     GC GGCTGGG ACC CGCGC CC
                     || ||||||| ||| ||||| ||
                     CG CCGGCCC TGG GCGCG GG
                       C AC    _  C    C CG|
GAM68  SORL1         CCGGCTGGGCCGGGACCGCGCGCGCC 757 C    G _   AC|
                      GGCTGGG ACC CGCGC
                      ||||||| ||| |||||
                      CCGGCCC TGG GCGCG
                       C    _  C    CG|
GAM68  TCF7          GCTGGGGACCCGGGGCAGCCT    777         C_ _ |||
                     GCTGGGGACCCG GCA CC
                     |||||||||||| ||| ||
```

```
                          CGACCCCTGGGC CGT GG
                            CC   C AII
GAM68  TEF          CCCGGACTCGG--CTCGCGCACCT  750 _  _ G  GACC      I
                        CCGG CT GG   CGCGCACC
                        IIII II II   IIIIIIII
                        GGCC GA CC   GCGCGTGG
                          G   T G GA__      I
GAM68  TEF          CCCGGACTCGG--CTCGCGCACCT  750 GC  _ G  GACC
                        CCGG CT GG   CGCGCACCT
                        IIII II II   IIIIIIIII
                        GGCC GA CC   GCGCGTGGA
                        __   T G GA__
GAM68  TNNC2           CCCTGGTGGGGACCCG-GCA    755 G C C    C  CC
                        CC GG TGGGGACCCG GCA
                        II II IIIIIIIII III
                        GG CC ACCCCTGGGC CGT
                          _ A _      _ CI
GAM68  TNNC2           CCCTGGTGGGGACCCG-GCA    755 _ _ C     C I
                        CC GG TGGGGACCCG GC
                        II II IIIIIIIII II
                        GG CC ACCCCTGGGC CG
                          G A _      _ I
GAM69  B3GAT1        TCAGTAGGCTGGGGCCCTTTCC  788   __  A__     GCTII
                        TCAG GGCT  GCCCTTTCC
                        IIII IIII  IIIIIIIII
                        AGTC CCGA  CGGGAAAGG
                          AT   CCC       IIITC
GAM69  COL4A4        TCAGGCGCCCAGCCCTTTCTCGC  789    _ _    _ TII
                        TCAGG GCT AGCCCTTTC CGC
                        IIIII III IIIIIIIII III
                        AGTCC CGG TCGGGAAAG GCG
                          G  G   A III
GAM69  CSRP1         AGGCCCAGCCCTTTCCCCT     784 TCAG G       G
                        G CTAGCCCTTTCC CT
                        I IIIIIIIIIIII II
                        C GGTCGGGAAAGG GA
                        ____ G      G
GAM69  EGR3          GGGCTAGACGCCACCTTTCCGC  787 TC _ GC       II
                        AGG GCTA CCTTTCCGCT
                        III IIII IIIIIIIIII
                        TCT CGGT GGAAAGGCGG
                          GA G __      GG
GAM69  NRXN2         CAGGGCTAGCGGTGTCTGC     785 TC     CCTT C
                        AGGGCTAGC  TC GCT
                        IIIIIIIII  II III
                        TCCCGATCG  AG CGG
                          __      CCAC A
GAM69  PART1         CAGTGC-AGCCCTTTCAGCT    786 TCAGG T     C
                        GC AGCCCTTTC GCT
                        II IIIIIIIII III
```

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                          CG TCGGGAAAG CGA
                     TCA__ _       T
GAM69  RFX2         TCAGCAC-AGCCCTTTCAGCT    790   G  T      C  I
                     TCAG GC AGCCCTTTC GCT
                     |||| || ||||||||| |||
                     AGTC TG TCGGGAAAG CGA
                        G _      T  I
GAM69  TAGLN        TCAGGGCTAGCCCTCTCCGCT    791               I
                     TCAGGGCTAGCCCTTTCCGCT
                     |||||||||||||||||||||
                     AGTCCCGATCGGGAGAGGCGA
                              I
GAM70  ADRA1A        GAGGCTGA---GGCAGGCA      800 TG    TGA      A
                      AGGCTGA GGCAGGCA
                      |||||||  |||||||||
                      TCCGACT  CCGTCCGT
                       __    ___       C
GAM70  ATP7B        TGAGGCCAA-GAGGCAGGCA     813    TG T      AGC
                     TGAGGC A GAGGCAGGCA
                     |||||| | ||||||||||
                     ACTCCG  T CTCCGTCCGT
                       GT _        |||
GAM70  COL5A3        GAGGAGTGAGGAGGCAGGCA     798 TG  C_  T      AGC
                      AGG  TGA GAGGCAGGCA
                      |||  ||| ||||||||||
                      TCC  ACT CTCCGTCCGT
                       __   TC  C        A||
GAM70  CYP1A2       TGAGGCAGGGGAGGCAGGCTAG    816       TGAT      AAGCG
                     TGAGGC   GAGGCAGGC
                     ||||||   |||||||||
                     ACTCCG   CTCCGTCCG
                       TCCC        ATC||
GAM70  DCTN1         TGAGCCAGAGGAGGCAGGC      810    G  _  T      AAGC
                      TGAG CT GA GAGGCAGGC
                      |||| || || ||||||||
                      ACTC GG CT CTCCGTCCG
                        _  T  C        |||G
GAM70  DMPK         TGAGGCTGAGTGACCCAGTAGCAA 809       _ GG __  GCGI
                     TGAGGCTGA TGA CAG GCAA
                     ||||||||| ||| ||| ||||
                     ACTCCGACT ACT GTC CGTT
                        C  GG  AT  |||G
GAM70  DYSF         GGCGGAGGAGGCAGGCCAG      807 TGAGGCT T     A  C
                      GA GAGGCAGGC AG
                      || |||||||| ||
                      CT CTCCGTCCG TC
                       C_____ C    G  A
GAM70  FCRH1        TGAGCCTGA-GAGGCAGGC      811    G  T      AAG
                     TGAG CTGA GAGGCAGGC
                     |||| |||| |||||||||
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                        ACTC GACT CTCCGTCCG
                        G    _      III
GAM70 FGF4      GAGGAGG-TGCGGGAGGCAAGCG  804 T_   C A A C
                        GAGG TG TG GG AGGCAAGCG

                        |||| || || || |||||||||
                        CTCC AC GC CC TCCGTTCGC
                        TC   _ _ _ _
GAM70 FGFR2     AGGCTCA-GAGCGCGCAGGCAAGC  797 TGAG  GAT  ___      GI
                        GCT  GAG  GCAGGCAAGC

                        ||| |||  |||||||||
                        CGA  CTC  CGTCCGTTCG
                        ____    GT_  GCG      AC
GAM70 FLNB      AGGCTGATGAAGGGCTGG--AGCG  795 TGAG     CA A__
                        GCTGATGAGG GGC  AGCG

                        |||||||||| ||| ||||
                        CGACTACTTC CCG  TCGC
                        ____       __   ACC
GAM70 HSPA2     AGGCACATGGCGGCAGGCAAG   796 TGAG TG A_      CG
                        GC ATG GGCAGGCAAG

                        || ||| |||||||||
                        CG TAC CCGTCCGTTC
                        ____   TG CG       TC
GAM70 HYAL4     GAGGCTGA---GGCAGGCA      800 TG    TGA     A
                        AGGCTGA  GGCAGGCA

                        ||||||| |||||||||
                        TCCGACT  CCGTCCGT
                        __       ___    C
GAM70 MATN2     AGGCAGGATGAGGCAGAAGCAAG  794 TGAG T_       __  CGI
                        GC GATGAGGCAG  GCAAG

                        || |||||||||| |||||
                        CG CTACTCCGTC CGTTC
                        ____   TC      TT  AAI
GAM70 MGST3     TGAGGCTGAT--GCCAGGTAAG   817         AGG  C C
                        TGAGGCTGATG CAGG AAG

                        |||||||||| |||| |||
                        ACTCCGACTAC GTCC TTC
                        G__  A I
GAM70 MPP5      GCTGATGAGGGAAGGGAAGC     805 TGAGGCTG   C_ C
                        ATGAGG AGG AAGC

                        |||||| ||| ||||
                        TACTCC TCC TTCG
                        _____   CT C
GAM70 ODF2      TGAGG---ATGAGGCAGACA     812     CTG      AG
                        TGAGG ATGAGGCAGGCA

                        ||||| |||||||||||
                        ACTCC TACTCCGTCTGT
                        ___        II
GAM70 PCDH7     GAGGCAGAAGTGGCAGGCAA     801 TG  T TGA     C
                        AGGC GA  GGCAGGCAAG

                        |||| || |||||||||
```

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                              TCCG CT  CCGTCCGTTT
                              ___  T TCA        I
GAM70  PFKL          GCAGCTGAGGCAGGGCAAG     806 TGAGGCTGA      _  C
                             TGAGGCAGG CAAG
                             ||||||||| ||||
                             ACTCCGTCC GTTC
                             G_____        C  C
GAM70  PMCHL1          TGAGGCTG---AGGCAGGAAA  815    TGA    CAAG
                       TGAGGCTGA GGCAGG
                       ||||||||| ||||||
                       ACTCCGACT CCGTCC
                             ___    TTTI
GAM70  PRKCM          TGAGGCACACCAGGCAGGCAA   814    TG G     GCG
                      TGAGGC AT AGGCAGGCAA
                      |||||| || |||||||||
                      ACTCCG TG TCCGTCCGTT
                          TG G       III
GAM70  SH3BP2         GAGGCTGA---GGCAGGAAA    802 TG    TGA   C
                        AGGCTGA GGCAGG AAG
                        ||||||| |||||| |||
                        TCCGACT CCGTCC TTT
                           __   ___   _
GAM70  SLC2A8         TGATGGCTGATGACCCAGGGAA  808  _     GG  CAAGCG
                      TGA GGCTGATGA CAGG
                      ||| ||||||||| ||||
                      ACT CCGACTACT GTCC
                          A     GG  CTTIII
GAM70  TRIM9          GAGGCCGAGCTGAGGCAGG     799 TG    __      CAAGC
                        AGGCTGA TGAGGCAGG
                        ||||||| |||||||||
                        TCCGGCT ACTCCGTCC
                           __   CG     TIIIG
GAM70  VPREB3         GAGGCAGG-GAGGCAGGCAAG   803 TG  TGAT      C
                      AGGC  GAGGCAGGCAAG
                      ||||  ||||||||||||
                      TCCG  CTCCGTCCGTTC
                         __  TCC_      A
GAM71  ANGPT1         GCATGTATA-TTATTTAAG     826 TGGC    GTGAGG
                        ATGTATA   TTAAGG
                        |||||||   ||||||
                        TACATAT   AATTCT
                          ____    AATAA_
GAM71  ATP8A2         TGGC---TAGAATGAGGTTAA   833   ATG T     G
                      TGGC  TA AGTGAGGTTAA
                      ||||  || |||||||||||
                      ACCG  AT TTACTCCAATT
                         ___  C      I
GAM71  ATP8A2         TGGC---TAGAATGAGGTTAA   833 _ ATG T
                       GGC  TA AGTGAGGTTA
                       |||  || ||||||||||
```

```
                        CCG   AT TTACTCCAAT
                        A    ___    C
GAM71   HAS2            GCATGGCTAGTGAGGTATATAGG  825 _   ATGTA      TA__ AI
                            TGGC   TAGTGAGGT  AGG
                            ||||   ||||||||| |||
                            ACCG   ATCACTCCA  TCC
                        T    _____        TATA  GG
GAM71   HAS2            GCATGGCTAGTGAGGTATATAGG  825 A  TA     TAAGI
                            TG TAGTGAGGT
                            || |||||||||
                            AC ATCACTCCA
                        _ CG       TATAT
GAM71   HK2            GCTTGTAGA-TGAGGTTAAAGA   827 CA_  TA         I
                            TGTA GTGAGGTTAAGG
                            |||| ||||||||||||
                            ACAT TACTCCAATTTC
                        CGA   C_        I
GAM71   HK2            GCTTGTAGA-TGAGGTTAAAGA   827 TGGCA  TA
                            TGTA GTGAGGTTAAGGA
                            |||| |||||||||||||
                            ACAT TACTCCAATTTCT
                        A____     C_
GAM71   JAM3          GCTTTTATAAATGAGGTTAA    824 ATG   _      II
                            GC  TATAG TGAGGTTA
                            ||  ||||| |||||||||
                            CG  ATATT ACTCCAAT
                        AAA   T    TI
GAM71   JAM3          GCTTTTATAAATGAGGTTAA    824 TGGCA  T        G
                            TGTA AGTGAGGTTAAG
                            |||| ||||||||||||
                            ATAT TTACTCCAATTT
                        AAA__  _        G
GAM71   LAMC2        GGCTAGGTATAGTGAGTGTTCTGGA 828 GCAT      _ AA I
                            GTATAGTGAG GTT GG
                            |||||||||| ||| ||
                            CATATCACTC CAA CC
                        ATC_      A GA I
GAM71   LAMC2        GGCTAGGTATAGTGAGTGTTCTGGA 828 TG AT_     _ AA II
                            GC  GTATAGTGAG GTT GGA
                            ||  |||||||||| ||| |||
                            CG  CATATCACTC CAA CCT
                        __ ATC       A GA CI
GAM71   MEN1         GGCAAATTCTTTAGTGAGG-TAAG  829 GGCATGTA      TI
                            TAGTGAGGT
                            |||||||||
                            ATCACTCCA
                        TAAGAA__      TT
GAM71   MEN1         GGCAAATTCTTTAGTGAGG-TAAG  829 TG TGTA___     T AI
                            GCA    TAGTGAGGT AAGG
                            |||    ||||||||| ||||
```

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                          CGT    ATCACTCCA TTCT
                          __   TTAAGAA      _   II
GAM71   MGAM           TGGCATGTAGGGAGGGTGGTTCAG 830      AT T  TTAA AI
                       TGGCATGT AG GAGG   GG
                       |||||||| || ||||   ||
                       ACCGTACA TC CTCC   CC
                          __  C   CA__  AA
GAM71   MGAM           TGGCATGTAGGGAGGGTGGTTCAG 830 G   AT T  TTAAI
                          CATGT AG GAGG
                          ||||| || ||||
                          GTACA TC CTCC
                          _   __ C  CACCA
GAM71   MPP5         CATGTATAGAGA-ATAAAGGA    823 _     T GTT  I
                        ATGTATAG GAG  AAGG
                        |||||||| ||| ||||
                        TACATATC CTT  TTCC
                           G    T AT_  I
GAM71   MPP5         CATGTATAGAGA-ATAAAGGA    823 TGGCAT   T GTT
                          GTATAG GAG  AAGG
                          |||||| ||| ||||
                          CATATC CTT  TTCC
                          _____     T  AT_
GAM71   MYH6        TGGCAAG---AGTGAGGTT      832    TGTAT
                       TGGCA   AGTGAGGT
                       |||||   ||||||||
                       ACCGT   TCACTCCA
                          TC___
GAM71   MYH6        TGGCAAG---AGTGAGGTT      832    TGTAT     AA
                       TGGCA   AGTGAGGTT
                       |||||   |||||||||
                       ACCGT   TCACTCCAA
                          TC___     II
GAM71   NEDD4       ATGAATCCAGAGAGGTTAAG     820   TA__ T     III
                       ATG  TAG GAGGTTAA
                       |||  ||| ||||||||
                       TAC  GTC CTCCAATT
                          TTAG  T    CII
GAM71   NEDD4       ATGAATCCAGAGAGGTTAAG     820 TGGCATGTA  T     G
                          TAG GAGGTTAAG
                          ||| |||||||||
                          GTC CTCCAATTC
                       TAG_____  T     A
GAM71   SLC17A4     CATTTGAAGTGAGGTTAGGG     822 CATGTAT       AI
                        AGTGAGGTTA
                        ||||||||||
                        TCACTCCAAT
                       AAACT__       CC
GAM71   SLC17A4     CATTTGAAGTGAGGTTAGGG     822 TGGCATGTAT       A
                        AGTGAGGTTA GG
                        |||||||||| ||
```

```
                          TCACTCCAAT CC
                      AACT_____        C
GAM71  SRD5A2         TGACTTATATAGTGAGTTT    831    A      GTII
                      TGGC TGTATAGTGAG
                      |||| |||||||||||
                      ACTG ATATATCACTC
                          A        AAAI
GAM71  SRD5A2         TGACTTATATAGTGAGTTT    831    A      GTTAAGG
                      TGGC TGTATAGTGAG
                      |||| |||||||||||
                      ACTG ATATATCACTC
                          A      AAAIIIA
GAM71  STK6      TGGGAGATA-AGTG--GTTAAGGA 834   CAT  T  GA
                      TGG  GTA AGT  GGTTAAGGA
                      |||  ||| |||  |||||||||
                      ACC  TAT TCA  CCAATTCCT
                       CTC   _  __
GAM71  STK6      TGGGAGATA-AGTG--GTTAAGGA 834 _  CAT  T  GA
                       GG  GTA AGT  GGTTAAGG
                       ||  ||| |||  ||||||||
                       CC  TAT TCA  CCAATTCC
                      A CTC   _  __
GAM71  ZNF138       ATGTATAGTAAGTGTTGAG      821        _  AAII
                      ATGTATAGTGAG GTT
                      ||||||||||| |||
                      TACATATCATTC CAA
                            A  CTCI
GAM71  ZNF138       ATGTATAGTAAGTGTTGAG      821 TGGCATGT    _  A
                        ATAGTGAG GTT AGG
                        |||||||| ||| |||
                        TATCATTC CAA TCT
                      _____       A  C
GAM72  GEMIN5        TGTTGGTTGATTGCTGGGCC     841   CT   _     CCAG
                      TGT  GTTGAT GCTGGGCC
                      |||  |||||| ||||||||
                      ACA  CAACTA CGACCCGG
                        AC    A     IIIG
GAM72  GEMIN5        TGTTGGTTGATTGCTGGGCC     841   CT   _     II
                      TGT  GTTGAT GCTGGGC
                      |||  |||||| |||||||
                      ACA  CAACTA CGACCCG
                        AC    A     GI
GAM72  GPC6     TGTCTGTTGGTG-TGAGCTCGAGG 842        A C    CCC  I
                      TGTCTGTTG TG TGGGC  AGG
                      ||||||||| || |||||   |||
                      ACAGACAAC AC ACTCG   TCC
                          C _    AGC   I
GAM72  GPC6     TGTCTGTTGGTG-TGAGCTCGAGG 842 _     A C    CCCAGI
                       GTCTGTTG TG TGGGC
                       |||||||| || |||||
```

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                    CAGACAAC AC ACTCG
                    A     C  _    AGCTCI
GAM72  HYAL3        TGTTGATGCT-GGCCTCTGG    844 _        G  CCAGI
                       GTTGATGCTGG CC
                       IIIIIIIIIII II
                       CAACTACGACC GG
                    A        _  AGACI
GAM72  HYAL3        TGTTGATGCT-GGCCTCTGG    844 TGTCTGTT    G  CCA
                       GATGCTGG CC   G
                       IIIIIIII II   I
                       CTACGACC GG   C
                    _____        _  AGA
GAM72  MEF2B        TGTCTGCCTTG-TGCTGGGCC    840        GA_      CCAG
                       TGTCTGTT TGCTGGGCC
                       IIIIIIII IIIIIIIII
                       ACAGACGG ACGACCCGG
                    AAC       IIIG
GAM72  MEF2B        TGTCTGCCTTG-TGCTGGGCC    840        GA_     II
                       TGTCTGTT TGCTGGGC
                       IIIIIIII IIIIIIII
                       ACAGACGG ACGACCCG
                    AAC      GI
GAM72  NDUFV3       GTCTGTTGGAAGCTGGGCCC    838        AT_     II
                       GTCTGTTG GCTGGGCC
                       IIIIIIII IIIIIIII
                       CAGACAAC CGACCCGG
                    CTT      GI
GAM72  NDUFV3       GTCTGTTGGAAGCTGGGCCC    838 TG     AT_      CAG
                       TCTGTTG GCTGGGCCC
                       IIIIIII IIIIIIIII
                       AGACAAC CGACCCGGG
                    __     CTT      AII
GAM72  OGG1         GTTTGTCTGGGGCTGGGCCC    837 __   TTGAT      CAG
                       TGTCTG  GCTGGGCCC
                       IIIIII  IIIIIIIII
                       ACAGAC  CGACCCGGG
                    AA    CC___      TII
GAM72  OGG1         GTTTGTCTGGGGCTGGGCCC    837 ____  TTGAT     II
                       GTCTG  GCTGGGCC
                       IIIII  IIIIIIII
                       CAGAC  CGACCCGG
                    CAAA   CC___      GI
GAM72  SFTPD        TCTTTT--TGTTAGGCCCCAGG   839 CTGTTGA C      I
                       TG TGGGCCCCAG
                       II IIIIIIIIII
                       AC ATCCGGGGTC
                    AGAAAA_ A      I
GAM72  TNFRSF7      TGCTGATGCT-GGCCTCTGG    843 _        G  CCAGI
                       GTTGATGCTGG CC
                       IIIIIIIIIII II
```

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                          CGACTACGACC GG
                         A          _ AGACI
GAM72  TNFRSF7        TGCTGATGCT-GGCCTCTGG    843 TGTCTGTT      G CCA
                         GATGCTGG CC  G
                         |||||||| || |
                         CTACGACC GG  C
                         _____      _ AGA
GAM73  AVPR1A         GGGTTTCTTCCTTCTCACC    848        G___     III
                         GGGTTTCTT  CTCAC
                         ||||||||   |||||
                         CCCAAAGAA  GAGTG
                          GGAA    GII
GAM73  AVPR1A         GGGTTTCTTCCTTCTCACC    848 TGTGGGG    G    CCC
                         TTTCTT CTCACC
                         |||||| ||||||
                         GAAGGA GAGTGG
                          AA_____    A   CTC
GAM73  C14orf1       TGTGG----TCTTGCTCACACACA 859   GGTT       CCCC
                         TGTGG  TCTTGCTCAC
                         |||||  ||||||||||
                         ACACC  AGAACGAGTG
                          ____        TGTG
GAM73  C14orf1       TGTGG----TCTTGCTCACACACA 859   GGTT       CI
                         TGTGG  TCTTGCTCAC
                         |||||  ||||||||||
                         ACACC  AGAACGAGTG
                          ____        TG
GAM73  ELMO1         TGTGGGGTTTGGTCTT-CTCA    854        ___  G  CCCCC
                         TGTGGGGTT  TCTT CTCA
                         |||||||||  |||| ||||
                         ACACCCCAA  AGAA GAGT
                          ACC   _  IIIAC
GAM73  ELMO1         TGTGGGGTTTGGTCTT-CTCA    854        ___  G  III
                         TGTGGGGTT  TCTT CTC
                         |||||||||  |||| |||
                         ACACCCCAA  AGAA GAG
                          ACC   _  TII
GAM73  G2A           TGTCGTGTCCCTTGCTCACC    858  GGG TT        CCC
                         TGT GT CTTGCTCACC
                         ||| || ||||||||||
                         ACA CA GAACGAGTGG
                          GCA GG       III
GAM73  G2A           TGTCGTGTCCCTTGCTCACC    858 GTGGG TT       I
                          GT CTTGCTCAC
                          || |||||||||
                          CA GAACGAGTG
                          CAGCA GG      I
GAM73  GCK           TGGGGTTTCTTCCTGAGCC    853       G CACCII
                         TGGGGTTTCTT CT
                         |||||||||| ||
```

```
                          ACCCCAAAGAA GA
                            G  CTCGGI
GAM73  GCK          TGGGGTTTCTTCCTGAGCC    853 TGTG     G  CAC  CC
                          GGGTTTCTT CT  CC
                          ||||||||| ||  ||
                          CCCAAAGAA GA  GG
                             G  CTC  TC
                         ____
GAM73  HSF4         GGGGCTTC--GCTCACCCCC    847 _    TT      I
                          GGGTTTC GCTCACCCC
                          ||||||| |||||||||
                          CCCGAAG CGAGTGGGG
                          C    __    I
GAM73  HSF4         GGGGCTTC--GCTCACCCCC    847 TGTGGG   TT
                          GTTTC GCTCACCCC
                          ||||| |||||||||
                          CGAAG CGAGTGGGG

                       _____    __
GAM73  IL13RA1      GTGAGGGTTTCTT-ATCTCCCC  850 T T      C A  CA
                       G GGGGTTTCTTG TC CCCC
                       | ||||||||||| || ||||
                       A TCCCAAAGAAT AG GGGG
                       _ C        _ A  AI
GAM73  IL13RA1      GTGAGGGTTTCTT-ATCTCCCC  850 T_      _ A CI
                          GGGGTTTCTTG CTC CC
                          ||||||||||| ||| ||
                          TCCCAAAGAAT GAG GG
                          AC      A _ ||
GAM73  MMP14       TGTGGCCTT-CAGGCTCACCCCCA 860   G G  TT        I
                          TGTG G TTTC GCTCACCCCCA
                          |||| | |||| |||||||||||
                          ACAC C GAAG CGAGTGGGGGT
                           _ G  TC        I
GAM73  MMP14       TGTGGCCTT-CAGGCTCACCCCCA 860 _ G G  TT        I
                          GTG G TTTC GCTCACCCCC
                          ||| | |||| ||||||||||
                          CAC C GAAG CGAGTGGGGG
                          A _ G  TC        I
GAM73  MYO1D        TGTGGG-TGACTCTGCTCACCC   855    GT_  T     CCA
                          TGTGGG  TTCT GCTCACCC
                          ||||||  |||| ||||||||
                          ACACCC  GAGA CGAGTGGG
                           ACT  _      |||
GAM73  MYO1D        TGTGGG-TGACTCTGCTCACCC   855    GT_  T    I
                          GTGGG  TTCT GCTCACC
                          |||||  |||| |||||||
                          CACCC  GAGA CGAGTGG
                           ACT  _     I
GAM73  PCDHA11       GGGTTTCTT-----CCCCCA    849       TGC A
                          GGGTTTCT TC CCCC
                          |||||||| || ||||
```

```
                         CCCAAAGA  AG GGGG
                                          __  _
GAM73  PYCR1        TGTGGGGTGTCAACTTCACCCCCA 861      T TT  _     I
                   TGTGGGGT TC  GCT CACCCCCA
                   |||||||| || ||| ||||||||
                   ACACCCCA AG  TGA GTGGGGGT
                        C  T_  A     I
GAM73  PYCR1        TGTGGGGTGTCAACTTCACCCCCA 861      T TT  _     I
                     GTGGGGT TC  GCT CACCCCC
                     |||||| || ||| |||||||
                     CACCCCA AG  TGA GTGGGGG
                          C  T_  A     I
GAM73  RALBP1       TGTGGGGTTTGTT-TTCGACCCC  857       C GC  _   CA
                   TGTGGGGTTT TT  TC ACCCC
                   |||||||||| ||  || |||||
                   ACACCCCAAA AA  AG TGGGG
                        C A_   C   II
GAM73  RALBP1       TGTGGGGTTTGTT-TTCGACCCC  857       C GC  _   I
                    GTGGGGTTT TT  TC ACCC
                    ||||||||| ||  || ||||
                    CACCCCAAA AA  AG TGGG
                         C A_   C   I
GAM73  TIA1      GTGGGGTTTCTCGGCTGACC      851          _ CACII
                GTGGGGTTTCTTG CT
                ||||||||||||| ||
                CACCCCAAAGAGC GA
                     C CTGGI
GAM73  TIA1      GTGGGGTTTCTCGGCTGACC      851 TG        _ C  CCC
                  TGGGGTTTCTTG CT ACC
                  ||||||||||| || |||
                  ACCCCAAAGAGC GA TGG
                  __           C  C  TII
GAM73  TRPM6     TGGGATCTTCTTGCTCCTCCC      852  GG       AC I
                   GG TTTCTTGCTC CC
                   || ||||||||| ||
                   CC GAAGAACGAG GG
                      TA        GA I
GAM73  TRPM6     TGGGATCTTCTTGCTCCTCCC      852 TGT GG      AC CA
                  GG TTTCTTGCTC CCC
                  || ||||||||| |||
                  CC GAAGAACGAG GGG
                  ___ TA        GA AA
GAM73  VASP       TGTGGGGTTCATTGGTGCATCCCCA 856      C CT_ C   II
                  TGTGGGGTTT TTG  CA CCCCA
                  |||||||||| ||| || |||||
                  ACACCCCAAG AAC  GT GGGGT
                       T  CAC A    II
GAM73  VASP       TGTGGGGTTCATTGGTGCATCCCCA 856 G     C CT_ _  CI
                   TGGGGTTT TTG  CA CCCC
                   ||||||| ||| || ||||
```

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                        ACCCCAAG AAC   GT GGGG
                           T  CAC  A    ll
GAM74  ADORA1       AGTCCTCCGGCTCCCGCCG     864 TGGAAGT        A
                        CTCCGGCTCC GTCGT
                        lllllllll lllll
                        GAGGCCGAGG CGGCG
                        _____         G
GAM74  AK1         GGAAG----CGGCTCCAG-CGT    869 TG  TCTC      T
                        GAAG   CGGCTCCAG CG
                        llll   lllllllll ll
                        CTTC   GCCGAGGTC GC
                          __   ____    _
GAM74  CCBL1         TGGAAGTCTACCG--TCC-GTC   872        _ GC  A  GT
                        TGGAAGTCT CCG TCC GTC
                        lllllllll lll lll lll
                        ACCTTCAGA GGC AGG CAG
                           T __  _   ll
GAM74  DTR         TGGAAGTCTTTCCCCTCTGCAGTC  871        ___ GG  C   GTCl
                        TGGAAGTCT  CC CT CAGTC
                        lllllllll  ll ll lllll
                        ACCTTCAGA  GG GA GTCAG
                         AAG  GA  C    lllC
GAM74  ERBB4        TGGAAGTCT-CAGATCCCGT     874        C CT AGTCGT
                        TGGAAGTCTC GG  CC
                        llllllllll ll  ll
                        ACCTTCAGAG CT  GG
                           T  AG  CAlllC
GAM74  ITK       GGAAGTCTCCTAGCT-CAGT      867 TG      _    C  CGT
                        GAAGTCTCC GGCTC AGT
                        lllllllll lllll lll
                        CTTCAGAGG TCGAG TCA
                          __       A   _  Tll
GAM74  MAN2C1      GGAAGTCTCTCCGGCGTCAG     865 TG    __    TC  TCGT
                        GAAGTC TCCGGC CAG
                        llllll lllllll lll
                        CTTCAG AGGCCG GTC
                          __     AG    CA  Clll
GAM74  OSCAR       TGGAAGTCTCGGGCTGCAGT     875        C  C  CGT
                        TGGAAGTCTC GGCT CAGT
                        lllllllll llll llll
                        ACCTTCAGAG CCGA GTCA
                          C   C   lll
GAM74  SLC2A1       TGGAAGTCTC---ATCCAG      873        CGGC  TC
                        TGGAAGTCTC  TCCAG
                        llllllllll  lllll
                        ACCTTCAGAG  AGGTC
                            T___   ll
GAM74  SORBS1      GGAAGTCTCCTTCTACCCAG     868 TG     GG __  TCGT
                        GAAGTCTCC CT CCAG
                        lllllllll ll llll
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                        CTTCAGAGG GA GGTC
                        __      AA TG  TIII
GAM74  TNFRSF6B         GGAACTCAACCGACTCCAGTCG   866 TG  G T_        TC
                        GAA TC  CCGGCTCCAGTCG
                        ||| ||  ||||||||||||
                        CTT AG  GGCTGAGGTCAGC
                        __  G TT          TI
GAM74  TNXB             GGAAGTCTCC--CT-CACTTGTC   870 TG      GG CA__ GT
                        GAAGTCTCC CTC   GTC
                        ||||||||| |||   |||
                        CTTCAGAGG GAG   CAG
                        __        __ TGAA  GI
GAM75  ABCD1            CCTGAGGTCAGGGCCTTGAGA   878 TCGCCT       AG
                           GAGGTCGGG TTTGAGA
                           ||||||||| ||||||
                           CTCCAGTCC GAACTCT
                           _____        CG
GAM75  ABCD1            CCTGAGGTCAGGGCCTTGAGA   878          AG   I
                           CTGAGGTCGGG TTTGAG
                           |||||||||| ||||||
                           GACTCCAGTCC GAACTC
                             CG     I
GAM75  ALX4             CGCCTTGGCT-GGGAGTTTG   879 TC  GA C     AG
                           GCCT GGT GGGAGTTTG
                           |||| ||| |||||||||
                           CGGA CCG CCCTCAAAC
                           __ A_ A   CI
GAM75  ALX4             CGCCTTGGCT-GGGAGTTTG   879 _  GA C   I
                           GCCT GGT GGGAGTTT
                           |||| ||| ||||||||
                           CGGA CCG CCCTCAAA
                           G  A_ A   I
GAM75  AQP6             TCGCCTCAGGTCAGGAGTTTGAGA 902     G          I
                           TCGCCT AGGTCGGGAGTTTGAGA
                           |||||| ||||||||||||||||
                           AGCGGA TCCAGTCCTCAAACTCT
                             G          I
GAM75  AQP6             TCGCCTCAGGTCAGGAGTTTGAGA 902     G          I
                           CGCCT AGGTCGGGAGTTTGAG
                           ||||| |||||||||||||||
                           GCGGA TCCAGTCCTCAAACTC
                             G          I
GAM75  ARSF             TCACTTGAGGTCGGGAGTTCGAGA 899   C          I
                           TCGC TGAGGTCGGGAGTTTGAGA
                           |||| |||||||||||||||||||
                           AGTG ACTCCAGCCCTCAAGCTCT
                             A          I
GAM75  ARSF             TCACTTGAGGTCGGGAGTTCGAGA 899   C          I
                           CGC TGAGGTCGGGAGTTTGAG
                           ||| |||||||||||||||||
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                              GTG ACTCCAGCCCTCAAGCTC
                               A          I
GAM75  ATP1B2      TCACCTGAGGTCGGGAGTTCGAGA 895                    I
                      TCGCCTGAGGTCGGGAGTTTGAGA
                      IIIIIIIIIIIIIIIIIIIIIIII
                      AGTGGACTCCAGCCCTCAAGCTCT
                               I
GAM75  ATP1B2      TCACCTGAGGTCGGGAGTTCGAGA 895                   I
                       CGCCTGAGGTCGGGAGTTTGAG
                       IIIIIIIIIIIIIIIIIIIIII
                       GTGGACTCCAGCCCTCAAGCTC
                               I
GAM75  ATP6V1A1      TCACCTGAGGTCTGGAGTTCGAGA 897            G      I
                        TCGCCTGAGGTC GGAGTTTGAGA
                        IIIIIIIIIIII IIIIIIIIII
                        AGTGGACTCCAG CCTCAAGCTCT
                               A     I
GAM75  ATP6V1A1      TCACCTGAGGTCTGGAGTTCGAGA 897            G      I
                        CGCCTGAGGTC GGAGTTTGAG
                        IIIIIIIIIII IIIIIIIII
                        GTGGACTCCAG CCTCAAGCTC
                               A     I
GAM75  AVPR1A        TCGGC-GAGGTCGGGAAGGTGAG 890    CC       TT A
                        TCG TGAGGTCGGGAG TGAG
                        III IIIIIIIIIII IIII
                        AGC GCTCCAGCCCTT ACTC
                        C_          CC  I
GAM75  AVPR1A        TCGGC-GAGGTCGGGAAGGTGAG 890 C__ CT       TT I
                          GC GAGGTCGGGAG TGA
                          II IIIIIIIIIII III
                          CG CTCCAGCCCTT ACT
                        AGC __         CC  I
GAM75  CACNG6        TCCCTTGGGCTCAG-AGTTTGAGA 901  G  GA  CG         I
                        TC CCT GGT GGAGTTTGAGA
                        II III III IIIIIIIIIII
                        AG GGA CCG TCTCAAACTCT
                         _  AC  AG        I
GAM75  CACNG6        TCCCTTGGGCTCAG-AGTTTGAGA 901 CG  GA  CG        I
                          CCT GGT GGAGTTTGAG
                          III III IIIIIIIIII
                          GGA CCG TCTCAAACTC
                        AG  AC  AG        I
GAM75  CBFA2T2       TCACCTGAGGTCCGGGGTTTGAGA 894           _  A   I
                        CGCCTGAGGTC GGG GTTTGAG
                        IIIIIIIIIII III IIIIIII
                        GTGGACTCCAG CCC CAAACTC
                               G  _  I
GAM75  CBFA2T2       TCACCTGAGGTCCGGGGTTTGAGA 894           _  A   I
                        TCGCCTGAGGTC GGG GTTTGAGA
                        IIIIIIIIIII III IIIIIII
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                        AGTGGACTCCAG CCC CAAACTCT
                             G    _        I
GAM75  CYP1A2      TCACTTGAGGTCAGGAGTTTGAGA  898    C              I
                        TCGC TGAGGTCGGGAGTTTGAGA
                        IIII IIIIIIIIIIIIIIIII
                        AGTG ACTCCAGTCCTCAAACTCT
                             A          I
GAM75  CYP1A2      TCACTTGAGGTCAGGAGTTTGAGA  898    C              I
                         CGC TGAGGTCGGGAGTTTGAG
                         III IIIIIIIIIIIIIIIII
                         GTG ACTCCAGTCCTCAAACTC
                             A          I
GAM75  DFFB        TCACCTGAGGTCAGGAGTTCGAGA  892                  I
                        TCGCCTGAGGTCGGGAGTTTGAGA
                        IIIIIIIIIIIIIIIIIIIIIIII
                        AGTGGACTCCAGTCCTCAAGCTCT
                                    I
GAM75  DFFB        TCACCTGAGGTCAGGAGTTCGAGA  892                  I
                        CGCCTGAGGTCGGGAGTTTGAG
                        IIIIIIIIIIIIIIIIIIIIII
                        GTGGACTCCAGTCCTCAAGCTC
                                    I
GAM75  DFFB        TCACCTGAGGTCAGGAGTTTGAGA  893                  I
                        TCGCCTGAGGTCGGGAGTTTGAGA
                        IIIIIIIIIIIIIIIIIIIIIIII
                        AGTGGACTCCAGTCCTCAAACTCT
                                    I
GAM75  DFFB        TCACCTGAGGTCAGGAGTTTGAGA  893                  I
                        CGCCTGAGGTCGGGAGTTTGAG
                        IIIIIIIIIIIIIIIIIIIIII
                        GTGGACTCCAGTCCTCAAACTC
                                    I
GAM75  DISC1       TCGCCTGAGGTCAGGAGTTTGAGA  904                  I
                        TCGCCTGAGGTCGGGAGTTTGAGA
                        IIIIIIIIIIIIIIIIIIIIIIII
                        AGCGGACTCCAGTCCTCAAACTCT
                                    I
GAM75  DISC1       TCGCCTGAGGTCAGGAGTTTGAGA  904                  I
                        CGCCTGAGGTCGGGAGTTTGAG
                        IIIIIIIIIIIIIIIIIIIIII
                        GCGGACTCCAGTCCTCAAACTC
                                    I
GAM75  FCAR        TCACCTGAGGTCGGGAGTTCGAGA  895                  I
                        TCGCCTGAGGTCGGGAGTTTGAGA
                        IIIIIIIIIIIIIIIIIIIIIIII
                        AGTGGACTCCAGCCCTCAAGCTCT
                                    I
GAM75  FCAR        TCACCTGAGGTCGGGAGTTCGAGA  895                  I
                        CGCCTGAGGTCGGGAGTTTGAG
                        IIIIIIIIIIIIIIIIIIIIII
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                         GTGGACTCCAGCCCTCAAGCTC
                                   |
GAM75  FCAR          TCACCTGAGGTCAGGAGTTCGAGA  892                   |
                         TCGCCTGAGGTCGGGAGTTTGAGA
                         ||||||||||||||||||||||||
                         AGTGGACTCCAGTCCTCAAGCTCT
                                   |
GAM75  FCAR          TCACCTGAGGTCAGGAGTTCGAGA  892                   |
                          CGCCTGAGGTCGGGAGTTTGAG
                          ||||||||||||||||||||||
                          GTGGACTCCAGTCCTCAAGCTC
                                   |
GAM75  HCS          GCTTGAGCTCAGGAGTTTGAGA    885 CC    G          |
                            TGAG TCGGGAGTTTGAG
                            |||| |||||||||||||
                            ACTC AGTCCTCAAACTC
                          GA    G          |
GAM75  HCS          GCTTGAGCTCAGGAGTTTGAGA    885 TCGCC    G
                            TGAG TCGGGAGTTTGAGA
                            |||| ||||||||||||||
                            ACTC AGTCCTCAAACTCT
                          A____    G
GAM75  HCS          TCACCCGACGTCGGGAGTTCAAGA  891        G      TG  |
                         TCGCCTGA GTCGGGAGTT AGA
                         |||||||| |||||||||| |||
                         AGTGGGCT CAGCCCTCAA TCT
                            G      GT  |
GAM75  HCS          TCACCCGACGTCGGGAGTTCAAGA  891        G      TG  |
                         CGCCTGA GTCGGGAGTT AG
                         ||||||| |||||||||| ||
                         GTGGGCT CAGCCCTCAA TC
                          G      GT  |
GAM75  LTB4R         TCACTTGATGTTAGCAGTTTGAGA 900    C  G CG G       |
                         TCGC TGA GT G AGTTTGAGA
                         |||| ||| || | |||||||||
                         AGTG ACT CA  C TCAAACTCT
                          A  A AT G        |
GAM75  LTB4R         TCACTTGATGTTAGCAGTTTGAGA 900    C  G CG G      |
                         CGC TGA GT G AGTTTGAG
                         ||| ||| || | |||||||||
                         GTG ACT CA  C TCAAACTC
                          A  A AT G        |
GAM75  MAK          TCACCTGAGGTCAGGAGTTTGAGA  893                |
                         TCGCCTGAGGTCGGGAGTTTGAGA
                         ||||||||||||||||||||||||
                         AGTGGACTCCAGTCCTCAAACTCT
                                   |
GAM75  MAK          TCACCTGAGGTCAGGAGTTTGAGA  893                 |
                         CGCCTGAGGTCGGGAGTTTGAG
                         ||||||||||||||||||||||
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                              GTGGACTCCAGTCCTCAAACTC
                                        I
GAM75  MEFV        TCACCTGAGGTCAGGAGTTTGAGA  893              I
                       TCGCCTGAGGTCGGGAGTTTGAGA
                       IIIIIIIIIIIIIIIIIIIIIIII
                       AGTGGACTCCAGTCCTCAAACTCT
                                        I
GAM75  MEFV        TCACCTGAGGTCAGGAGTTTGAGA  893              I
                        CGCCTGAGGTCGGGAGTTTGAG
                        IIIIIIIIIIIIIIIIIIIIII
                        GTGGACTCCAGTCCTCAAACTC
                                        I
GAM75  MEFV        TCACCTGAGGTCAGGAGTTCGAGA  892              I
                       TCGCCTGAGGTCGGGAGTTTGAGA
                       IIIIIIIIIIIIIIIIIIIIIIII
                       AGTGGACTCCAGTCCTCAAGCTCT
                                        I
GAM75  MEFV        TCACCTGAGGTCAGGAGTTCGAGA  892              I
                        CGCCTGAGGTCGGGAGTTTGAG
                        IIIIIIIIIIIIIIIIIIIIII
                        GTGGACTCCAGTCCTCAAGCTC
                                        I
GAM75  MLANA        TCACCTGAGGTCAGGAGTTTGAGA  893             I
                        TCGCCTGAGGTCGGGAGTTTGAGA
                        IIIIIIIIIIIIIIIIIIIIIIII
                        AGTGGACTCCAGTCCTCAAACTCT
                                         I
GAM75  MLANA        TCACCTGAGGTCAGGAGTTTGAGA  893             I
                         CGCCTGAGGTCGGGAGTTTGAG
                         IIIIIIIIIIIIIIIIIIIIII
                         GTGGACTCCAGTCCTCAAACTC
                                          I
GAM75  MTRF1        CTGAGGTCGGAACCTTCCGAGA    880  TG      G__   I
                        AGGTCGGGA  TTTGAG
                        IIIIIIIII  IIIIII
                        TCCAGCCTT  AGGCTC
                        __         GGA    I
GAM75  NCOA6        TCACTTGAGGTCAGGAGTTTGAGA  898    C          I
                        TCGC TGAGGTCGGGAGTTTGAGA
                        IIII IIIIIIIIIIIIIIIIIIII
                        AGTG ACTCCAGTCCTCAAACTCT
                         A              I
GAM75  NCOA6        TCACTTGAGGTCAGGAGTTTGAGA  898    C          I
                        CGC TGAGGTCGGGAGTTTGAG
                        III IIIIIIIIIIIIIIIIII
                        GTG ACTCCAGTCCTCAAACTC
                         A             I
GAM75  NDRG3        TCACCTGAGGTCAGGAGTTTGAGA  893              I
                        TCGCCTGAGGTCGGGAGTTTGAGA
                        IIIIIIIIIIIIIIIIIIIIIIII
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                        AGTGGACTCCAGTCCTCAAACTCT
                                   I
GAM75  NDRG3        TCACCTGAGGTCAGGAGTTTGAGA  893                I
                     CGCCTGAGGTCGGGAGTTTGAG
                     IIIIIIIIIIIIIIIIIIIIII
                     GTGGACTCCAGTCCTCAAACTC
                                I
GAM75  NQO1         TCACCTGAGGTCAGGAGTTTGAGA  893                I
                     TCGCCTGAGGTCGGGAGTTTGAGA
                     IIIIIIIIIIIIIIIIIIIIIIII
                     AGTGGACTCCAGTCCTCAAACTCT
                                I
GAM75  NQO1         TCACCTGAGGTCAGGAGTTTGAGA  893                I
                     CGCCTGAGGTCGGGAGTTTGAG
                     IIIIIIIIIIIIIIIIIIIIII
                     GTGGACTCCAGTCCTCAAACTC
                                I
GAM75  NXF3         GCCTGGGGACGGGAGTTTGGAGA  883  C  A  T     AGI
                      CTG GG CGGGAGTTTG
                      III II IIIIIIIIII
                      GAC CC GCCCTCAAAC
                       _  C  T       CTC
GAM75  NXF3         GCCTGGGGACGGGAGTTTGGAGA  883 TCGC  A  T     _  I
                      CTG GG CGGGAGTTTG AGA
                      III II IIIIIIIIII III
                      GAC CC GCCCTCAAAC TCT
                      ____  C  T     C  T
GAM75  ODF2         TCGC-TGATGGTTTCGGGAGTTT  886    C  _ __      GAGA
                     TCGC TGA GG  TCGGGAGTTT
                     IIII III II  IIIIIIIIII
                     AGCG ACT CC  AGCCCTCAAA
                      _   A  AA      IIIA
GAM75  ODF2         TCGC-TGATGGTTTCGGGAGTTT  886 CGC   _ __       I
                     CTGA GG  TCGGGAGTT
                     IIII II  IIIIIIIII
                     GACT CC  AGCCCTCAA
                     ___   A  AA      I
GAM75  RGS9         TCGCTTGAGCCCAGGAGTTTGAG  889    C  G      AI
                     TCGC TGAG TCGGGAGTTTGAG
                     IIII IIII IIIIIIIIIIIII
                     AGCG ACTC GGTCCTCAAACTC
                       A   G       II
GAM75  RGS9         TCGCTTGAGCCCAGGAGTTTGAG  889    C  G       I
                     CGC TGAG TCGGGAGTTTGA
                     III IIII IIIIIIIIIIII
                     GCG ACTC GGTCCTCAAACT
                       A   G      I
GAM75  SAS          TCACCTGAGGTCAGGAGTTCGAGA  892                I
                     TCGCCTGAGGTCGGGAGTTTGAGA
                     IIIIIIIIIIIIIIIIIIIIIIII
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                         AGTGGACTCCAGTCCTCAAGCTCT
                                    |
GAM75  SAS         TCACCTGAGGTCAGGAGTTCGAGA  892                    |
                          CGCCTGAGGTCGGGAGTTTGAG
                          ||||||||||||||||||||
                          GTGGACTCCAGTCCTCAAGCTC
                                    |
GAM75  SCML2         TCACCTGAGGTCAGGAGTTTGAGA  893                    |
                          TCGCCTGAGGTCGGGAGTTTGAGA
                          ||||||||||||||||||||||
                          AGTGGACTCCAGTCCTCAAACTCT
                                    |
GAM75  SCML2         TCACCTGAGGTCAGGAGTTTGAGA  893                    |
                          CGCCTGAGGTCGGGAGTTTGAG
                          ||||||||||||||||||||
                          GTGGACTCCAGTCCTCAAACTC
                                    |
GAM75  SIL       TCACCTGAGGTCGGGAGTTTGAGA  896                    |
                          TCGCCTGAGGTCGGGAGTTTGAGA
                          |||||||||||||||||||||
                          AGTGGACTCCAGCCCTCAAACTCT
                                    |
GAM75  SIL       TCACCTGAGGTCGGGAGTTTGAGA  896                    |
                          CGCCTGAGGTCGGGAGTTTGAG
                          |||||||||||||||||||
                          GTGGACTCCAGCCCTCAAACTC
                                    |
GAM75  SPN        TCACCTGAGGTCAGGAGTTTGAGA  893                    |
                          TCGCCTGAGGTCGGGAGTTTGAGA
                          ||||||||||||||||||||||
                          AGTGGACTCCAGTCCTCAAACTCT
                                    |
GAM75  SPN        TCACCTGAGGTCAGGAGTTTGAGA  893                    |
                          CGCCTGAGGTCGGGAGTTTGAG
                          ||||||||||||||||||||
                          GTGGACTCCAGTCCTCAAACTC
                                    |
GAM75  SULT2B1       TCACCTGAGGTCAGGAGTTTGAGA  893                    |
                          TCGCCTGAGGTCGGGAGTTTGAGA
                          ||||||||||||||||||||||
                          AGTGGACTCCAGTCCTCAAACTCT
                                    |
GAM75  SULT2B1       TCACCTGAGGTCAGGAGTTTGAGA  893                    |
                          CGCCTGAGGTCGGGAGTTTGAG
                          ||||||||||||||||||||
                          GTGGACTCCAGTCCTCAAACTC
                                    |
GAM75  TAT       GCCTGAGGTCAGGAGTTTGAGA  884                    |
                          CCTGAGGTCGGGAGTTTGAG
                          ||||||||||||||||||
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                              GGACTCCAGTCCTCAAACTC
                                       I
GAM75  TAT          GCCTGAGGTCAGGAGTTTGAGA    884  TCGC
                         CTGAGGTCGGGAGTTTGAGA

                         |||||||||||||||||||
                         GACTCCAGTCCTCAAACTCT
                                   _____

GAM75  TES          CTGAGGTCAGGAGTTTGAGA    881                I
                         TGAGGTCGGGAGTTTGAG

                         ||||||||||||||||
                         ACTCCAGTCCTCAAACTC
                                   I

GAM75  TES          CTGAGGTCAGGAGTTTGAGA    881  TCGCCTGA
                           GGTCGGGAGTTTGAG

                           |||||||||||||
                           CCAGTCCTCAAACTC
                                 _____

GAM75  TNFRSF10B      TCACCTGAGGTCAGGAGTTCGAGA  892              I
                        CGCCTGAGGTCGGGAGTTTGAG

                        |||||||||||||||||||||
                        GTGGACTCCAGTCCTCAAGCTC
                                   I

GAM75  TNFRSF10B      TCACCTGAGGTCAGGAGTTCGAGA  892               I
                        TCGCCTGAGGTCGGGAGTTTGAGA

                        |||||||||||||||||||||||
                        AGTGGACTCCAGTCCTCAAGCTCT
                                   I

GAM75  TP53          TCGCCTGAGCCCAGGAGTTTGAGA  903         G        I
                        TCGCCTGAG TCGGGAGTTTGAGA

                        ||||||||| |||||||||||||
                        AGCGGACTC GGTCCTCAAACTCT
                             G            I

GAM75  TP53          TCGCCTGAGCCCAGGAGTTTGAGA  903         G        I
                         CGCCTGAG TCGGGAGTTTGAG

                         ||||||||| ||||||||||||
                         GCGGACTC GGTCCTCAAACTC
                             G            I

GAM75  VHL           TCACCTGAGGTCAGGAGTTTGA    888              GA
                         TCGCCTGAGGTCGGGAGTTTGA

                         |||||||||||||||||||||
                         AGTGGACTCCAGTCCTCAAACT
                                   II

GAM75  VHL           TCACCTGAGGTCAGGAGTTTGA    888             I
                         CGCCTGAGGTCGGGAGTTTG

                         ||||||||||||||||||||
                         GTGGACTCCAGTCCTCAAAC
                                   I

GAM75  WARS          GCCTGAGGTCAGAGGA-TTTG     882        AGTTTII
                         GCCTGAGGTCGGG

                         ||||||||||||
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                    CGGACTCCAGTCT
                     CCTAAAC
GAM75  WARS        GCCTGAGGTCAGAGGA-TTTG   882  TCGC        _AG   AG
                     CTGAGGTCGG G TTTG
                     ||||||||| | ||||
                     GACTCCAGTC C AAAC
                     ____        T CT   AA
GAM75  ZNF133      TCACCTGAGGTCAGCAGTT    887         G   TGAG
                     TCGCCTGAGGTCGG AGTT
                     |||||||||||| ||||
                     AGTGGACTCCAGTC TCAA
                         G  |||A
GAM75  ZNF133      TCACCTGAGGTCAGCAGTT    887         G  ||
                     TCGCCTGAGGTCGG AGT
                     |||||||||||| |||
                     AGTGGACTCCAGTC TCA
                         G  A|
GAM76  ADORA2A       TGTCACCTCTGGGC-CCAGC    917  TGA      C T    CCT
                     CACCTCTGG C CCAGC
                     ||||||||| | |||||
                     GTGGAGACC G GGTCG
                     ACA        C _    |||
GAM76  BSN         TGACCCC-CTAGC-TCCAGCCC   918   A      C      T
                     TGAC CCTCTGGC TCCAGCCC
                     |||| ||||||| ||||||||
                     ACTG GGGGATCG AGGTCGGG
                         _       _       |
GAM76  CCNF        CACCCTTCGCCTCCAGCCC      910  TGACA  CTG
                     CCT  GCCTCCAGCCCT
                     |||  |||||||||||
                     GGA  CGGAGGTCGGGG
                     _____   AG_
GAM76  EN2         TGAGACCT--GGCCTCCATGCCC  915   C   CT     _   TG
                     TGA ACCT  GGCCTCCA GCCC
                     ||| ||||  ||||||||| ||||
                     ACT TGGA  CCGGAGGT CGGG
                         C  __    A  ||
GAM76  EPHA2       TGACACCCTCTGTCC-CCAGCCCTG 914       _   GC        |
                     TGACACC TCTG CTCCAGCCCTG
                     ||||||| |||| |||||||||||
                     ACTGTGG AGAC GGGGTCGGGAC
                         G  A_      |
GAM76  FGFR3       TGACACCTCTGGCCACCATGCACTG 916            T _ C ||
                     TGACACCTCTGGCC CCA GC CTG
                     |||||||||||||| ||| || |||
                     ACTGTGGAGACCGG GGT CG GAC
                         T A T ||
GAM76  GARP        ACACCT-TGGCCTCCAGGCCT    907  TGAC  C      C
                     ACCT TGGCCTCCAG CCT
                     |||| ||||||||||| |||
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                       TGGA ACCGGAGGTC GGA
                       ____    _       C
GAM76  LNK            CACCACTGCACTCCAGCCC    908 TGACACCTCTG _      T
                        GC CTCCAGCCC
                        || |||||||||
                        CG GAGGTCGGG
                       GTGA_____ T      C
GAM76  PLXNA1        DACACCGCTGGCCTCCAGTCCCT  912 TG   T      _  GI
                       ACACC CTGGCCTCCAG CCCT
                       ||||| |||||||||| ||||
                       TGTGG GACCGGAGGTC GGGA
                        __   C     A  GI
GAM76  POU2F2         CACCACTGGCCTCCTGCCC     909 TGACACCT        A
                       CTGGCCTCC GCCCT
                       ||||||||| |||||
                       GACCGGAGG CGGGG
                       GT_____     A
GAM76  RET          CCTCTTCCCCTCCAGCCCTG    911 TGACACCTCTGG
                       CCTCCAGCCCT
                       |||||||||||
                       GGAGGTCGGGA
                       AGG_____
GAM76  XRCC3         GACACCCCAGGC-TCCAGCCCTG  913 TG    T C
                       ACACCTC GGC TCCAGCCCTG
                       ||||||| ||| ||||||||||
                       TGTGGGG CCG AGGTCGGGAC
                       __     T  _
GAM77  ABCB4          ATCATCCTGCATTCCTC-TCTT   921      _ GC  G  GG
                       ATCATCCTG GT CCTC TCTT
                       ||||||||| || |||| ||||
                       TAGTAGGAC TA GGAG AGAA
                         G A_  _  II
GAM77  ABCB4          ATCATCCTGCATTCCTC-TCTT   921 _    _ GC  G  I
                       TCATCCTG GT CCTC TCT
                       |||||||| || |||| |||
                       AGTAGGAC TA GGAG AGA
                       T    G A_  _ I
GAM77  AQP6          TCCTGGTGCCTTGGCCGTTCTTG  935      C___ _ IIIC
                       TCCTGGTGCC   TCGT CTT
                       ||||||||||   |||| |||
                       AGGACCACGG   GGCA GAA
                        AACC  A CIII
GAM77  AQP6          TCCTGGTGCCTTGGCCGTTCCTTG 936      CTC TTIIIC
                       TCCTGGTGCC  GTC
                       ||||||||||  |||
                       AGGACCACGG  CGG
                        AAC  CAAGGA
GAM77  BCL7A          CCTGGTG-CCTGGTGCTTGG    926      CTC _ II
                       CCTGGTGCC  GT CTTG
                       |||||||| || ||||
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                              GGACCACGG  CA GAAC
                               AC_  C   CI
GAM77  BLTR2          TCATCCTGG-G-CCTC-TCCTGG  932        T  _  GTCTI
                      TCATCCTGG GCC CTC
                      |||||||| ||| |||
                      AGTAGGACC CGG GAG
                               _  A  GACCI
GAM77  BLTR2          TCATCCTGG-G-CCTC-TCCTGG  932 AT      T  C  G
                       CATCCTGG GCC TC TCTTG
                       |||||||| ||| || |||||
                       GTAGGACC CGG AG AGGAC

                          __    _  _  _
GAM77  CACNA1D          CCTGGTGCCCTGGTACATGG     927         C CTTGII
                        CCTGGTGCCCT GT
                        |||||||||| ||
                        GGACCACGGGA CA
                             C  TGTACC
GAM77  COX6A1           CCTGGTGCCCGGGTAGTGG      929        TCGTCTTGII
                        CCTGGTGCCC
                        ||||||||||
                        GGACCACGGG
                             CCCATCACCI
GAM77  FKRP           TCGTCCTGGTGCTCTCCTCCTG  931 ATCA      C  G   G
                        TCCTGGTGC CTC TCTTG
                        ||||||||| ||| |||||
                        AGGACCACG GAG AGGAC
                      GC__       A  G   G
GAM77  FKRP           TCGTCCTGGTGCTCTCCTCCTG  931 CA        C  G  I
                        TCCTGGTGC CTC TCTT
                        ||||||||| ||| ||||
                        AGGACCACG GAG AGGA
                      GC      A  G   I
GAM77  GAS            CCTGGTGCCTCTCAGGTCT      925          _  TCIII
                        CCTGGTGCC CTCG
                        ||||||||| ||||
                        GGACCACGG GAGT
                          A   CCAGA
GAM77  IHPK2          TCCGTGTGTCCCTCTCGTCTTGG  933 ATCATCCTG G _      I
                        GT CC CTCGTCTTGG
                        || || ||||||||||
                        CA GG GAGCAGAACC
                      ACA_____ G  A      G
GAM77  IHPK2          TCCGTGTGTCCCTCTCGTCTTGG  933 CCTG G _     I
                        GT CC CTCGTCTTG
                        || || |||||||||
                        CA GG GAGCAGAAC
                      ACA_  G  A      I
GAM77  LEP           CATCCTGGTGGCCTGGCCTGGG    924        C  C  TGI
                      ATCCTGGTG CCT GTCT
                      |||||||| ||| ||||
```

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                       TAGGACCAC GGA CGGA
                           C   C   CCI
GAM77  LEP            CATCCTGGTGGCCTGGCCTGGG   924 ATCA     C   C   T
                       TCCTGGTG CCT GTCT GG
                       |||||||| ||| |||| ||
                       AGGACCAC GGA CGGA CC
                       ____        C   C   C
GAM77  MGAT4B          CCTGGTGCCTGTGTCTCTGG    928       CTC    GII
                       CCTGGTGCC  GTCTT
                       |||||||||  |||||
                       GGACCACGG  CAGAG
                           ACA    ACC
GAM77  PRKCABP         ATGACCCTGGTG-CCT-GTCCTGG  922 ATC        CTC
                       ATCCTGGTGCC  GTCTTGG
                       ||||||||||   |||||||
                       TGGGACCACGG  CAGGACC
                       TAC          A__
GAM77  PRKCABP         ATGACCCTGGTG-CCT-GTCCTGG  922 TC_        CTC    I
                       ATCCTGGTGCC  GTCTTG
                       ||||||||||   ||||||
                       TGGGACCACGG  CAGGAC
                       TAC          A__   I
GAM77  SLA             TCCTGGTGCCCT-TTCTTG      937         CG   I
                       TCCTGGTGCCCT TCTT
                       ||||||||||| ||||
                       AGGACCACGGGA AGAA
                           A_   C
GAM77  SLA             TCCTGGTGCCCT-TTCTTG      937 ATCATCCT      CG
                       GGTGCCCT TCTT
                       |||||||| ||||
                       CCACGGGA AGAA
                       _____        A_
GAM77  SUV39H2         CATCCTGGTCCCATTATCATG     923       G TC_ TTI
                       ATCCTGGT CCC  GTC
                       |||||||| ||| |||
                       TAGGACCA GGG  TAG
                         _  TAA  TAI
GAM77  SUV39H2         CATCCTGGTCCCATTATCATG     923 ATCA     G TC_  T G
                       TCCTGGT CCC  GTC TG
                       ||||||| ||| ||| ||
                       AGGACCA GGG  TAG AC
                       ____        _  TAA  T A
GAM77  SYN3           TCAGCCT--TGGCCTCGTCTT      930 _ T _ TGC      I
                       CA CCT GG  CCTCGTCT
                       || ||| ||  |||||||||
                       GT GGA CC  GGAGCAGA
                       A C  A ___     I
GAM77  SYN3           TCAGCCT--TGGCCTCGTCTT      930 AT T _ TGC       G
                       CA CCT GG  CCTCGTCTT
                       || ||| ||  |||||||||
```

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                            GT GGA CC  GGAGCAGAA
                            __ C A ___      G
GAM77  ZNF146       TCCTGGTGCCTCTCAAGTCCTGG  934 CCT    _ __      I
                            GGTGCC CTC GTCTTG
                            |||||| ||| ||||||
                            CCACGG GAG CAGGAC
                                 A  TT   I
                            ___
GAM78  ABCA1        AAACACAA--GTTGTGTTTTC  940  _ TC     G CC
                            AAAC CAA  GTTGTGTTT TC
                            |||| ||| |||||||||| ||
                            TTTG GTT  CAACACAAA AG
                                T __      A II
GAM78  ABCA1        AAACACAA--GTTGTGTTTTC  940  _ TC     GI
                            AAC CAA  GTTGTGTTT
                            ||| ||| |||||||||
                            TTG GTT  CAACACAAA
                                T __     AA
GAM78  BBS4       AATCTAATATTTGTGTTG      946 AAACCAATCG    TCCC
                              TTGTGTTTG
                              |||||||||
                              AACACAAAC
                            TTAGATTATA     IIIC
GAM78  CALM1        AAACCAATTTTAAATGTGTTTGT 944    CGT___     CCCCI
                            AAACCAAT    TGTGTTTGT
                            ||||||||    |||||||||
                            TTTGGTTA    ACACAAACA
                            AAATTT     IIICC
GAM78  CFTR         AAACAATATAGTTGTGTTT    941 AAAC  C__    GTCCC
                            CAAT  GTTGTGTTT
                            ||||  |||||||||
                            GTTA  CAACACAAA
                            TTT_  TAT     IIICC
GAM78  ENAM       CAA-CGTTGTGTT--TCCCC     950  T     G  I
                            CAA CGTTGTGTTT TCC
                            ||| |||||||||| |||
                            GTT GCAACACAAA GGG
                              _     G  I
GAM78  FOXG1B       CAATCGTTAATTTTGTCCCC   951      TG     I
                            AATCGTTG TTTGTCCC
                            |||||||| |||||||||
                            TTAGCAAT AAACAGGG
                              TA    I
GAM78  FOXG1B       CAATCGTTAATTTTGTCCCC   951 AAACCAAT   TG
                            CGTTG TTTGTCCC
                            ||||| ||||||||
                            GCAAT AAACAGGG
                            _____    TA
GAM78  KLHL1        AAAACAATCCTTTGTGTTTG   945 AAAC  G_    TCCC
                            CAATC TTGTGTTTG
                            ||||| |||||||||
```

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                          GTTAG AACACAAAC
                          TTTT  GA       IIIC
GAM78 KLHL1      AAAACAATCCTTTGTGTTTG   945 AAAC   G_       II
                          CAATC TTGTGTTT
                          IIIII IIIIIIII
                          GTTAG AACACAAA
                          TTTT  GA      CI
GAM78 LANCL1     AAACCAAACTCTAATTGTGTTTGT  942 AACCAATC      I
                          GTTGTGTTTG
                          IIIIIIIIII
                          TAACACAAAC
                          TTTGAGAT      I
GAM78 LANCL1     AAACCAAACTCTAATTGTGTTTGT  942   __ __      CCCCI
                          AAACCAA TC GTTGTGTTTGT
                          IIIIIII II IIIIIIIIIII
                          TTTGGTT AG TAACACAAACA
                          TG AT        IIICC
GAM78 PBX2       ACCA---GTTCTGTTTGTCCCC  949 _ ATC  G
                          CCA  GTT TGTTTGTCCC
                          III  III IIIIIIIIII
                          GGT  CAA ACAAACAGGG
                          T ___  G
GAM78 PBX2       ACCA---GTTCTGTTTGTCCCC  949 AAACCAATC  G
                          GTT TGTTTGTCCC
                          III IIIIIIIIII
                          CAA ACAAACAGGG
                          GT_____ G
GAM78 SCML1      AAACCAATCTACAGATTGTTTCTTGTCC943        _____  G_   CCIII
                          AAACCAATC  GTTGT TTTGTCC
                          IIIIIIIII  IIIII IIIIIII
                          TTTGGTTAG  TAACA GAACAGG
                          ATGTC  AA   IIICC
GAM78 SCNN1A     ACCCTTGGTTGTGTTTTGTCC    948 AAA AATC    _  CC
                          CC  GTTGTGTTT GTCC
                          II  IIIIIIIII IIII
                          GG  CAACACAAA CAGG
                          ___  AAC_     A  AC
GAM78 SCNN1A     ACCCTTGGTTGTGTTTTGTCC    948 CCAATC    _  I
                          GTTGTGTTT GTC
                          IIIIIIIII III
                          CAACACAAA CAG
                          GGAAC_      A  I
GAM78 TNS        ACCCATAGCTTGGTTGTTTGTCCC  947 AAA  ATCG __     CI
                          CCA  TTG TGTTTGTCCC
                          III  III IIIIIIIIII
                          GGT  AAC ACAAACAGGG
                          ___  ATCG CA      AG
GAM78 TNS        ACCCATAGCTTGGTTGTTTGTCCC  947 CCAATCGTTG       I
                          TGTTTGTCC
                          IIIIIIIII
```

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                              ACAAACAGG
                            TATCGAACCA        I
GAM79   ABR              GGGAGCCGGGGGAGGCCGAA    959    A_   _    CAIII
                           GGGA CGGGG AGGCC
                           |||| ||||| |||||
                           CCCT GCCCC TCCGG
                             CG    C   CTTII
GAM79   ABR              GGGAGCCGGGGGAGGCCGAA    959  T  AAC        CAACCCT
                            GGG  GGGGAGGCC
                            |||  |||||||||
                            CTC  CCCCTCCGG
                             C  GGC       CTTCIII
GAM79   ADCY8          GGGAA---GGAGGCCCAGAACCT   961    ACG        __   I
                          GGGA  GGGAGGCCCA ACC
                          |||| ||||||||||| |||
                          CCCT  TCCTCCGGGT TGG
                          ___          CT  A
GAM79   ADCY8          GGGAA---GGAGGCCCAGAACCT   961  TG ACG        __ CT
                           GGA  GGGAGGCCCA ACC
                           |||  ||||||||||| |||
                           CCT  TCCTCCGGGT TGG
                            __  ___        CT AA
GAM79   CDKN2D        TGGGAGCCGGG---CCCAACCCT    970    A_  GGAG
                          TGGGA CGG   GCCCAACCCT
                          ||||| |||   ||||||||||
                          ACCCT GCC   CGGGTTGGGA
                            CG   ____
GAM79   CDKN2D        TGGGAGCCGGG---CCCAACCCT    970  _  A_  GGAG
                          GGGA CGG   GCCCAACCC
                          |||| |||   |||||||||
                          CCCT GCC   CGGGTTGGG
                           A  CG   ____
GAM79   CHRNA4        TGGGA-CGCAGAG-CCCAACCC     969    A  G   G     T
                          TGGGA CG GGAG CCCAACCC
                          ||||| || |||| ||||||||
                          ACCCT GC TCTC GGGTTGGG
                           _  G   _    I
GAM79   CHRNA4        TGGGA-CGCAGAG-CCCAACCC     969  _  A  G   G    I
                          GGGA CG GGAG CCCAACC
                          |||| || |||| |||||||
                          CCCT GC TCTC GGGTTGG
                           A  _ G   _    I
GAM79   CTF1         TGGGTAAAGGGGGAGGCCAAA       964    AAC__       CAACCCT
                         TGGG   GGGGAGGCC
                         ||||   |||||||||
                         ACCC   CCCCTCCGG
                          ATTTC       TTTIIIT
GAM79   CTF1         TGGGTAAAGGGGGAGGCCAAA       964    AAC__       CAIII
                         TGGG   GGGGAGGCC
                         ||||   |||||||||
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                    ACCC   CCCCTCCGG
                   ATTTC       TTTII
GAM79  CTF1       GGGACAGGGCTGAGGCCCAA    960    A   ___      III
                   GGGA CGGGG  AGGCCCA
                   |||| ||||| ||||||||
                   CCCT GTCCC  TCCGGGT
                    _    GAC      TII
GAM79  CTF1       GGGACAGGGCTGAGGCCCAA    960 TG  A   ___       CCCT
                    GGA CGGGG  AGGCCCAA
                    ||| ||||| |||||||||
                    CCT GTCCC  TCCGGGTT
                    __ _  GAC      TIII
GAM79  DGKG        GAA-GTGGAGGCCCAGCCC      954  GAACGG      A  I
                      GGAGGCCCA CC
                      ||||||||| ||
                      CCTCCGGGT GG
                   CTTCA_       C  G
GAM79  DPP6       GGAAAGGGAAACAAGGCCCAACCC 956  GAAC  ____        I
                     GGG  GAGGCCCAACC
                     |||  |||||||||||
                     CCC  TTCCGGGTTGG
                     ____  TTTG        I
GAM79  DPP6       GGAAAGGGAAACAAGGCCCAACCC 956  T__   CG G        II
                     GGGAA G GAGGCCCAACCCT
                     ||||| | |||||||||||||
                     CCCTT T TTCCGGGTTGGGG
                     TTT  __ G        TI
GAM79  FE65L2     TGGGTCCGGGGGAGGCCCA     965    AA  _    ACCC
                   TGGG CGGGG AGGCCCA
                   |||| ||||| ||||||||
                   ACCC GCCCC TCCGGGT
                    AG    C    IIIT
GAM79  FE65L2     TGGGTCCGGGGGAGGCCCA     965    AA  _   II
                   TGGG CGGGG AGGCCC
                   |||| ||||| |||||||
                   ACCC GCCCC TCCGGG
                    AG    C    TI
GAM79  GTF2F1     GAGCGAGGAC-CCCAACCCT     955  AA_    GG      I
                    CGGGGA CCCAACCC
                    |||||| |||||||||
                    GCTCCT GGGTTGGG
                   CTC   G_     I
GAM79  GTF2F1     GAGCGAGGAC-CCCAACCCT     955  TGGGAA    GG
                    CGGGGA CCCAACCC
                    |||||| |||||||||
                    GCTCCT GGGTTGGG
                    _____    G_
GAM79  IRS2       GGGAAGGTCCGGGGAGGCCC     958    ____      IIIG
                   GGGAA  CGGGGAGGCC
                   |||||  ||||||||||
```

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                          CCCTT  GCCCCTCCGG
                          CCAG        GIII
GAM79 IRS2        GGGAAGGTCCGGGGAGGCCC   958  T__  AA        AACCCT
                          GGG  CGGGGAGGCCC
                          III  IIIIIIIIII
                          TCC  GCCCCTCCGGG
                          CCT  AG        CIIITC
GAM79 MAP2K1        TGGGAA---GGAGGCCCAA      967    ACG
                          TGGGA  GGGAGGCCCA
                          IIIII  IIIIIIIIII
                          ACCCT  TCCTCCGGGT
                          ___
GAM79 MAP2K1        TGGGAA---GGAGGCCCAA      967    ACG        CC
                          TGGGA  GGGAGGCCCAA
                          IIIII  IIIIIIIIIII
                          ACCCT  TCCTCCGGGTT
                          ___         II
GAM79 MYO15A        GGGAA--GGGAGGCCCAGCCC    962    AC      ACI
                          GGGA  GGGGAGGCCCA
                          IIII  IIIIIIIIIII
                          CCCT  TCCCTCCGGGT
                           __         CGG
GAM79 MYO15A        GGGAA--GGGAGGCCCAGCCC    962 TG  AC      A
                           GGA  GGGGAGGCCCA CCC
                           III  IIIIIIIIIII III
                           CCT  TCCCTCCGGGT GGG
                           __  __         C
GAM79 NCF4        TGGGA--GGGGAGGCCACGAGCCT  966    AC      CAAC_  I
                          TGGGA  GGGGAGGCC    CCT
                          IIIII  IIIIIIIII    III
                          ACCCT  CCCCTCCGG    GGA
                           __        TGCTC  I
GAM79 NCF4        TGGGA--GGGGAGGCCACGAGCCT  966 _  AC      CAACCCI
                           GGGA  GGGGAGGCC
                           IIII  IIIIIIIII
                           CCCT  CCCCTCCGG
                           A  __        TGCTCGG
GAM79 SLC1A4        GGGAA---GGAGGCCCATCTCT    963    ACG      ACI
                           GGGA  GGGAGGCCCA
                           IIII  IIIIIIIIII
                           CCCT  TCCTCCGGGT
                           ___        AGA
GAM79 SLC1A4        GGGAA---GGAGGCCCATCTCT    963 TG  ACG      ACCC
                           GGA  GGGAGGCCCA
                           III  IIIIIIIIII
                           CCT  TCCTCCGGGT
                           __  ___        AGAG
GAM79 SMARCA5        GGGATGGACGGGGAGGCCTAGGCCT 957 _  A      CAA_  CI
                           GGA  CGGGGAGGCC    CC
                           III  IIIIIIIIII    II
```

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                            CCT GCCCCTCCGG   GG
                          A  _        ATCC  II
GAM79  SMARCA5        GGGATGGACGGGGAGGCCTAGGCCT 957 TG__  A       CAAC  II
                          GGA CGGGGAGGCC   CCT
                          ||| ||||||||||   |||
                          CCT GCCCCTCCGG   GGA
                         CCTA  _       ATCC  CI
GAM79  WHSC1         TGAGAA---GTAGGCCCAACCC   968    AC GG
                         TGGGA GG AGGCCCAACCC
                         ||||| || ||||||||||
                         ACTCT TC TCCGGGTTGGG
                           __ A_
GAM79  WHSC1         TGAGAA---GTAGGCCCAACCC   968 _  AC GG
                          GGGA GG AGGCCCAACC
                          |||| || ||||||||||
                          CTCT TC TCCGGGTTGG
                        A  __ A_
GAM80  ACCN1          TGATCGAA--TTTCAGAGA      992      AG       GGT
                         TGATTGA ATTTCAGAGA
                         ||||||| ||||||||||
                         ACTAGCT TAAAGTCTCT
                              __         |||
GAM80  ADH7         GATACATGATTTCAGATGAGG   985 TGATTGAA     _  TCA
                            GATTTCAGA GAGG
                            ||||||||| ||||
                            CTAAAGTCT CTCC
                        TATGTA__       A  CII
GAM80  BCL11B        GAATGTAGGTTTCAGAGAG     986 TGAT A A       GTC
                           TG AG TTTCAGAGAG
                           || || ||||||||||
                           AC TC AAAGTCTCTC
                        TT__  A C        GII
GAM80  COMT        TTGCAG--TTCAGAGAGGT        995 TGATTGAAGAT
                            TTCAGAGAGGT
                            |||||||||||
                            AAGTCTCTCCA
                        GTC_____
GAM80  DAZ         AGCCTGAACGTG-CTGA-GTTAC   976              CTTATGTCI
                           AGCCTGAACGTGT
                           |||||||||||||
                           TCGGACTTGCACG
                               ACTCAATGI
GAM80  DAZ         AGCCTGAACGTG-CTGA-GTTAC   976 CA           CTTATGTCAC
                           GCCTGAACGTGT
                           ||||||||||||
                           CGGACTTGCACG
                           __          ACTCAATGTI
GAM80  DAZ         CAGACTGAACGTG-CTGA-GTTAC  982    C          CTTATGTCAC
                           CAG CTGAACGTGT
                           ||| ||||||||||
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                              GTC GACTTGCACG
                                T      ACTCAATGII
GAM80  DAZ           CAGACTGAACGTG-CTGA-GTTAC  982   C        CTTATGTCI
                       CAG CTGAACGTGT
                       ||| ||||||||||
                       GTC GACTTGCACG
                         T      ACTCAATGI
GAM80  DCX           TGAATCACAATTTCAGAGTAGGT  991   TTGAA       _   CAI
                       TGA    GATTTCAGAG AGGT
                       |||    ||||||||||| ||||
                       ACT    TTAAAGTCTC TCCA
                         TAGTG       A   III
GAM80  DPYSL3          GCCTGTTTGATGTGTCTTATG   987   AAC___        III
                       GCCTG    GTGTCTTAT
                       |||||    |||||||||
                       CGGAC    CACAGAATA
                         AAACTA       CII
GAM80  DPYSL3          GCCTGTTTGATGTGTCTTATG   987 CAGCCTGAAC      TCAC
                               GTGTCTTATG
                               ||||||||||
                               CACAGAATAC
                       GACAAACTA_       TTII
GAM80  GABRP         CTGTAACGTGTCTCATTGTTAC   983 CAGCCTG       _ CAC
                       AACGTGTCTTAT GT
                       |||||||||||| ||
                       TTGCACAGAGTA CA
                       _____       A ATG
GAM80  GABRP         CTGTAACGTGTCTCATTGTTAC   983 TG         _ CAI
                       AACGTGTCTTAT GT
                       |||||||||||| ||
                       TTGCACAGAGTA CA
                       A_        A ATI
GAM80  GPD2         ATTCATTATTTCAGAGTGGT    978 TGATTGAAG     A  C
                       ATTTCAGAG GGT
                       ||||||||| |||
                       TAAAGTCTC CCA
                       AGTAA____      A  A
GAM80  GPR17        CAGCCTGAAATGTGTGGCCTGTGTC 980        C_ __ A  ACII
                       CAGCCTGAA GTGT CTT TGTC
                       ||||||||| |||| ||| ||||
                       GTCGGACTT CACA GGA ACAG
                         TA   CC  C   IIIC
GAM80  HEM1         TGTTTGA-GATT-CAGAGAGG    993  A A  T     TC
                       TG TTGA GATT CAGAGAGG
                       || |||| |||| |||||||||
                       AC AACT CTAA GTCTCTCC
                         A  _  _     II
GAM80  HSPD1        TGTAGTTAACAGAGAGGTCA    988 TGATTGAAGATTT
                       CAGAGAGGTC
                       ||||||||||
```

```
                            GTCTCTCCAG
                        CAATT_____
GAM80  IL1RAPL2     GAAGATTTC-TAGAGTTCA     984  TGATTGA  T    _  GGT
                        AGA TTCAG AGA
                        ||| ||||| |||
                        TCT AAGTC TCT
                    AAAGA__   C   G  III
GAM80  LRP1         AGCCTTGGCAAAGTGTCTTAT    973     GAAC___       III
                        AGCCT    GTGTCTTA
                        |||||    ||||||||
                        TCGGA    CACAGAAT
                          ACCGTTT    AII
GAM80  LRP1         AGCCTTGGCAAAGTGTCTTAT    973  CA   GAAC___      TCAC
                        GCCT    GTGTCTTATG
                        ||||    |||||||||||
                        CGGA    CACAGAATAT
                        __    ACCGTTT      IIIC
GAM80  MCP         ATTGAAGATTTTAATAGA-GTCA  977  TGAT      CAG_  G
                        TGAAGATTT  AGAG TCA
                        |||||||||  |||| |||
                        ACTTCTAAA  TCTC AGT
                          ____        ATTA    _
GAM80  MFAP3        TGACTGAAAAGTATCAGAGAGG   990       TT_    TCA
                        TGATTGAAGA  TCAGAGAGG
                        ||||||||||  |||||||||
                        ACTGACTTTT  AGTCTCTCC
                           CAT       III
GAM80  PMX1        AGCAGGATAGGTGTCTTATG     974  CA CT AC_      TCA
                        GC GA  GTGTCTTATG
                        || ||  |||||||||||
                        CG CT  CACAGAATAC
                        __  TC ATC       CII
GAM80  PMX1        AGCAGGATAGGTGTCTTATG     974    CT AC_      II
                        AGC GA  GTGTCTTAT
                        ||| ||  |||||||||
                        TCG CT  CACAGAATA
                         TC ATC       CI
GAM80  PPP1CC      TGACTGAGAAAGATTTCACGAGA  989      ___     _  GGTCAI
                        TGATTGA  AGATTTCA GAGA
                        |||||||  |||||||| ||||
                        ACTGACT  TCTAAAGT CTCT
                          CTT       G   IIIACT
GAM80  RECQL5      AGCCT--ACGGGCTGTCTTATGTCA 975  CA   AAC _       CI
                        GCCTG  G TGTCTTATGTCA
                        |||||  | ||||||||||||
                        CGGAT  C ACAGAATACAGT
                          __    GCC G        CI
GAM80  RECQL5      AGCCT--ACGGGCTGTCTTATGTCA 975  G   AAC _       I
                        CCTG  G TGTCTTATGTC
                        ||||  | |||||||||||
```

```
                         GGAT  C ACAGAATACAG
                         _   GCC G       I
GAM80  SCN3A        TTGCAG-TGACAGAGAGGTCA    996 TGATTGAAGATTT
                              CAGAGAGGTC
                              |||||||||
                              GTCTCTCCAG
                         GTCACT_____
GAM80  SLC1A1       TTGTAGATTTCAGATGTAGGTC   994 TGATTGA      G__   A
                              AGATTTCAGA AGGTC
                              |||||||||| |||||
                              TCTAAAGTCT TCCAG
                         A_____         ACA   C
GAM80  USP9Y        CACCCTGCATGTGTCTTAT     981  G  AAC     GTCA
                              CA CCTG GTGTCTTAT
                              || |||| |||||||||
                              GT GGAC CACAGAATA
                               G  GTA      IIIC
GAM80  USP9Y        CACCCTGCATGTGTCTTAT     981  G  AAC     II
                              CA CCTG GTGTCTTA
                              || |||| ||||||||
                              GT GGAC CACAGAAT
                               G  GTA     AI
GAM80  WBSCR1       ATTGAAGATGTAAG-TAGGTCA   979 TGAT     TTCA  _
                              TGAAGAT  GAG AGGTCA
                              |||||||  ||| ||||||
                              ACTTCTA  TTC TCCAGT
                         ____        CA__  A
GAM81  ABCB6        CAGGATGAAATAAGCCAGG      1011      CAT  II
                              CAGGATGAAAT CTAG
                              ||||||||||| ||||
                              GTCCTACTTTA GGTC
                               TTC  CI
GAM81  CCND1        AGGGGCAGGGGATAAGAATTCATC 999      AT____ A  TAGGI
                              AGGGGCAGG   GAA TCATC
                              |||||||||   ||| |||||
                              TCCCCGTCC   CTT AGTAG
                               CCTATT  A  IIIGG
GAM81  CCND1        AGGGGCAGGGGATAAGAATTCATC 999     C__  GAA AI
                              AGGGG AGGAT ATC
                              ||||| ||||| |||
                              TCCCC TCTTA TAG
                               TAT   AG_  II
GAM81  DGAT2        AGGGGCAAAAAGTGAATCATCTA 1003      __ A   GGI
                              AGGGGCAGGA TGAA TCATCTA
                              |||||||||| |||| |||||||
                              TCCCCGTTTT ACTT AGTAGAT
                                TC  _    III
GAM81  DGAT2        AGGGGCAAAAAGTGAATCATCTA 1003 G    __ A  I
                               GGGCAGGA TGAA TCATCT
                              ||||||| |||| ||||||
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```
                        CCCGTTTT ACTT AGTAGA
                        _       TC    _    I
GAM81  DUSP5           AGGGGCAGGGAGGAAAACA      1000      AT_   T TCTAG
                        AGGGGCAGG  GAAA CA
                        |||||||||  |||| ||
                        TCCCCGTCC  CTTT GT
                          CTC   T IIIGG
GAM81  DUSP5           AGGGGCAGGGAGGAAAACA      1000      AT_   TCII
                        AGGGGCAGG  GAAA
                        |||||||||  ||||
                        TCCCCGTCC  CTTT
                          CTC   TGTI
GAM81  ENTPD6          CAGGATGAAGTCACGTCCAGG    1010       A   __   III
                        CAGGATGAA TCA  TCTAG
                        ||||||||| ||| |||||
                        GTCCTACTT AGT  AGGTC
                          C  GC    CII
GAM81  EPB49           AGGGGCAGGTGAGGAAAGCAGCTGGG 1001      AT__   T T A II
                        AGGGGCAGG  GAAA CA CT GG
                        |||||||||  |||| || || ||
                        TCCCCGTCC  CTTT GT GA CC
                          ACTC   C C C II
GAM81  EPB49           AGGGGCAGGTGAGGAAAGCAGCTGGG 1001 G    AT__   T T AGI
                        GGCAGG   GAAA CA CT
                        ||||||   |||| || ||
                        CCGTCC   CTTT GT GA
                        _   ACTC   C C CII
GAM81  FAAH            AGGGGCAGGA--ACCTCATCT    1005       TGAAA   AG
                        AGGGGCAGGA   TCATCT
                        ||||||||||   ||||||
                        TCCCCGTCCT   AGTAGA
                          TGG__   II
GAM81  FAAH            AGGGGCAGGA--ACCTCATCT    1005 _     TGAAA   I
                        GGGGCAGGA   TCATC
                        |||||||||   |||||
                        CCCCGTCCT   AGTAG
                        T    TGG__   I
GAM81  GABRE           GGGGCAGGA--AAAAC-TCTAG    1016      T A ATCI
                        GGGGCAGGA GAA TC
                        ||||||||| ||| ||
                        CCCCGTCCT TTT AG
                          T  G  ATCI
GAM81  GABRE           GGGGCAGGA--AAAAC-TCTAG    1016 AG     T  CA
                        GGGCAGGA GAAAT  TCTAG
                        |||||||| ||||| |||||
                        CCCGTCCT TTTTG AGATC
                          __    _   __
GAM81  ICA1            AGGGGCAGGAAAAAAGCAT       1004      T  T CTAG
                        AGGGGCAGGA GAAA CAT
                        |||||||||| |||| |||
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                        TCCCCGTCCT TTTT GTA
                          T  C  IIIG
GAM81  ICA1      AGGGGCAGGAAAAAAGCAT    1004        T   TCAII
                   AGGGGCAGGA GAAA
                   |||||||||| ||||
                   TCCCCGTCCT TTTT
                     T   CGTAI
GAM81  IGBP1     GCTGGTTCATATCATCTAGG     1012 AGGGGCAGGATGAA
                          ATCATCTAG
                          |||||||||
                          TAGTAGATC
                   CAAGTA_____
GAM81  IGBP1     GCTGGTTCATATCATCTAGG    1012 CA ATGAA       I
                     GG   ATCATCTAG
                     ||   |||||||||
                     CC   TAGTAGATC
                   GA  AAGTA       I
GAM81  KLHL3     AGGGGCAGG--GAATTCACCTA   1006      AT  A    G
                   AGGGGCAGG GAA TCATCTA
                   ||||||||| ||| |||||||
                   TCCCCGTCC CTT AGTGGAT
                    __  A    I
GAM81  KLHL3     AGGGGCAGG--GAATTCACCTA   1006_      AT  A    I
                   GGGGCAGG GAA TCATCT
                   |||||||| ||| ||||||
                   CCCCGTCC CTT AGTGGA
                    T   __  A    I
GAM81  LCP1    AGGCGGAGGGGGGAAATCATCTGAGG 1002  _  C  AT_       _ II
                   AGG GG AGG   GAAATCATCT AGG
                   ||| || |||   |||||||||| |||
                   TCC CC TCC   CTTTAGTAGA TCC
                    G  _  CCC        C  II
GAM81  LCP1    AGGCGGAGGGGGGAAATCATCTGAGG 1002_  CA AT      AGI
                   GGGG GG GAAATCATCT
                   |||| || ||||||||||
                   CCTC CC CTTTAGTAGA
                    G   CC __       CTC
GAM81  MKI67     GGACTGGATGAAATGATCTTGG   1015 A      C   AGI
                   GGC GGATGAAAT ATCT
                   ||| |||||||||| ||||
                   CTG CCTACTTTA TAGA
                    A      C   ACI
GAM81  MKI67     GGACTGGATGAAATGATCTTGG   1015 AGGGGCA      C  A
                      GGATGAAAT ATCT GG
                      ||||||||| |||| ||
                      CCTACTTTA TAGA CC
                   TGA____       C  A
GAM81  MX2      CAGGATGGAGAAATCATCT    1008    ___       III
                   CAGGAT GAAATCATC
                   |||||| |||||||||
```

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                        GTCCTA CTTTAGTAG
                          CCT       AII
GAM81  PKIA        CAGGAAGAATCATCATCTAGG   1009    T  __       III
                        CAGGA GAA  ATCATCTAG
                        ||||| ||| |||||||||
                        GTCCT CTT  TAGTAGATC
                          T  AG       CII
GAM81  PKIA        CAGGAAGAATCATCATCTAGG   1009 AGGGGCA  TGAA
                          GGA  ATCATCTAGG
                          |||  ||||||||||
                          TCT  TAGTAGATCC
                        _____    TAG_
GAM81  SNX1        GGCAGGATG-CATCA-CTAGG   1014      AA   CTAI
                        GGCAGGATG ATCAT
                        ||||||||| |||||
                        CCGTCCTAC TAGTG
                          G_    ATCC
GAM81  SNX1        GGCAGGATG-CATCA-CTAGG   1014 AGGGGC   AA   T
                        AGGATG ATCA CTAG
                        |||||| |||| ||||
                        TCCTAC TAGT GATC
                        _____   G_   _
GAM81  TSGA10      GGCTGGTT-AAATCATCTA     1013   A ATG      I
                        GGC GG  AAATCATCT
                        ||| ||  |||||||||
                        CCG CC  TTTAGTAGA
                         A AA_      T
GAM81  TSGA10      GGCTGGTT-AAATCATCTA     1013 AGGGGCA ATG
                          GG  AAATCATCTA
                          ||  ||||||||||
                          CC  TTTAGTAGAT
                        A_____   AA_
GAM81  VIPR1       AGAGTCAGGATGAAAGTATGTAG 1007    G     TC C  GI
                        AGGG CAGGATGAAA  AT TAG
                        |||| ||||||||||| || |||
                        TCTC GTCCTACTTT  TA ATC
                          A      CA C  II
GAM81  VIPR1       AGAGTCAGGATGAAAGTATGTAG 1007  _       TCATCTAI
                        GGG CAGGATGAAA
                        ||| ||||||||||
                        CTC GTCCTACTTT
                          A     CATACAII
GAM82  APLP2       GTCAGTGCCTTTGGAGAAAG    1024 ____  ATG        ATAAC
                        TGTC TTTGGAGAAAG
                        |||| |||||||||||
                        ACGG AAACCTCTTTC
                        AGTC   ___       AIIIA
GAM82  CPO         ATGTTCTCTGGAGAAAGATA    1019 TGTCATG         AC
                        TTTGGAGAAAGATA
                        ||||||||||||||
```

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                              AGACCTCTTTCTAT
                         AG_____             AT
GAM82  DAPP1        ATGTT-GGATAAAGATAAC      1020 TGTCATGTT   G
                         TGGA AAAGATAA
                         |||| |||||||||
                         ACCT TTTCTATT
                         _____      A
GAM82  GUCY1A3        TGTCATGTTAAACAGGAGAAAGAT 1028      T____       AACAI
                     TGTCATGTT   GGAGAAAGAT
                     |||||||||   ||||||||||
                     ACAGTACAA   CCTCTTTCTA
                         TTTGT      IIIAC
GAM82  MCM2         CAGGCTTGGAGAAACA-AACA      1023 TGTCAT        GAT
                         GTTTGGAGAAA  AAC
                         |||||||||||  |||
                         CGAACCTCTTT  TTG
                         _____          GT_
GAM82  MS4A1        TGTCAAATTTGGAGAAACAAAA     1033    T        GATAACA
                     TGTCA GTTTGGAGAAA
                     ||||| |||||||||||
                     ACAGT TAAACCTCTTT
                         T      GTTTTII
GAM82  MS4A2        TGTCAGCCCTGTAGAAAGATAA     1034   T GG_       CA
                     TGTCA GTTT  AGAAAGATAA
                     ||||| ||||  ||||||||||
                     ACAGT CGGG  TCTTTCTATT
                         _   ACA        II
GAM82  NRIP1        TGTCATGTTAGGATGAACAT       1031      T _ AGATAAC
                     TGTCATGTT GGA GAA
                     ||||||||| ||| |||
                     ACAGTACAA CCT CTT
                         T  A  GTAIIIA
GAM82  PCDH8         TGTTTCAGGTGAAAGATAA       1036 TGTCATGTTT A     C
                         GG GAAAGATAA
                         || |||||||||
                         CC CTTTCTATT
                         GT_____ A    T
GAM82  PIK3CG       TGCCATGCT-GGAGAAAGCTA      1032      T    ATAAC
                     TGTCATGTT GGAGAAAG
                     ||||||||| ||||||||
                     ACGGTACGA CCTCTTTC
                         _      GATII
GAM82  PPP1R12B      TGTCATGTTAGGAAAGAATTAACA  1035      T A   __    I
                     TGTCATGTT GG GAAAGA TAACA
                     ||||||||| || |||||| ||||
                     ACAGTACAA TC CTTTCT ATTGT
                         _ _      TA   I
GAM82  RNTRE        TCAGGTTTTGGAGAAAAACATAAC   1026 TGTCATG          ACAI
                         TTTGGAGAAAGATA
                         ||||||||||||||
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                         AAACCTCTTTTTGT
                       TCCA___          ATTG
GAM82  SLN             CATCTTTGGAGAACACATAA    1022 TGTCATG        AG_   C
                         TTTGGAGAA  ATAA
                         ||||||||| ||||
                         AAACCTCTT  TATT
                       G_____          GTG   A
GAM82  SMT3H1          TCATTTTACCTGAACAAAGATAACA 1025 TGTCA TT   G         II
                         TG  TGGA AAAGATAACA
                         II ||||  |||||||||
                         AT ACTT TTTCTATTGT
                       TAAA_ GG  G      TA
GAM82  TDG             TGTCATGTTAGGAAAAACAT     1030           T   G AAC
                         TGTCATGTT GGAGAAA AT
                         ||||||||| ||||||| ||
                         ACAGTACAA CCTTTTT TA
                           T   G III
GAM82  TUFT1           CAAGTTTGAAGGAGAAAGA      1021 TGTCA TTT        TAAC
                         TG  GGAGAAAGA
                         II  ||||||||||
                         AC  CCTCTTTCT
                       CAA__ TT_        CTCI
GAM82  UC28            TCAAGATTG-AGAAAGATCAACA   1027 TGTCATGTTTG         _
                         GAGAAAGAT AACA
                         ||||||||| ||||
                         CTCTTTCTA TTGT
                       TTCTAA_____          G
GAM82  WHSC1           TGTCATGTT---ACAATGAT     1029       TG___ GAAAGATAA
                         TGTCATGTT  GA
                         |||||||||   ||
                         ACAGTACAA   CT
                           TGTTA AIIIACAAT
GAM83  ATP1A2          GATTGCAAGGTCTGAAGGGGA    1049    T            III
                         GATT CAAGGTCTGGGG
                         |||| ||||||||||||
                         CTAA GTTCCAGACTTC
                           C        CCC
GAM83  BLAME           TCAAACTGCAGGGTCTGGGG     1056     T A      AGT
                         TCAGATT CA GGTCTGGGG
                         ||||||| || ||||||||
                         AGTTTGA GT CCAGACCCC
                           C C     III
GAM83  BLAME           TCAAACTGCAGGGTCTGGGG     1056     T A      I
                         CAGATT CA GGTCTGGG
                         |||||| || |||||||||
                         GTTTGA GT CCAGACCC
                           C C     I
GAM83  BYSL            ACTGCCCTGATCTGGGTCTTCAGC 1039    ____ A      G TCTI
                         ACTGT  GT CTGGGTCTT AGC
                         |||||   || |||||||| |||
```

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                        TGACG   TA GACCCAGAA TCG
                          GGAC _      G  IIIT
GAM83   CCR9            CAGCTCTCAGTGTCTGGGGA    1043  A   AG       I
                          AG TTTCA GTCTGGGG
                          II IIIII IIIIIIIII
                          TC AGAGT CAGACCCC
                             G   CA       I
GAM83   CCR9            CAGCTCTCAGTGTCTGGGGA    1043 TC  A   AG        T
                          AG TTTCA GTCTGGGGAG
                          II IIIII IIIIIIIIII
                          TC AGAGT CAGACCCCTT
                          __ G   CA       I
GAM83   CIT          CTGTGAGCTGGCGCTTGAGCTC    1046 AC   TA   _ T
                          TGTG CTGG G CTTGAGCTCT
                          IIII IIII I IIIIIIIIII
                          ACAC GACC C GAACTCGAGG
                          __   TC   G _
GAM83   DDB2            GATTGAGAGGCCTCTGGGGAG    1048    TCA   __     III
                          GATT  AGGT CTGGGGA
                          IIII  IIII IIIIIII
                          CTAA  TCCG GACCCCT
                          CTC   GA      CII
GAM83   DDB2            GATTGAGAGGCCTCTGGGGAG    1048 TCAGATTTCA   __      TA
                             AGGT CTGGGGAG
                             IIII IIIIIIIII
                             TCCG GACCCCTC
                          ACTC_____   GA      TT
GAM83   DPH2L2        ATTTGCCAAGGTCTGGAGA    1041 ATT__          III
                          TCAAGGTCTGGGG
                          IIIIIIIIIIIII
                          GGTTCCAGACCTC
                          TAAAC        TII
GAM83   DPH2L2        ATTTGCCAAGGTCTGGAGA    1041 TCAGATT        GT
                          TCAAGGTCTGGGGA
                          IIIIIIIIIIIIII
                          GGTTCCAGACCTCT
                          C_____        AT
GAM83   EN1         GATTTAAA----TGGGGAGTA    1051 ATTTCAAGGTC
                          TGGGGAGT
                          IIIIIIII
                          ACCCCTCA
                          CTAAATTT___
GAM83   EPB49          GATGTCAGGGTCTGGGCAG    1050   T   A      GAII
                          GAT TCA GGTCTGGG
                          III III IIIIIIII
                          CTA AGT CCAGACCC
                             C   C      GTCI
GAM83   EPB49          GATGTCAGGGTCTGGGCAG    1050 TCAGATT  A     G  T
                          TCA GGTCTGGG AG
                          III IIIIIIII II
```

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                              AGT CCAGACCC TC
                           C_____     C     G C
GAM83  GLTSCR1         TCAGATTTCAAAGTCGAGGG     1057         T  AGT
                       TCAGATTTCAAGGTC GGGG
                       |||||||||||||| ||||
                       AGTCTAAAGTTTCAG TCCC
                              C   |||
GAM83  GLTSCR1         TCAGATTTCAAAGTCGAGGG     1057         T  I
                        CAGATTTCAAGGTC GGG
                        ||||||||||||| |||
                        GTCTAAAGTTTCAG TCC
                              C  |
GAM83  GPR61         TCAGAATGGCAAGAGCTGCTGGGGAGTA1055     TTT_  _ __        |||
                     TCAGA   CAAG GT CTGGGGAGTA
                     |||||   |||| || ||||||||||
                     AGTCT   GTTC CG GACCCCTCAT
                        TACC   T AC        |||
GAM83  GPR61         TCAGAATGGCAAGAGCTGCTGGGGAGTA1055 CAGATTT  _ __       I
                           CAAG GT CTGGGGAGT
                           |||| || |||||||||
                           GTTC CG GACCCCTCA
                        TACC___   T AC       I
GAM83  IVD          TCAGATTTC-AGGATTAGGGA     1058        A TC    GT
                    TCAGATTTCA GG TGGGGA
                    |||||||||| || ||||||
                    AGTCTAAAGT CC ATCCCT
                         _ TA    ||
GAM83  IVD          TCAGATTTC-AGGATTAGGGA     1058 _      A TC    I
                     CAGATTTCA GG TGGGG
                     ||||||||| || |||||
                     GTCTAAAGT CC ATCCC
                         A   _ TA    I
GAM83  LOXL1        CAGCATTTCAAGGCCAAGGG     1042 _        T_  ||
                    CAG ATTTCAAGGTC GGG
                    ||| |||||||||| |||
                    GTC TAAAGTTCCGG CCC
                      G       TT  ||
GAM83  LOXL1        CAGCATTTCAAGGCCAAGGG     1042 TCAG        T_  AGT
                      ATTTCAAGGTC GGGG
                      ||||||||||| ||||
                      TAAAGTTCCGG CCCC
                    TCG_        TT  |||
GAM83  MX1          CAGATTTCAGGGAGT-GGGAGT     1044 _      A TC    AGI
                      AGATTTCA GG TGGGG
                      ||||||| || |||||
                      TCTAAAGT CC ACCCT
                        G   C TC   CII
GAM83  MX1          CAGATTTCAGGGAGT-GGGAGT     1044 TC      A TCTG    A
                      AGATTTCA GG   GGGAGT
                      ||||||| ||   |||||
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```
                              TCTAAAGT CC   CCCTCA
                          __    C TCA_   G
GAM83  NCOA6        TGTGGACTG---CTTGAGCTC    1059 ACTG  T  GGT
                          TG ACTG  CTTGAGCT
                          || |||| ||||||||
                          AC TGAC  GAACTCGA
                          ____   C   ___
GAM83  P2RY2        GTGTCATTGACCTTGAGCTCT    1053 ACTGTGTACTG GT
                              G CTTGAGCTCT
                              | ||||||||||
                              C GAACTCGAGA
                          AGTAA_____TG
GAM83  PPP1R8       TGTGTACTG----TTGAGATCT    1060 ACTG    GGTC   C
                          TGTACTG   TTGAG T
                          |||||||   ||||| |
                          ACATGAC   AACTC A
                          ____      ____    T
GAM83  RELN         GTGTACACTCGGTCTTGAG      1052 ACTGTG  G     CTC
                           TACT GGTCTTGAG
                           |||| ||||||||||
                           GTGA CCAGAACTC
                          AT____  G     TTC
GAM83  TMSB4Y       CTCTGTACTGGGAACTGTGCT    1045 ACTG    TC A CT
                          TGTACTGGG TTG GCT
                          ||||||||| ||| |||
                          ACATGACCC GAC CGA
                          AG__      TT A AI
GAM83  TRPM2        CTGTGCCCTG--TCTTGAGCTCT   1047 AC   A GG
                          TGTGT CT GTCTTGAGCTCT
                          ||||| || ||||||||||||
                          ACACG GG CAGAACTCGAGA
                          __   _ A_
GAM83  WNT8B        TCAGGATCCCTAGGTCTGGGAGAG  1054   _ TT A    _ TAI
                          TCAG AT C AGGTCTGGG GAG
                          |||| || | ||||||||| |||
                          AGTC TA  G TCCAGACCC CTC
                           C  GG A     T III
GAM83  WNT8B        TCAGGATCCCTAGGTCTGGGAGAG  1054 A  TT A    AI
                           GAT  C AGGTCTGGGG
                           ||| | |||||||||||
                           CTA  G TCCAGACCCT
                           C  GG A      CI
GAM83  ZNF147       AGATTTCCAGAACAATGGGGAGTA  1040 GA   AG TC_    I
                           TTTCA  G TGGGGAGT
                           ||||| | |||||||||
                           AAGGT  T ACCCCTCA
                          A_   CT GTT     I
GAM83  ZNF147       AGATTTCCAGAACAATGGGGAGTA  1040 TCAG   A TC__     I
                           ATTTC AGG  TGGGGAGTA
                           ||||| |||   |||||||||
```

```
                        TAAAG TCT   ACCCCTCAT
                        ____    G   TGTT      C
GAM84  BCL2     TATAAGTGATAA-GAAAGTCTAAAA 1075 AG  _  CT        I
                        AAGT ATA  GAGAGTCTAAA
                        |||| ||| ||||||||||
                        TTCA TAT  CTTTCAGATTT
                        TA   C  T_       I
GAM84  BCL2     TATAAGTGATAA-GAAAGTCTAAAA 1075 TAG  _ CT        I
                        AAGT ATA  GAGAGTCTAAAA
                        |||| ||| |||||||||||
                        TTCA TAT  CTTTCAGATTTT
                        ATA  C  T_        I
GAM84  CCNT2    AGAAATATACTGAGATGTGCAAA   1067          _ CTAAI
                        AAGTATACTGAGA GT
                        |||||||||||| ||
                        TTTATATGACTCT CA
                        A  CGTII
GAM84  CCNT2    AGAAATATACTGAGATGTGCAAA   1067 TA          _ C  AI
                        GAAGTATACTGAGA GT TAAA
                        ||||||||||||| || ||||
                        CTTTATATGACTCT CA GTTT
                        __         A C  GI
GAM84  CML66    AAGTATACTTGCTAGTACTA      1064        _ AG  CTIII
                        AAGTATACT G  AGT
                        ||||||||| |  |||
                        TTCATATGA C  TCA
                        A GA  TGATI
GAM84  CPO      TAGAAGTATAAATGAG-GTTTAA   1076        C_  A C  AA
                        TAGAAGTATA  TGAG GT TAA
                        |||||||||| |||| || |||
                        ATCTTCATAT  ACTC CA ATT
                        TT  _ A  II
GAM84  CPO      TAGAAGTATAAATGAG-GTTTAA   1076        C_  A  CTAI
                        AGAAGTATA  TGAG GT
                        ||||||||| |||| ||
                        TCTTCATAT  ACTC CA
                        TT  _  AATI
GAM84  CUL3     TAAAAGCATATTTGCAAGTCTAAAA 1077        C_ AG       II
                        TAGAAGTATA  TG AGTCTAAAA
                        |||||||||| || ||||||||||
                        ATTTTCGTAT  AC TCAGATTTT
                        AA  GT        II
GAM84  CUL3     TAAAAGCATATTTGCAAGTCTAAAA 1077 A      C_ AG      I
                        GAAGTATA  TG AGTCTAAA
                        |||||||| || ||||||||
                        TTTCGTAT  AC TCAGATTT
                        _    AA  GT      I
GAM84  CYP1B1       GAAGTATACCAGA-AGGCAAAA    1074      GA  TCTAAI
                        AAGTATACT GAG
                        ||||||||| |||
```

```
                              TTCATATGG TTC
                               TC  CGTTTI
GAM84  CYP1B1         GAAGTATACCAGA-AGGCAAAA   1074 TAGA     GA  TCTAAAA
                               AGTATACT GAG
                               |||||||| |||
                               TCATATGG TTC
                    ____         TC  CGTTTTC
GAM84  DBY           AGAAATGTACA-AGAGTCTAAA   1070 _   A  T       I
                               GAAGT TAC GAGAGTCTAA
                               ||||| ||| ||||||||||
                               CTTTA ATG TTCTCAGATT
                                T   C  _     I
GAM84  DBY           AGAAATGTACA-AGAGTCTAAA   1070 TA   A  T       A
                               GAAGT TAC GAGAGTCTAAA
                               ||||| ||| |||||||||||
                               CTTTA ATG TTCTCAGATTT
                               __   C  _       G
GAM84  FANCC        AACTATCAGGGAGAGTCTACAA   1063 AGTATACT      AI
                               GAGAGTCTA
                               |||||||||
                               CTCTCAGAT
                               ATAGTCC_       GT
GAM84  FANCC        AACTATCAGGGAGAGTCTACAA   1063 TAGAAGTATACT     AAA
                               GAGAGTCTA
                               |||||||||
                               CTCTCAGAT
                               ATAGTCC_____       GTT
GAM84  GRM6       AGAATGTATACTGA---TCTTAAA  1066   _      GAG  AAI
                               AGAA GTATACTGA  TCT
                               |||| ||||||||| |||
                               TCTT CATATGACT  AGA
                                 A      ___  ATT
GAM84  GRM6       AGAATGTATACTGA---TCTTAAA  1066 TA  _     GAG  AAAA
                               GAA GTATACTGA  TCT
                               ||| ||||||||| |||
                               CTT CATATGACT  AGA
                               __  A      ___  ATTT
GAM84  GSBS        AAGTGTAAT-AGAGTCTAAA   1065 A___   TACTG     I
                               GTA  AGAGTCTAA
                               |||   |||||||||
                               CAT   TCTCAGATT
                               TTCA  TA___       I
GAM84  GSBS        AAGTGTAAT-AGAGTCTAAA   1065 TAGAA  TACTG
                               GTA  AGAGTCTAAA
                               |||   ||||||||||
                               CAT   TCTCAGATTT
                               A____ TA___
GAM84  POU3F1       AGTATACTGCGA-TTTAAA     1073      A GTCTAAI
                               AGTATACTG GA
                               ||||||||| ||
```

```
                              TCATATGAC CT
                              G  AAATTTI
GAM84  RIG         AGATATCTACTGAGAGCCT      1068   A A        II
                         AGA GT TACTGAGAGTC
                         ||| || |||||||||||
                         TCT TA ATGACTCTCGG
                          A  G       AI
GAM84  RIG         AGATATCTACTGAGAGCCT      1068 TA A A      AAA
                          GA GT TACTGAGAGTCT
                          || || |||||||||||
                          CT TA ATGACTCTCGGA
                          __ A G        GII
GAM84  SCA1        AGTATACTGAAACAATAAA      1072        GTCTAAII
                           AGTATACTGAGA
                           ||||||||||||
                           TCATATGACTTT
                             GTTATTTI
GAM84  SLBP        AGTATTCTAAAGAGTCTAA      1071    A  _     II
                         AGTAT CTGA GAGTCTA
                         ||||| |||| |||||||
                         TCATA GATT CTCAGAT
                          A    T    TI
GAM84  SLBP        AGTATTCTAAAGAGTCTAA      1071 TAGAAGTATA   _     A
                           CTGA GAGTCTAA
                           |||| ||||||||
                           GATT CTCAGATT
                         AA_____   T    G
GAM84  SLC30A3     AGCAG-ATGCTGAGAGTCT      1069 AGA   TA__    I
                          AGTA   CTGAGAGTC
                          ||||   |||||||||
                          TCGT   GACTCTCAG
                          ___    CTAC    A
GAM84  SLC30A3     AGCAG-ATGCTGAGAGTCT      1069 TAGA T A     AA
                          AG AT CTGAGAGTCT
                          || || |||||||||||
                          TC TA GACTCTCAGA
                        CG__ _ C      CI
GAM85  APXL        AAGCTCTGCCAAACAAAATACTCT 1080 A  A_    G      I
                        GCT  GCTAAA AAAATACTC
                        ||| |||||| ||||||||||
                        CGA  CGGTTT TTTTATGAG
                        _  GA   G      I
GAM85  APXL        AAGCTCTGCCAAACAAAATACTCT 1080 TA  A_    G      I
                         AGCT  GCTAAA AAAATACTCT
                         |||| |||||| |||||||||||
                         TCGA  CGGTTT TTTTATGAGA
                         __  GA   G      C
GAM85  ATP11B      TAATCAAGCTAATACTAAAAAATACTCT1088    __  AA      I
                         AAGCTA  GCTA  GAAAATACTC
                         |||||| |||| ||||||||||
```

```
                    TTCGAT TGAT TTTTTATGAG
                     TA    __        I
GAM85  ATP11B      TAATCAAGCTAATACTAAAAAATACTCT1088 ____    __   AA        III
                    TAAGCTA GCTA GAAAATACTCT
                    ||||||| |||| ||||||||||
                    GTTCGAT TGAT TTTTTATGAGA
                    ATTA    TA   __        III
GAM85  C1D         CTGGCTTA-GAAAATACTC      1084 TAAGCTAGCTAA
                          AGAAAATACT
                          ||||||||||
                          TCTTTTATGA
                      GAA_____
GAM85  C1D         CTGGCTTA-GAAAATACTC      1084  A  AA       I
                    CT GCT AGAAAATACT
                    || ||| ||||||||||
                    GA CGA TCTTTTATGA
                     C  A_       G
GAM85  CD34        AAG-TAGAGAAAGAAAATAC     1082 TA C  CT      TC
                    AG TAG  AAAGAAAATAC
                    || ||| ||||||||||
                    TC ATC  TTTCTTTTATG
                     __ _  TC       TI
GAM85  CPD         CTTGCTAAAGAAAATCTTCT     1085 TA       A  CI
                    GCTAAAGAAAAT CT
                    ||||||||||| ||
                    CGATTTCTTTTA GA
                     AA      _  AG
GAM85  CPD         CTTGCTAAAGAAAATCTTCT     1085 TAAGCTAG     AC
                    CTAAAGAAAAT TC
                    |||||||||| ||
                    GATTTCTTTTA AG
                    _____      GA
GAM85  DCK         AAACTAG--AAAGAAAATA      1081      CT    I
                    AAGCTAG AAAGAAAAT
                    ||||||| |||||||||
                    TTTGATC TTTCTTTTA
                     __       T
GAM85  DCK         AAACTAG--AAAGAAAATA      1081 TA    CT    CT
                    AGCTAG AAAGAAAATA
                    |||||| ||||||||||
                    TTGATC TTTCTTTTAT
                     __   __    AI
GAM85  INSM1       AGCTAACAATTAAGAAAATA     1083       TA__      III
                    AGCTAGC  AAGAAAAT
                    |||||| |||||||||
                    TCGATTG  TTCTTTTA
                        TTAA     TII
GAM85  INSM1       AGCTAACAATTAAGAAAATA     1083 TAAG   TA__     CTC
                     CTAGC  AAGAAAATA
                     |||||  |||||||||
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                                    GATTG   TTCTTTTAT
                             ____        TTAA       TAI
GAM85  INSM1     GCTATACTAAAGAAA--ACTCT   1086 _  _        ACTCI
                         CTA GCTAAAGAAAAT
                         ||| |||||||||||
                         GAT TGATTTCTTTTG
                          C   A       AGIII
GAM85  INSM1     GCTATACTAAAGAAA--ACTCT   1086 TAAGCTA       AT
                           GCTAAAGAAA  ACTC
                           |||||||||| ||||
                           TGATTTCTTT  TGAG
                 TA_____        __
GAM85  M17S2     TAGCCAAAGAAAAATACTC      1093          _  II
                 TAGCTAAAGAAAA TACT
                 ||||||||||||| ||||
                 ATCGGTTTCTTTT ATGA
                         T  GI
GAM85  PCK1      TAGCTAAAGTGAAAAAACACT    1091         ____     CIII
                 TAGCTAAAG  AAAATACT
                 |||||||||  ||||||||
                 ATCGATTTC  TTTTGTGA
                        ACTT    IIIC
GAM85  PLSCR1    TAG-TAAAGAAAATTATCT      1094   C      ACTCI
                 TAG TAAAGAAAAT
                 ||| |||||||||
                 ATC ATTTCTTTTA
                   _        ATAGA
GAM85  RALBP1    TAAGTTAAC-AAAGAAAATTAATCT 1089   C   T     ACTCTI
                 TAAG TAGC AAAGAAAAT
                 |||| |||| |||||||||
                 ATTC ATTG TTTCTTTTA
                   A   _       ATTAGA
GAM85  RALBP1    TAAGTTAAC-AAAGAAAATTAATCT 1089   C   T     ACTCI
                 AAG TAGC AAAGAAAAT
                 ||| |||| |||||||||
                 TTC ATTG TTTCTTTTA
                   A   _       ATTAG
GAM85  TACC1     TAA-CTGGCTGGAAAGAAAAT    1087 TA  A  __     ACTC
                  AGCT GCT AAAGAAAAT
                  |||| ||| |||||||||
                  TTGA CGA TTTCTTTTA
                  A_  C  CC       IIIT
GAM85  TACC1     TAA-CTGGCTGGAAAGAAAAT    1087 TA  A  __     II
                  AGCT GCT AAAGAAAA
                  |||| ||| ||||||||
                  TTGA CGA TTTCTTTT
                  A_  C  CC     AI
GAM85  TMEM1     TAAGC-A-CTAAAGAAAAT      1090    TA      ACT
                 TAAGC GCTAAAGAAAAT
                 ||||| |||||||||||
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                              ATTCG TGATTTCTTTTA
                                __         |||
GAM85  TMEM1      TAAGC-A-CTAAAGAAAAT      1090    TA        I
                  TAAGC GCTAAAGAAAA
                  ||||| ||||||||||
                  ATTCG TGATTTCTTTT
                              __              A
GAM85  ZNF214     TAGGTAAAGAAAAATACACT      1092   C      _   TCII
                  TAG TAAAGAAAA TAC
                  ||| ||||||||| |||
                  ATC ATTTCTTTT ATG
                       C    T  TGAI
GAM86  BBOX1      TATGGTCATTGGAATCTTATT     1102      GT   AAATTTGA
                  TATGGTCAT GAATC
                  ||||||||| |||||
                  ATACCAGTA CTTAG
                        AC    AATAAIII
GAM86  CDH6       ATGGTCATG-AAAGCAAAGTT     1098 TA     T  T  TTTG
                  TGGTCATG GAA CAAA
                  |||||||| ||| ||||
                  ACCAGTAC TTT GTTT
                     __      _   C   CAAT
GAM86  FGF13      TGGTAAATGTCACTGACAAATTTGA  1105 TATG__   G  AT      II
                  GTCAT TGA CAAATTTGA
                  ||||| ||| |||||||||
                  CAGTG ACT GTTTAAACT
                  CATTTA  _  __        TG
GAM86  FIGF       TGATCATACGAATCAAATT       1109 TATG           G
                  GTCATGTGAATCAAATTT
                  ||||||||||||||||||
                  TAGTATGCTTAGTTTAAG
                     ____              A
GAM86  GJA1       CATGAGAAAGGTTCAAATTTGA    1100 TAT  CATGTGAA
                  GGT     TCAAATTTGA
                  |||     ||||||||||
                  CCA     AGTTTAAACT
                  TTT  _____
GAM86  HMGB3      TATGATC--GTGA-TCAAATTT    1103     AT  A    G
                  TATGGTC GTGA TCAAATTT
                  ||||||| |||| ||||||||
                  ATACTAG CACT AGTTTAAA
                     __    _     I
GAM86  ICMT       TATGGTAAAATGAGAATCAAAT    1101    C__ T      TTGA
                  TATGGT ATG GAATCAAAT
                  |||||| ||| |||||||||
                  ATACCA TAC CTTAGTTTA
                     TTT  T      IIIA
GAM86  KCNJ6      TGGTCATGTAAAAATTAAAT      1106 TATG        TCAAATTTG
                  GTCATGTGAA
                  ||||||||||
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                              CAGTACATTT
                              ____        TTAATTTAT
GAM86  MAPK4      TGGTCATGTGAGTTAATTCTG  1110 TATG      ATCAAATTTGA
                              GTCATGTGA
                              |||||||||
                              CAGTACACT
                              ____        CAATTAAGACA
GAM86  RB1        ATGGGCA-GTCAATCAAATT   1097 TA  T T G     TG
                              TGG CA GT AATCAAATT
                              ||| || || |||||||||
                              ACC GT CA TTAGTTTAA
                              __  C _ G   CI
GAM86  SLC6A6     TGGTCCTATGTGAATCTAAT    1104 TATG  __      AAATTTG
                              GTC ATGTGAATC
                              ||| |||||||||
                              CAG TACACTTAG
                              ____ GA       ATTACAI
GAM86  TACC1      ATGGTT-TGAGT-TCAAATTTG  1099 TA  CATG  A_
                              TGGT  TGA TCAAATTTG
                              ||||  ||| |||||||||
                              ACCA  ACT AGTTTAAAC
                              __  A___  CA
GAM86  TPM4       TGGTCATGT-ATTCATAATTTG  1108 TATG    AA _   A
                              GTCATGTG TCA AATTTG
                              |||||||| ||| ||||||
                              CAGTACAT AGT TTAAAC
                              ____      A_ A   G
GAM86  TPX1       TGCTCTT-TGAAATCAAATTTG  1107 TATGGTCA T      A
                              TG GAATCAAATTTG
                              || |||||||||||
                              AC TTTAGTTTAAAC
                              GAGAA___ _       A
GAM87  ACCN2      ATGGTGTGAGAGAGTGGGGCTG-AGG 1113 TA    AAT___  T  II
                              TGGTGTGAGA     GGCTG AGG
                              ||||||||||     ||||| |||
                              ACCACACTCT     CCGAC TCC
                              __        CTCACC _ AI
GAM87  CALB2      GGTGTGTGCA--GGCTGTAGG   1117 TATG   AGAAAT
                              GTGTG    GGCTGTAG
                              |||||    ||||||||
                              CACAC    CCGACATC
                              ____    GT____
GAM87  CARD10     GGTGTGAGAACAGACTCCAGG   1115 TATGGT    AT  G
                              GTGAGAA GGCT TAGG
                              ||||||| |||| ||||
                              CACTCTT CTGA GTCC
                              _____     GT  G
GAM87  GNAT2      GGTGAGAGAGCAGGCTGTAGG   1114 TATGGTGT  AAT
                              GAGA  GGCTGTAGG
                              ||||  |||||||||
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                              CTCT  CCGACATCC
                        CT_____    CGT
GAM87  KIAA0857        TGGCTGTGGGAAGAAATGGCTG   1121 TATG  T_        TAGG
                        GTG  GAGAAATGGCTG
                        |||  |||||||||||
                        CAC  TTCTTTACCGAC
                      CGA_  CC          TGII
GAM87  MBL2        TATGTGTGTGAGAATTTG-TGAAG   1118  _       ATGGCTGTAGGI
                        TATG  GTGTGAGAA
                        ||||  |||||||||
                        ATAC  CACACTCTT
                        A        AAACACTTCIII
GAM87  METTL1        TGAGAAATGGCAGAATAGG      1120 TA  GTG  AT  _  AG
                        TGGT  AGAA  GGC  TGT
                        ||||  ||||  |||  |||
                        ACCG  TCTT  CCG  ACA
                        __    ___   AT  T  CA
GAM87  PSCDBP        TATAGATGTGAGAAACAGCTG    1119 TAT_        TAGG
                        GGTGTGAGAAATGGCTG
                        |||||||||||||||||
                        CTACACTCTTTGTCGAC
                      ATAT            IIIG
GAM87  RAB1A        TGCTGTGAGAAAAGGATGGAGG    1123 TATGG    T C T
                        TGTGAGAAA GG TG AGG
                        ||||||||| || || |||
                        ACACTCTTT CC AC TCC
                      G____      T T C
GAM87  ROBO1        GGTGTGAGAGCT-GCTG-AGG    1116 TATGGT    AATG  T
                        GTGAGA   GCTG AG
                        ||||||   |||| ||
                        CACTCT   CGAC TC
                      _____    CGA_  _
GAM87  YWHAG        TGATGTTACATATGGCTGTA     1122 TATG  GAGAA
                        GTGT  ATGGCTGTAG
                        ||||  |||||||||
                        TACA  TACCGACATT
                      ____    ATGTA
GAM88  ACTR1B        TGGGCTGCAC--CCCCTTGC    1139  G  CT     AT
                        TGGG TGTA CCCCCTTGC
                        |||| |||| |||||||||
                        ACCC ACGT GGGGGAACG
                        G    __        II
GAM88  AP2S1        AAGTGGGGTGAAGTCTCCTC     1127 TCACAAGT   TACTG_
                        GGGGTG   CCTC
                        ||||||   ||||
                        CCCCAC   GGAG
                      _____    TTCAGA
GAM88  BCL11B        CACAATT----TGTACTGCCT    1130 TCACAA TG GG
                        G  G TGTACTGCCT
                        |  | |||||||||
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                          T T ACATGACGGA
                     _____GT AA
GAM88  BTG2          AAGTGGGGTGAAGATTCCTC   1126 TCACAAGT     TACTG_
                          GGGGTG    CCTC
                          ||||||    ||||
                          CCCCAC    GGAG
                          _____     TTCTAA
GAM88  CARD15        CACAAATGAAATGGAACTGCCTCT 1129 TC    GG  T_     I
                         ACAAGTG GTG ACTGCCTCT
                         ||||||| ||| |||||||||
                         TGTTTAC TAC TGACGGAGA
                         __    TT  CT      A
GAM88  CD8A          TGGGCTTTAGCCTCCCCCTT     1137 TG  GTA___       GCATA
                          GGGT    CTCCCCCTT
                          ||||    |||||||||
                          CCCG    GAGGGGGAA
                          A_  AAATCG      IIITA
GAM88  CYP8B1        TCACAGG-GGGGTGTACTG      1134  A T       CCT
                          TCACA G GGGGTGTACTG
                          ||||| | |||||||||||
                          AGTGT C CCCCACATGAC
                           _ C        III
GAM88  EDG8          TCACATTGTGGGGTGTCGCTGC   1133   A_    A_   CTCT
                          TCACA GTGGGGTGT CTGC
                          ||||| ||||||||| ||||
                          AGTGT CACCCCACA GACG
                          AA       GC   IIIT
GAM88  GHRHR         TGGGGATGTGG-CCCCCTTGC    1136  _ ACT     ATA
                          TGGGG TGT  CCCCCTTGC
                          ||||| |||  |||||||||
                          ACCCC ACA  GGGGGAACG
                           T CC_      III
GAM88  KCNJ5         TGGGGT----TCCCCCTTG      1138   GTAC     CA
                          TGGGGT TCCCCCTTG
                          |||||| |||||||||
                          ACCCCA AGGGGGAAC
                          ____        II
GAM88  KLHL3         TGGGGATGTCAAGAC-CCCCCTTGC 1135  _ AC___       ATATI
                          TGGGG TGT   TCCCCCTTGC
                          ||||| |||   ||||||||||
                          ACCCC ACA   GGGGGGAACG
                           T GTTCT       IIITA
GAM88  PCTK1         ACAAGTGGGCAGGTGAACATGGCTC 1128 TCAC      ___  T _ C TII
                          AAGTGGG  GTG AC TG CTC
                          |||||||  ||| || || |||
                          TTCACCC  CAC TG AC GAG
                          ____       GTC  T T  C  TCI
GAM88  PPP1R12B      GGTGTACTCCCCAGAGCAT      1132 TGGGGT      CTT  A
                          GTACTCCCC  GCAT
                          |||||||||  ||||
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                      CATGAGGGG  CGTA
                      _____      TCT    A
GAM88  SLC17A5     GGTGTACTCGCCACCTGGCA    1131 TGGGGT    _ _  T  TA
                      GTACTC CC CCT GCA
                      |||||| || ||| |||
                      CATGAG GG GGA CGT
                      _____      C  T  C  CT
GAM89  ADRB3       CACTGCTTGAGAGCAGTAATAAGG  1149 ACA  GT___  C      I
                      GCT   GC AGTAATAAG
                      |||   || |||||||||
                      CGA   CG TCATTATTC
                        A__  ACTCT _    I
GAM89  AGRN        CAGAGCTGTGCCCAGCAGTAA    1150 AC      _  ATAI
                      AGCTGTGCC AGTA
                      |||||||||| ||||
                      TCGACACGG TCGT
                        C_    G  CATI
GAM89  AGRN        CAGAGCTGTGCCCAGCAGTAA    1150 TCAC      _  A  GGA
                      AGCTGTGCC AGTA TAA
                      |||||||||| |||| |||
                      TCGACACGG TCGT ATT
                        TC__    G  C  GII
GAM89  AKAP13      TCACAGCTGGGCGGGGAGTAAG   1158     T C___    TAAGGA
                      TCACAGCTG GC   AGTAA
                      ||||||||| ||   |||||
                      AGTGTCGAC CG   TCATT
                        C CCCC    CIIIAG
GAM89  AKAP13      TCACAGCTGGGCGGGGAGTAAG   1158     T C___    TAAI
                      CACAGCTG GC   AGTAA
                      |||||||| ||   |||||
                      GTGTCGAC CG   TCATT
                        C CCCC   IIIA
GAM89  AKAP2       AAACATAACTGTGA-AAATGTG    1142 CA  C      C  C  A
                      AAC TAACTGTGA AG TGTG
                      ||| |||||||| || ||||
                      TTG ATTGACACT TT ACAC
                        __  T     T _  A
GAM89  CCND1       ACAGCTGTGC--TTTATCAGGA    1145         _____  TAATAAGI
                      ACAGCTGTGC   CAG
                      ||||||||||   |||
                      TGTCGACACG   GTC
                        AAATA  CTIIIGAA
GAM89  CCND1       ACAGCTGTGC--TTTATCAGGA    1145 TCAC     CAG ATA
                      AGCTGTGC TA AGG
                      |||||||| || |||
                      TCGACACG AT TCC
                        ____     AA_ AG_
GAM89  EPHA3       TCAAAGCCAGTGAGCCAGTAAT    1156  C  ___T     AAGGA
                      TCA AGCT  G GCCAGTAAT
                      ||| ||||  | |||||||||
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                              AGT TCGG  C CGGTCATTA
                               T  TCA T      IIIAG
GAM89  EPHA3        TCAAAGCCAGTGAGCCAGTAAT   1156  C   ___T      III
                              TCA AGCT  G GCCAGTAA
                              III IIII  I IIIIIIII
                              AGT TCGG  C CGGTCATT
                               T  TCA T      AII
GAM89  FMOD         GCTTTTCCTGTAATAAGGA      1154  GTG A      II
                              GCT  CC GTAATAAGG
                              III  II IIIIIIIII
                              CGA  GG CATTATTCC
                              AAA  A     TI
GAM89  GALNT2       CAATACTAGCGTGTGACAGCTG   1146  AC  AC_       TGA
                              CAA CTA  TGTGACAGCTG
                              III III  IIIIIIIIIII
                              GTT GAT  ACACTGTCGAC
                              AT  CGC        III
GAM89  GRINL1A      AACCTATCATCTGTGACAGC     1143 CAAA  A___       TGTG
                              CCTA  CTGTGACAGC
                              IIII  IIIIIIIIII
                              GGAT  GACACTGTCG
                              ____  AGTA      TTII
GAM89  HDAC4        CACAGCTGTGC--GGAA-AAGG   1153         CAGTAATAI
                              CACAGCTGTGC
                              IIIIIIIIIII
                              GTGTCGACACG
                                   CCTTTTCCI
GAM89  HDAC4        CACAGCTGTGC--GGAA-AAGG   1153 TC        CAGTAAT
                              ACAGCTGTGC    AAGG
                              IIIIIIIIII    IIII
                              TGTCGACACG    TTCC
                              __        CCTT___
GAM89  HOXC6        CACATCAATTGTGCCAGTGATAA  1148 A  C       AATAI
                              CAG TGTGCCAGT
                              III IIIIIIIII
                              GTT ACACGGTCA
                              A  A      CTATI
GAM89  HOXC6        CACATCAATTGTGCCAGTGATAA  1148 TCA_ C      A   GAI
                              CAG TGTGCCAGT ATAAG
                              III IIIIIIIII IIIII
                              GTT ACACGGTCA TATTT
                              TGTA A     C   III
GAM89  MIPEP        TCACAGCTGTAGCATTTATAA    1157        C GTA  GGA
                              TCACAGCTGTG CA  ATAA
                              IIIIIIIIIII II  IIII
                              AGTGTCGACAT GT  TATT
                               C AAA   III
GAM89  MIPEP        TCACAGCTGTAGCATTTATAA    1157        C GTAATAI
                              CACAGCTGTG CA
                              IIIIIIIIII II
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                  GTGTCGACAT GT
                   C  AAATATI
GAM89  NDUFA6        ACAGCTGTGCACCTAAGCAGG     1144        C____     ATAAGI
                      CAGCTGTGC    AGTA
                      ||||||||  ||||
                      GTCGACACG   TCGT
                       TGGAT  CIIIGA
GAM89  NDUFA6        ACAGCTGTGCACCTAAGCAGG    1144 TCAC      CAGTAATA  A
                        AGCTGTGC      AGG
                        ||||||||    |||
                        TCGACACG      TCC
                      ____        TGGATTCG  C
GAM89  NPAT        CAAACCTAACTGTAGTACAG    1147           __   CTGTG
                      CAAACCTAACTGTG  ACAG
                      ||||||||||||  ||||
                      GTTTGGATTGACAT  TGTC
                         CA   IIIAG
GAM89  SCN8A        CACAGCTGTTCTGCATTGATAA    1151 TC     GCCA  ATAAGGA
                       ACAGCTGT   GTA
                       ||||||||   |||
                       TGTCGACA   CGT
                        __      AGA_  AACTATT
GAM89  SLC11A3      CACAGCTGTG---GTAAAAA    1152        CCA    TI
                      CACAGCTGTG  GTAA
                      ||||||||||  ||||
                      GTGTCGACAC  CATT
                          ___    TT
GAM89  SLC11A3      CACAGCTGTG---GTAAAAA    1152 TC      CCA    TAAG
                       ACAGCTGTG  GTAA
                       |||||||||  ||||
                       TGTCGACAC  CATT
                       __    ___  TTTG
GAM89  TEX15       TCAAAGGCCTGTGCCAG--ATAA    1155  C  __       TAATAAGGA
                       TCA AG  CTGTGCCAG
                       ||| ||  |||||||||
                       AGT TC  GACACGGTC
                        T  CG      TATTIIIAG
GAM89  TEX15       TCAAAGGCCTGTGCCAG--ATAA    1155 TCACAG      TAAI
                          CTGTGCCAG
                          |||||||||
                          GACACGGTC
                       TTCCG_      TATT
GAM90  COG8        TCTCCATT-GGGGTCCAGCCCG    1165 TGTCA      G
                        CCATTGGGG TTCGGCTCG
                        ||||||||| |||||||||
                        GGTAACCCC AGGTCGGGC
                       A____       _
GAM90  CRLF1       TGGCCCCAGTTTGGGTTCGGC    1167 T_ A TTGG      TCG
                        GTC CCA  GGGTTCGGC
                        ||| |||  |||||||||
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                        CGG GGT    CCCAAGCCG
                        AC    _   CAAA        III
GAM90  DPEP1    GTCACAAGGCTTGGGGGTT   1162 TG   CA___      CGGCTC
                        TCAC    TTGGGGGTT
                        IIII    IIIIIIIII
                        AGTG    AACCCCCAA
                        __    TTCCG      CIIIGC
GAM90  EGLN2    TCACCTCGTGGGGGTTCCGC   1164 TGTC  AT_      G  C
                        ACC   TGGGGGTTC GCT
                        III   IIIIIIIII III
                        TGG   ACCCCCAAG CGG
                        ____   AGC     G  C
GAM90  GLP1R    TGTCACCATGGCTTGGGGCTTC   1166      ____   G GGCTCG
                        TGTCACCAT   TGGGG TTC
                        IIIIIIIII   IIIII III
                        ACAGTGGTA   ACCCC AAG
                         CCGA    G  IIIGCT
GAM90  PVR      TCATCCATTGGGG--TCGGGTC   1163 TGTCA     GT  C
                        CCATTGGGG  TCGG TC
                        IIIIIIIII  IIII II
                        GGTAACCCC  AGCC AG
                        TA___      __  C
GAM90  TDRD1    ACCCCTGGGGGTTCAGTTC   1161 TGTCACCAT        C
                        TGGGGGTTCGG TC
                        IIIIIIIIIII II
                        ACCCCCAAGTC AG
                        G_____     A
GAM91  CPNE3    TGGC-GTACTTTATGTGTC   1170   C AA     GCG
                        TGGC GTA  TTATGTGTC
                        IIII III  IIIIIIIII
                        ACCG CAT  AATACACAG
                         _ GA      III
GAM91  CPNE3    TGGC-GTACTTTATGTGTC   1170   C AA    I
                        TGGC GTA  TTATGTGT
                        IIII III  IIIIIIII
                        ACCG CAT  AATACACA
                         _ GA     G
GAM92  ADCY6    GAGACTTGGGAGGG--CAGG   1180          GCCAI
                        GAGATTTGGGAGGG
                        IIIIIIIIIIIII
                        CTCTGAACCCTCCC
                         GTCCI
GAM92  ADCY6    GAGACTTGGGAGGG--CAGG   1180 TG       GC  G
                        AGATTTGGGAGGG CAGG
                        IIIIIIIIIIIII IIII
                        TCTGAACCCTCCC GTCC
                        __      __  A
GAM92  ALOX15   TGGGACTTGGGAGGG--CAGGG   1190 A      GC  G
                        TG GATTTGGGAGGG CAGGG
                        II IIIIIIIIIII IIIII
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```
                         AC CTGAACCCTCCC GTCCC
                         C            __    I
GAM92  ALOX15        TGGGACTTGGGAGGG--CAGGG   1190 _ A        GC   I
                         G GATTTGGGAGGG  CAGG
                         I IIIIIIIIIIII IIII
                         C CTGAACCCTCCC GTCC
                         A C           __    I
GAM92  BCL3          AGCTCTGGGAGGGGACATGG   1175 AGA       C  GI
                         TTTGGGAGGGG CA
                         IIIIIIIIIIII II
                         AGACCCTCCCC GT
                         G__       T AC
GAM92  BCL3          AGCTCTGGGAGGGGACATGG   1175 TGAGA         C  G
                         TTTGGGAGGGG CA GGG
                         IIIIIIIIIIII II III
                         AGACCCTCCCC GT CCT
                         G____       T A
GAM92  CD74          GACATGGGGGAGGGGCTGGGGGC   1182 AGATTT      CA   I
                         GGGAGGGGC GGGG
                         IIIIIIIIII IIII
                         CCCTCCCCG CCCC
                         TGTACC        AC   I
GAM92  CD74          GACATGGGGGAGGGGCTGGGGGC   1182 TGAGATTT      CA    I
                         GGGAGGGGC GGGGC
                         IIIIIIIIII IIIII
                         CCCTCCCCG CCCCG
                         TGTACC__       AC   A
GAM92  COX15        TGAGATTT-GGAGGGGACA   1187       GA   CAGGG
                         TGAGATTTGG GGGGC
                         IIIIIIIIII IIIII
                         ACTCTAAACC CCCTG
                         TC   TIIIC
GAM92  COX15        TGAGATTT-GGAGGGGACA   1187       GA   CI
                         TGAGATTTGG GGGGC
                         IIIIIIIIII IIIII
                         ACTCTAAACC CCCTG
                         TC   TI
GAM92  CRAT         AGATTTGGG-GGGACCAGGG   1174 _    A      I
                         GATTTGGG GGGGCCAGG
                         IIIIIIII IIIIIIIII
                         CTAAACCC CCCTGGTCC
                         T     _    I
GAM92  CRAT         AGATTTGGG-GGGACCAGGG   1174 TGAG    A
                         ATTTGGG GGGGCCAGGGG
                         IIIIIII IIIIIIIIII
                         TAAACCC CCCTGGTCCCT

                         ____    _
GAM92  DRPLA       GATCGGGGAGGGG-CAGGGG   1185 _ T      C  I
                         ATT GGGAGGGGC AGGG
                         III IIIIIIIII IIII
```

```
                         TAG CCCTCCCCG TCCC
                          C  C      _   I
GAM92  DRPLA        GATCGGGGAGGGG-CAGGGG     1185 TGAGATTT      C
                        GGGAGGGGC AGGG
                        ||||||||| |||||
                        CCCTCCCCG TCCCC
                    GC_____        _
GAM92  F2RL3        AGATTTGTG-GTTGCCAGGGGC  1178 _    _ AGGG     I
                       GATTTG GG   GCCAGGGG
                       |||||| ||   ||||||||
                       CTAAAC CC   CGGTCCCC
                     T   A  AA__     I
GAM92  F2RL3        AGATTTGTG-GTTGCCAGGGGC  1178 TGAG   _ AGGG
                        ATTTG GG   GCCAGGGGC
                        ||||| ||   |||||||||
                        TAAAC CC   CGGTCCCCG
                    ____     A  AA__
GAM92  FUT4         TGAGATTTGGAAGCTG-CACGGGC  1192      GG  C G   I
                       TGAGATTTGGGAG  GC A GGGC
                       |||||||||||| || | ||||
                       ACTCTAAACCTTC  CG T CCCG
                          GA _ G   I
GAM92  FUT4         TGAGATTTGGAAGCTG-CACGGGC  1192 _        GG  CA  GI
                        GAGATTTGGGAG  GC  GGG
                        ||||||||||| ||  |||
                        CTCTAAACCTTC  CG  CCC
                      A      GA  TG  II
GAM92  HOXB5        GATT--GGAGGGGCCAGGG     1184 GATTTG         I
                         GGAGGGGCCAGG
                         ||||||||||||
                         CCTCCCCGGTCC
                    CTAA__        C
GAM92  HOXB5        GATT--GGAGGGGCCAGGG      1184 TGAGATTTG
                         GGAGGGGCCAGGG
                         |||||||||||||
                         CCTCCCCGGTCCC
                    A_____
GAM92  LDLR         GAGATTGGTGGATGAGGCAGGGCCAGGGG1179 _____ A  TT  A       CIIIC
                       TG GAT  GGG GGGGCCAGGGG
                       || ||| ||| ||||||||||||
                       AC CTA  TCC TCCCGGTCCCC
                    TCTAACC  _  C_  G       CIIIC
GAM92  LDLR         GAGATTGGTGGATGAGGCAGGGCCAGGGG1179 A_  TT  A        I
                        GAT  GGG GGGGCCAGGG
                        ||| ||| |||||||||||
                        CTA  TCC TCCCGGTCCC
                    AC  C_  G       I
GAM92  MUC5B        TGACATCAGGGAGGGGCAAGG     1189  G  T      C  GC
                       TGA ATT GGGAGGGGC AGGG
                       ||| ||| ||||||||| ||||
```

```
                         ACT TAG CCCTCCCCG TTCC
                          G  T       _   II
GAM92  MUC5B        TGACATCAGGGAGGGGCAAGG   1189  G  T      C I
                         GA ATT GGGAGGGGC AG
                         II III IIIIIIIII II
                         CT TAG CCCTCCCCG TC
                          G  T       T I
GAM92  MYO1C        TTGGGAGGGTCCAGTGGGC    1194        G  _  II
                         TTGGGAGGG CCAG GGG
                         IIIIIIIII IIII III
                         AACCCTCCC GGTC CCC
                           A   A  GI
GAM92  PACSIN1      GAGAGT--GG-GGGGCCAGGGG   1181 T  ATT   AG
                          GAG  TGGG GGGCCAGGGG
                          III  IIII IIIIIIIIII
                          CTC  ACCC CCCGGTCCCC
                          T   ___   __
GAM92  PACSIN1      GAGAGT-GGGAGGGG--AGGGGC   1183 _  TT      CC
                          AGA TGGGAGGGG AGGGG
                          III IIIIIIIII IIIII
                          TCT ACCCTCCCC TCCCC
                          C  C_       __
GAM92  PACSIN1      GAGAGT-GGGAGGGG--AGGGGC   1183 T  ATT     CC
                          GAG  TGGGAGGGG AGGGG
                          III  IIIIIIIII IIIII
                          CTC  ACCCTCCCC TCCCC
                          T   ___      __
GAM92  PACSIN1      GAGAGT--GG-GGGGCCAGGGG   1181 AGATTTG A
                             GG GGGGCCAGGG
                             II IIIIIIIIII
                             CC CCCCGGTCCC
                          CTCTCA_  _
GAM92  PKIA         TGACATT-GTGAGGGGCCAG    1188 GA  _  G     I
                          GAT TTG GAGGGGCCA
                          III III IIIIIIIIII
                          CTG AAC CTCCCCGGT
                          A_  T  A     I
GAM92  PKIA         TGACATT-GTGAGGGGCCAG    1188 TGA  _  G    GGG
                          GAT TTG GAGGGGCCAG
                          III III IIIIIIIIII
                          CTG AAC CTCCCCGGTC
                          A__ T  A      III
GAM92  PPP2R5D      AGAGTATGGAGGG-CCAGGG    1173 _ TTTG   G  I
                          GA   GGAGGG CCAGG
                          II   IIIIII IIIII
                          CT   CCTCCC GGTCC
                          T CATA   _  I
GAM92  PPP2R5D      AGAGTATGGAGGG-CCAGGG    1173 TGAGATTTG   G   G
                             GGAGGG CCAGGG
                             IIIIII IIIIII
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                              CCTCCC GGTCCC
                         TCATA____    _     G
GAM92  PPP5C      TGGGATT--GGAGGGGCCCTGGG  1191  A  TG     AG  C
                       TG GATT  GGAGGGGCC  GGG
                       || |||| ||||||||| |||
                       AC CTAA  CCTCCCCGG  CCC
                         C    __        GA  I
GAM92  PPP5C      TGGGATT--GGAGGGGCCCTGGG  1191 _ A  TG     AG  I
                          G GATT  GGAGGGGCC  GG
                          | |||| ||||||||| ||
                          C CTAA  CCTCCCCGG  CC
                          A C    __        GA  I
GAM92  SYNGR1       AGATG-GGGAGGGG-CGGGGGC  1177 _  TT     CA  I
                          GAT GGGAGGGGC GGGG
                          ||| ||||||||| ||||
                          CTA CCCTCCCCG CCCC
                          T   C_        C_  I
GAM92  SYNGR1       AGATG-GGGAGGGG-CGGGGGC  1177 TGAGATTT     CA
                             GGGAGGGGC GGGG
                             ||||||||| ||||
                             CCCTCCCCG CCCC
                         TAC_____        C_
GAM92  TFAP2A     TGAGGCGTGGGAGGGGC--GGGGC  1193   ATT      CA
                          TGAG  TGGGAGGGGC GGGGC
                          ||||  ||||||||| |||||
                          ACTC  ACCCTCCCCG CCCCG
                          CGC          __
GAM92  TFAP2A     TGAGGCGTGGGAGGGGC--GGGGC  1193 _  ATT      CA  I
                          GAG  TGGGAGGGGC GGGG
                          |||  ||||||||| ||||
                          CTC  ACCCTCCCCG CCCC
                          A CGC        __  I
GAM92  WARS       TTTGGGAGGGGGCATGGGC        1195       C _ GII
                          TTTGGGAGGGG CA GGG
                          |||||||||| || |||
                          AAACCCTCCCC GT CCC
                          C  A  GII
GAM92  WDR1       TGAGAGCCGCGGCGGGGCCAGGGGC  1186   T _ A       II
                          TGAGA TTG GG GGGGCCAGGGGC
                          ||||| ||| || |||||||||||
                          ACTCT GGC CC CCCCGGTCCCCG
                          C  G  G        II
GAM92  WDR1       TGAGAGCCGCGGCGGGGCCAGGGGC  1186 _ ATT GA        I
                          GAG  TGG  GGGGCCAGGGG
                          |||  |||  |||||||||||
                          CTC  GCC  CCCCGGTCCCC
                          T  GGC  G_        I
GAM92  ZNF179     AGATTTGGGAAGGGTCATGGG      1176          C _ GI
                          GATTTGGGAGGGG CA GG
                          ||||||||||||| || ||
```

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                         CTAAACCCTTCCC GT CC
                            A A II
GAM92  ZNF179        AGATTTGGGAAGGGTCATGGG   1176 TGAG      C _ C
                        ATTTGGGAGGGG CA GGGG
                        IIIIIIIIIII II IIII
                        TAAACCCTTCCC GT CCCT
                         ____         A A  T
GAM93  AOC3          GAGCAACTCCTAC-TCCCAATA   1201 TG G    AA
                        AG AACTCCTAC  CTCAATAG
                        II IIIIIIIII  IIIIIIII
                        TC TTGAGGATG  GGGTTATT
                        __ G      A_
GAM93  CAPN10        TGAGGAACTCCTCCTCCTC      1203       ACAA  AATA
                        TGAGGAACTCCT   CTC
                        IIIIIIIIIII   III
                        ACTCCTTGAGGA   GAG
                          GGAG  IIIG
GAM93  DLK1          TGAGGAACTCCAAGAA-TCTAGAG 1205        TACAACTCAATAGI
                        TGAGGAACTCC
                        IIIIIIIIII
                        ACTCCTTGAGG
                            TTCTTAGATCTCII
GAM93  GCMB          GAATCTCC--CAACTCAATA     1200 TGAGGAA  TA
                        CTCC  CAACTCAAT
                        IIII  IIIIIIIII
                        GAGG  GTTGAGTTA

                        _____  __
GAM93  IL10          AGGAACTCCT-GACCTCAA      1199 TGAG    ACAA  T
                        GAACTCCT   CTCAA
                        IIIIIIII   IIIII
                        CTTGAGGA   GAGTT
                        ____       CTG_  C
GAM93  LMO2          TGTGGAACTCCT-CCCCTCAA    1204 TGA     ACAA  TA
                        GGAACTCCT   CTCAA
                        IIIIIIII   IIIII
                        CCTTGAGGA   GAGTT
                        ACA      GGG_  II
GAM93  MEN1          AGAAACTCCTACAAGTCAA      1198 TGAG       C
                        GAACTCCTACAA TCAATA
                        IIIIIIIIIII IIIIII
                        TTTGAGGATGTT AGTTGT
                        ____       C
GAM93  TBX3          GGAACTCCTAC-CCCCAGTAG    1202 TGAGGA    AA  A
                        ACTCCTAC  CTCA TA
                        IIIIIIII  IIII II
                        TGAGGATG  GGGT AT
                        _____    G_  C
GAM94  AKAP2         ATGAAGCACATGGTTTCCT      1211 C  T    GTTC
                        ATG AGTAT TGGTTTCCT
                        III IIIII IIIIIIIII
```

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                          TAC TCGTG ACCAAAGGA
                           T    T      IIIC
GAM94  AKAP2        ATGAAGCACATGGTTTCCT      1211  C    T      II
                          ATG AGTAT TGGTTTCC
                          III IIIII IIIIIIII
                          TAC TCGTG ACCAAAGG
                           T    T     AI
GAM94  ATP2B2       CAGTATTTGGTTTCCGATTGTT   1214              TGTIII
                          CAGTATTTGGTTTCC
                          IIIIIIIIIIIIIII
                          GTCATAAACCAAAGG
                              CTAACA
GAM94  ATP2B2       CAGTATTTGGTTTCCGATTGTT   1214 ATGCAG         ___     CC
                          TATTTGGTTTCC  TGTT
                          IIIIIIIIIII  IIII
                          ATAAACCAAAGG  ACAA
                          _____        CTA   CG
GAM94  C21orf33     ATGTGGTATTTCTGGTTTCCTGATC 1210  CA   __      T CII
                          ATG GTATT TGGTTTCCTG TC
                          III IIIII IIIIIIIIII II
                          TAC CATAA ACCAAAGGAC AG
                           AC   AG        T III
GAM94  C21orf33     ATGTGGTATTTCTGGTTTCCTGATC 1210 GCA   __        TI
                              GTATT TGGTTTCCTG
                              IIIII IIIIIIIIII
                              CATAA ACCAAAGGAC
                          C__   AG        TI
GAM94  GALNT7       TGCAATATTTGGTTTTCCT      1219              _ II
                          TGCAGTATTTGGTTT CC
                          IIIIIIIIIIIIIII II
                          ACGTTATAAACCAAA GG
                              A AI
GAM94  GALNT7       TGCAATATTTGGTTTTCCT       1219 AT          _  TTC
                          GCAGTATTTGGTTT CCTG
                          IIIIIIIIIIIIII IIII
                          CGTTATAAACCAAA GGAT
                          __        A III
GAM94  HIP12        CAGTATTTGGTAGCCT-TTCC     1216 _      TT  GTTCI
                          AGTATTTGGT CCT
                          IIIIIIIIII III
                          TCATAAACCA GGA
                          G      TC AAGII
GAM94  HIP12        CAGTATTTGGTAGCCT-TTCC     1216 ATGCAG     TT  G
                          TATTTGGT CCT TTC
                          IIIIIIII III III
                          ATAAACCA GGA AAG
                          _____        TC  _
GAM94  HNF3B        CATTATTTTTTTTCCTGTT       1215 ATGCAG    GG     C
                          TATTT TTTCCTGTT
                          IIIII IIIIIIIII
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                        ATAAA AAAGGACAA
                        _____    AA        A
GAM94  HNF3B    CATTATTTTTTTTCCTGTT    1215 CAG    GG      II
                        TATTT TTTCCTGT
                        IIIII IIIIIIII
                        ATAAA AAAGGACA
                        GTA   AA     AI
GAM94  IGHMBP2    GCAGTCTT--GTTCCTGTT    1217   ATTTG      I
                        GCAGT   GTTCCTG
                        IIIII   IIIIIIII
                        CGTCA   CAAAGGAC
                         GAA__        A
GAM94  IGHMBP2    GCAGTCTT--GTTCCTGTT     1217 ATGC  ATTTG
                        AGT   GTTTCCTGTT
                        III   IIIIIIIIII
                        TCA   CAAAGGACAA
                        ____  GAA__
GAM94  KCND2    ATGCATTATGATGGTTTCCT    1208    G  T_     GTTC
                        ATGCA TAT TGGTTTCCT
                        IIIII III IIIIIIIII
                        TACGT ATA ACCAAAGGA
                         A   CT      IIIC
GAM94  KCND2    ATGCATTATGATGGTTTCCT    1208    G  T_     II
                        ATGCA TAT TGGTTTCC
                        IIIII III IIIIIIII
                        TACGT ATA ACCAAAGG
                         A   CT      AI
GAM94  PHKA2    ATGCAGTATT---TTTCCT     1212        GGT
                        ATGCAGTATTT TTCC
                        IIIIIIIIIII IIII
                        TACGTCATAAA AAGG
                        ___
GAM94  PHKA2    ATGCAGTATT---TTTCCT     1212        GGT  GT
                        ATGCAGTATTT TTCCT
                        IIIIIIIIIII IIIII
                        TACGTCATAAA AAGGA
                        ___    II
GAM94  RABIF    ATGAAATACTATGGTTTCCTATTC 1209  C    _       CI
                        ATG AGTATT TGGTTTCCTGTTC
                        III IIIIII IIIIIIIIIIIII
                        TAC TTATGA ACCAAAGGATAAG
                         T    T       II
GAM94  RABIF    ATGAAATACTATGGTTTCCTATTC 1209 TGC    _        I
                        AGTATT TGGTTTCCTGTT
                        IIIIII IIIIIIIIIIII
                        TTATGA ACCAAAGGATAA
                        CT_    T        I
GAM94  SDPR    GCATTCTTTG-TTCCTGTT     1218 ATGCAGTATTTG      C
                        GTTTCCTGTT
                        IIIIIIIIII
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                              CAAAGGACAA
                         TAAGAAA_____          A
GAM94  SDPR          GCATTCTTTG-TTTCCTGTT    1218 CA    G__       I
                         GTATTT  GTTTCCTGT
                         ||||||  |||||||||
                         CGTAAG  CAAAGGACA
                           __     AAA      I
GAM94  TGIF          CAGTATGTGGGCATCCTGTTCC   1213 A   T  TT_      I
                         GTAT TGG  TCCTGTTC
                         |||| |||  ||||||||
                         CATA ACC  AGGACAAG
                          _   C   CGT      I
GAM94  TGIF          CAGTATGTGGGCATCCTGTTCC   1213 ATGCAGTATTT  T
                             GGT TCCTGTTCC
                             ||| |||||||||
                             CCG AGGACAAGG
                         ATACAC_____    T
GAM95  ARNT2         GATCCAAAACCTATTTTGTGC   1222   ___   __    IIIG
                         GATC AACCT TTTTGTG
                         |||| ||||| |||||||
                         CTAG TTGGA AAAACAC
                          GTT   TA   GIII
GAM95  CCND1         TGAAACAG--CAACCTTTTTG    1225  C   AT       TG
                         TGA ACGG CAACCTTTTTG
                         ||| |||| |||||||||||
                         ACT TGTC GTTGGAAAAAC
                           T   __       II
GAM95  CCND1         TGAAACAG--CAACCTTTTTG    1225 _ C   AT        I
                         GA ACGG CAACCTTTTT
                         || |||| ||||||||||
                         CT TGTC GTTGGAAAAA
                         A T   __      I
GAM95  NCOA4         TGACCAGGTT-AATTTTTTTGTGC 1226   A ATCAACC       I
                         TGAC CGG    TTTTGTGC
                         |||| |||    ||||||||
                         ACTG GTC    AAAAACACG
                          _  CAATTAA      I
GAM95  NCOA4         TGACCAGGTT-AATTTTTTTGTGC 1226 _ A ATCAACC       I
                         GAC CGG    TTTTGTG
                         ||| |||    ||||||||
                         CTG GTC    AAAAACAC
                         A _  CAATTAA      I
GAM95  PTEN          TGACACAGCTACACAACCTTTTT  1224       AT___        GTGCI
                         TGACACGG   CAACCTTTTT
                         ||||||||   ||||||||||
                         ACTGTGTC   GTTGGAAAAA
                             GATGT       IIICG
GAM95  PTEN          TGACACAGCTACACAACCTTTTT  1224 GAC   AT___         I
                         ACGG    CAACCTTTT
                         ||||    |||||||||
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                          TGTC   GTTGGAAAA
                          ___    GATGT         I
GAM95  RFPL1      TGACAAGTGA-CAACCTTTTCATGC 1223    CG_ T      TG  I
                          TGACA  GA CAACCTTTT TGC
                          |||||  || |||||||||| |||
                          ACTGT  CT GTTGGAAAA ACG
                            TCA  _       GT  I
GAM95  RFPL1      TGACAAGTGA-CAACCTTTTCATGC 1223    CG_ T      TG  I
                           GACA  GA CAACCTTTT TG
                           ||||  || |||||||||| ||
                           CTGT  CT GTTGGAAAA AC
                            TCA  _       GT  I
GAM95  RFPL2      TGACAAGTGA-CAACCTTTTCATGC 1223    CG_ T      TG  I
                          TGACA  GA CAACCTTTT TGC
                          |||||  || |||||||||| |||
                          ACTGT  CT GTTGGAAAA ACG
                            TCA  _       GT  I
GAM95  RFPL2      TGACAAGTGA-CAACCTTTTCATGC 1223    CG_ T      TG  I
                           GACA  GA CAACCTTTT TG
                           ||||  || |||||||||| ||
                           CTGT  CT GTTGGAAAA AC
                            TCA  _       GT  I
GAM95  RFPL3      TGACAAGTGA-CAACCTTTTCATGC 1223    CG_ T      TG  I
                          TGACA  GA CAACCTTTT TGC
                          |||||  || |||||||||| |||
                          ACTGT  CT GTTGGAAAA ACG
                            TCA  _       GT  I
GAM95  RFPL3      TGACAAGTGA-CAACCTTTTCATGC 1223    CG_ T      TG  I
                           GACA  GA CAACCTTTT TG
                           ||||  || |||||||||| ||
                           CTGT  CT GTTGGAAAA AC
                            TCA  _       GT  I
GAM96  ADCY3        GTCCTGCCCCACCAAGCCC       1245 TCAGA  TG      CA
                           GTCC  CACCAAGCCC
                           ||||  ||||||||||
                           CGGG  GTGGTTCGGG
                           _____  __       AC
GAM96  AQP6      GGGTCTTGGTGTCGGGGAACAGGA 1240 GGT      ___    CC  I
                          CTTGGT  GGGG  CAGG
                          ||||||  ||||  ||||
                          GAACCA  CCCC  GTCC
                            ___      CAG  TT  I
GAM96  AQP6      GGGTCTTGGTGTCGGGGAACAGGA 1240 TG        ___    CC   ATI
                         GGTCTTGGT  GGGG  CAGGA
                         |||||||||  ||||  |||||
                         CCAGAACCA  CCCC  GTCCT
                           __        CAG  TT  GII
GAM96  AXUD1      AGTC-TGCACCAAAGCCCAG      1231 TCAGAGTCC       C
                          TGCACCAAG CCCA
                          ||||||||| ||||
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                              ACGTGGTTT GGGT
                              _____    C
GAM96  B4GALT2       CAGACTTACTGATCCAAGCCCCA  1233 TC  GTC_  CA       GI
                             AGA   CTG  CCAAGCCCCA
                             III   III  IIIIIIIIII
                             TCT   GAC  GGTTCGGGGT
                             __  GAAT  TA       GI
GAM96  BTNL3         TGGGTCTGTGGTGTGGGGCCC    1252    _  __       AGGAAT
                             TGGGTCT TGGT GGGGCCC
                             IIIIIII IIII IIIIIII
                             ACCCAGA ACCA CCCCGGG
                                C   CA    IIITAA
GAM96  BTNL3         TGGGTCTGTGGTGTGGGGCCC    1252    _  __       III
                             TGGGTCT TGGT GGGGCC
                             IIIIIII IIII IIIIII
                             ACCCAGA ACCA CCCCGG
                                C   CA    GII
GAM96  C1QB          TCAGCAG-CATTCACCAAGCCC   1248   _  CCTG      CAG
                             TCAG AGT  CACCAAGCCC
                             IIII III  IIIIIIIIII
                             AGTC TCG  GTGGTTCGGG
                               G  TAA_      III
GAM96  CCND2         TGGGACTCCTTGGGGCCCAGGA   1257  T GG        AT
                             TGGG CTT TGGGGCCCAGGA
                             IIII III IIIIIIIIIIII
                             ACCC GAG ACCCCGGGTCCT
                               T  GA       II
GAM96  CCND2         TGGGACTCCTTGGGGCCCAGGA   1257  T GG        I
                             GGG CTT TGGGGCCCAGG
                             III III IIIIIIIIIII
                             CCC GAG ACCCCGGGTCC
                               T  GA      I
GAM96  CD79B         TGGCTCTTC-TGGGGCCCAG     1256  G  GG       GAA
                             TGG TCTT TGGGGCCCAG
                             III IIII IIIIIIIIII
                             ACC AGAA ACCCCGGGTC
                               G  G_       III
GAM96  CD79B         TGGCTCTTC-TGGGGCCCAG     1256_ G  GG      I
                             GG TCTT TGGGGCCCA
                             II IIII IIIIIIIIII
                             CC AGAA ACCCCGGGT
                             A  G  G_      I
GAM96  CHRM1         GGGTCTCTCTGGGCTGCCCAGGAA 1242 GG  GG   __      I
                             TCTT TGGG GCCCAGGA
                             IIII IIII IIIIIIII
                             AGAG ACCC CGGGTCCT
                               __  AG  GA      I
GAM96  CHRM1         GGGTCTCTCTGGGCTGCCCAGGAA 1242 TG   GG   __     TI
                             GGTCTT TGGG GCCCAGGAA
                             IIIIII IIII IIIIIIIIII
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                              CCAGAG  ACCC  CGGGTCCTT
                                __    AG  GA      CI
GAM96  CORO2B        GGGTCTTGGTCGTGGGCCCA    1241        __      III
                        GGGTCTTGGT G GGGCCC
                        IIIIIIIII I IIIIII
                        CCCAGAACCA C CCCGGG
                             G A    TII
GAM96  CORO2B        GGGTCTTGGTCGTGGGCCCA    1241 TG     __      GGAA
                        GGTCTTGGT G GGGCCCA
                        IIIIIIIII I IIIIIII
                        CCAGAACCA C CCCGGGT
                           __      G A    AIII
GAM96  F2RL3       TGGGCCT-GGTGGGGCCACAG    1255     T     _  GAA
                        TGGGTCT GGTGGGGCC CAG
                        IIIIIII IIIIIIIII III
                        ACCCGGA CCACCCCGG GTC
                           _       T  III
GAM96  F2RL3       TGGGCCT-GGTGGGGCCACAG    1255     T     _  I
                        GGGTCT GGTGGGGCC CA
                        IIIIII IIIIIIIII II
                        CCCGGA CCACCCCGG GT
                           _       T  I
GAM96  FLOT2       AGTGCAACATCCAAGCCCCAG    1230 TCAGAGTCCT  _
                           GCA CCAAGCCCCAG
                           III IIIIIIIIII
                           TGT GGTTCGGGGTC
                        GT_____    A
GAM96  GJB3      GAGCTCCAGCTC-AAGCCCCAG    1236 TCAGAG  T AC
                        TCC GC  CAAGCCCCAG
                        III II  IIIIIIIIII
                        AGG CG  GTTCGGGGTC
                        G_____  T A_
GAM96  H4F2      TCAGAGTCCGACA-CAAGCCCC    1251      T  C    AG
                        TCAGAGTCC GCAC AAGCCCC
                        IIIIIIIII IIII IIIIIII
                        AGTCTCAGG TGTG TTCGGGG
                            C  _    II
GAM96  HIRA     CAGAGCTCCAGC-CCTAGCTCC    1232 TC  _  T A A  C AG
                        AGAG TCC GC CC AGC CC
                        IIII III II II III II
                        TCTC AGG CG GG TCG GG
                           __   G  T _ A A CI
GAM96  HOXC5      GTCT--GTGGGGCCCGGGA    1246    TG      A I
                        GTCT GTGGGGCCC GG
                        IIII IIIIIIIII II
                        CAGA CACCCCGGG CC
                           __       C T
GAM96  HOXC5      GTCT--GTGGGGCCCGGGA    1246 TGGGTCTTG      A
                        GTGGGGCCC GGA
                        IIIIIIIII III
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```
                              CACCCCGGG CCT
                          A_____        C
GAM96  NKX3A        TGGGTCTTGCTCGTTGCCCAGG   1254      G_ GG    AAT
                       TGGGTCTTG TG GCCCAGG
                       ||||||||| || |||||||
                       ACCCAGAAC GC CGGGTCC
                          GA AA     |||
GAM96  NKX3A        TGGGTCTTGCTCGTTGCCCAGG   1254 G    G_ GG   I
                         GGTCTTG TG GCCCAG
                         |||||| || ||||||
                         CCAGAAC GC CGGGTC
                       _    GA AA   I
GAM96  PRDM4          CAGAGTCCTCTACTCCAGCCC     1234 TC    __ A  A   CAG
                        AGAGTCCT GC CCA GCCC
                        |||||||| || ||| ||||
                        TCTCAGGA TG GGT CGGG
                        __    GA A _ T||
GAM96  RBP4       TCAGAGTCTGGAATCTTAAGCCCCAG 1250      C CACC___      ||
                      TCAGAGTC TG    AAGCCCCAG
                      |||||||| ||    |||||||||
                      AGTCTCAG AC    TTCGGGGTC
                        _ CTTAGAA       ||
GAM96  RFX2        GGTCT-GGTGGGGCCCTGG      1244    T      AG|
                      GGTCT GGTGGGGCCC
                      ||||| |||||||||||
                      CCAGA CCACCCCGGG
                        _      ACC
GAM96  RFX2        GGTCT-GGTGGGGCCCTGG      1244 TGGGTC     A A
                       TTGGTGGGGCCC GG
                       ||||||||||| ||
                       GACCACCCCGGG CC
                       A_____        A A
GAM96  SERPINE1       GGGTCTTGGTATGTTGCCCAGG    1239 GG     GG__    I
                        TCTTGGTG  GCCCAG
                        |||||||| ||||||
                        AGAACCAT  CGGGTC
                        __    ACAA   I
GAM96  SERPINE1       GGGTCTTGGTATGTTGCCCAGG    1239 TG     GG__    AAT
                        GGTCTTGGTG  GCCCAGG
                        ||||||||| |||||||
                        CCAGAACCAT  CGGGTCC
                          __    ACAA   G||
GAM96  SYNGR1        GGGTCTAGAGTGGGGGCCCAGGA  1238 GG  T_   _    I
                        TCT  GGTGGGG CCCAGG
                        |||  |||||||  ||||||
                        AGA  TCACCCC  GGGTCC
                        __   TC    C   I
GAM96  SYNGR1        GGGTCTAGAGTGGGGGCCCAGGA  1238 TG  T_   _   AT|
                         GGTCT GGTGGGG CCCAGGA
                         ||||| ||||||| |||||||
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                              CCAGA  TCACCCC GGGTCCT
                              __     TC    C    AII
GAM96  SYNGR1         GGGTCTT----GGGCCAAGG    1243      GGTG    CA
                          GGGTCTT  GGGCC
                          |||||||  |||||
                          CCCAGAA  CCCGG
                          ____        TT
GAM96  SYNGR1         GGGTCTT----GGGCCAAGG    1243 TG    GGTG    C
                           GGTCTT  GGGCC AGG
                           ||||||  ||||| |||
                           CCAGAA  CCCGG TCC
                           __  ____        T
GAM96  TCTA           TGGGTCTTGCTCTGTTGCCCAGG  1253      G__ GG    AATI
                         TGGGTCTTG  TG GCCCAGG
                         ||||||||| || |||||||
                         ACCCAGAAC  AC CGGGTCC
                             GAG AA      IIIT
GAM96  TCTA           TGGGTCTTGCTCTGTTGCCCAGG  1253 GG    G__ GG    I
                          GTCTTG  TG GCCCAG
                          |||||| || ||||||
                          CAGAAC  AC CGGGTC
                          __    GAG AA    I
GAM96  TLR4           TCAGAGTCC--CAGCCAGGCGCGAG 1249      GCA  A CCCAGI
                         TCAGAGTCCT  CCA GC
                         ||||||||||  ||| ||
                         AGTCTCAGGG  GGT CG
                            TC_  C CGCTCI
GAM96  TNFRSF10B        AGCGTCCTGCACAGAAGGCCCAG  1229 TCAGA      C_ C    I
                           GTCCTGCAC AAG CCCAG
                           ||||||||| ||| |||||
                           CAGGACGTG TTC GGGTC
                           G____        TC  C   G
GAM96  VENTX2         TCAGGAGTC-TGCACCAAG    1247   _ C      CCCC
                         TCAG AGTC TGCACCAAG
                         |||| |||| |||||||||
                         AGTC TCAG ACGTGGTTC
                            C  _      IIIG
GAM96  WNT14          TGGG-CT-GGTCGAGCCCAGGAA  1258   CT  G      T
                          TGGGT TGGT GGGCCCAGGAA
                          ||||| |||| |||||||||||
                          ACCCG ACCA CTCGGGTCCTT
                             __   G        I
GAM96  WNT14          TGGG-CT-GGTCGAGCCCAGGAA  1258 _ CT  G      I
                           GGGT TGGT GGGCCCAGGA
                           |||| |||| ||||||||||
                           CCCG ACCA CTCGGGTCCT
                            A __   G      I
GAM96  WNT3A          GAGTCCTGCTCCA---CCCAG    1237 TCAGAG    A AGC
                          TCCTGC CCA  CCC
                          |||||| |||  |||
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                      AGGACG GGT   GGG
                      _____        A ___
GAM96  ZNF134      CAGGG-CCTGT-CCAAGCCCC      1235 TC  A T   CA       A
                      AG G CCTG  CCAAGCCCC
                      || | |||| ||||||||||
                      TC C GGAC  GGTTCGGGG
                      __  C _   A_        A
GAM97  CLCN6       AAAGCTGCAATGTTAAGAAT      1265 TAAA     CTG
                      AGCTGT  GTTAAGAAT
                      |||||| |||||||||
                      TCGACG  CAATTCTTA
                      ____       TTA
GAM97  DAG1        AAAAGCTGTTAGGCAAAAAT      1263 TA      CT  T    I
                      AAAGCTGT GGT AAGAAT
                      |||||||| ||| ||||||
                      TTTCGACA CCG TTTTTA
                      __       AT  T    T
GAM97  EXTL2       TAAACAGAGGCCTAGTTAAGAAT   1268 TAAA_ CT         II
                      AG GTCTGGTTAAGAAT
                      || ||||||||||||||
                      TC CGGATCAATTCTTA
                      ATTTG  TC          II
GAM97  GYPA        TAAATTCTGTAGCTCTGGTTAAGAA 1271 TAAA_____  TG        TIII
                      AGC TCTGGTTAAGAA
                      ||| |||||||||||
                      TCG AGACCAATTCTT
                      ATTTAAGACA  __         IIIT
GAM97  IL5RA       TAAAAGCTGTCT-GTTGTGAAT   1274          GTTAA  I
                      TAAAAGCTGTCTG   GAAT
                      |||||||||||||   ||||
                      ATTTTCGACAGAC   CTTA
                      AACA_   I
GAM97  MCL1        TACAAGCTGTC---TTAAGAAT   1275 TAA       GGT
                      AAGCTGTCT  TAAGAAT
                      ||||||||| |||||||
                      TTCGACAGA  ATTCTTA
                      ATG      ___
GAM97  MFAP3       AAAGGTGATGGGTTAAGAA      1264 TAAA  C  TCT       T
                      AG TG  GGTTAAGAA
                      || ||  |||||||||
                      TC AC  CCAATTCTT
                      ____   C  TAC       C
GAM97  MKLN1       TAAAAACTTGTGATGGTTAAGA   1269       _ C_      ATI
                      TAAAAGCT GT TGGTTAAGA
                      |||||||| || |||||||||
                      ATTTTTGA CA ACCAATTCT
                      A  CT      III
GAM97  NR3C2       TAAAAGCTGCTTTG-TAAG      1270       T GGT_ AAT
                      TAAAAGCTG CT   TAAG
                      |||||||||| ||   ||||
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                              ATTTTCGAC GA   ATTC
                              _   AAAC   III
GAM97  PHB           AAGGCTGT---GTTAAGAAT    1266 TAAAA    CTG
                              GCTGT  GTTAAGAA
                              IIIII  IIIIIIIII
                              CGACA   CAATTCTT
                              C____    ___
GAM97  RAI14         AAAAGTTGA--GGTTAAGAA    1262 TA   C TCT
                              AAAG TG  GGTTAAGAA
                              IIII II  IIIIIIIII
                              TTTC AC  CCAATTCTT
                              __   A T__
GAM97  SIRT2         AAGAACTG-CTGGTTAAGA     1261 TAAA    T      A
                              AGCTG CTGGTTAAGA
                              IIIII IIIIIIIIII
                              TTGAC GACCAATTCT
                              TC__   _       C
GAM97  TACC1         AAGCTGTCTTTGTTTAAAAAT   1267 TAAAAG    GG__     I
                              CTGTCT  TTAAGAAT
                              IIIIII  IIIIIIII
                              GACAGA   AATTTTA
                              _____    AACA      T
GAM97  Z39IG         TAAAAGCTGTCTGGCCCTGAAGAA 1272            AA  TII
                              TAAAAGCTGTCTGGTT GAA
                              IIIIIIIIIIIIIII III
                              ATTTTCGACAGACCGG CTT
                                     GA  CTT
GAM97  ZNF179        TAAAGGCTGTCTGGCTTAGCTCAGAAT1273    A        A AATIIIA
                              TAAA GCTGTCTGGTT AG
                              IIII IIIIIIIIIII II
                              ATTT CGACAGACCGA TC
                                     C      A GAGTCTT
GAM98  ABCC3         TGGTGTAGTCCATGATAGTGTT   1286       GC C_ TTI
                              GTGTAGTC TG AGT
                              IIIIIIII II III
                              CACATCAG AC TCA
                                     GT TA CII
GAM98  APPBP2        TTGGCATGTGTTCACTGCAGTTTT 1288 TATTG  AG          I
                              GTGT TCGCTGCAGTTTT
                              IIII IIIIIIIIIIIII
                              TACA AGTGACGTCAAAA
                              CCG__   CA          G
GAM98  APPBP2        TTGGCATGTGTTCACTGCAGTTTT 1288 TG   AG          I
                              GTGT TCGCTGCAGTTT
                              IIII IIIIIIIIIII
                              TACA AGTGACGTCAAA
                              CG   CA          I
GAM98  CAPN1         TTGGGG--GTCGCTGCAGT      1290    TGTA       I
                              TTGG  GTCGCTGCAG
                              IIII  IIIIIIIIII
```

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                              AACC    CAGCGACGTC
                              CC__         A
GAM98  CAPN1          TTGGGG--GTCGCTGCAGT     1290 TATTGGTGTA
                              GTCGCTGCAGTT

                              IIIIIIIIIII
                              CAGCGACGTCAG
                              CCCC_____
GAM98  CASP6          TTTGTGTAACC-CTGCAGTTT   1291 TATTG   GT G
                            GTGTA C CTGCAGTTT

                            IIIII I IIIIIIIII
                            CACAT G GACGTCAAA
                            A____    TG _
GAM98  CASP6          TTTGTGTAACC-CTGCAGTTT   1291 TG_   GT G     I
                            GTGTA C CTGCAGTT

                            IIIII I IIIIIIIII
                            CACAT G GACGTCAA
                            AAA   TG _    I
GAM98  CYFIP2         GTGGTCATGGCTGCAGTTT     1282 A ___       III
                            GT GTC  GCTGCAGTT

                            II III  IIIIIIIII
                            CA CAG  CGACGTCAA
                             C  TAC      AII
GAM98  FLNB           TGCTGTAGTCGCCTGGCAG     1285 G      __  III
                             TG TGTAGTCGCT GCA

                             II IIIIIIIIII III
                             AC ACATCAGCGG CGT
                              G     AC  CII
GAM98  FLNB           TGCTGTAGTCGCCTGGCAG     1285 TATTGG      __ TTT
                              TGTAGTCGCT GCAG

                              IIIIIIIIII IIII
                              ACATCAGCGG CGTC
                              _____         AC  TCA
GAM98  GLRX           TTGGTGTAGGGGGCTGTAAGTTTT 1289 TATT    TC_  C_   I
                              GGTGTAG  GCTG AGTTTT

                              IIIIIII  IIII IIIIII
                              CCACATC  CGAC TCAAAA
                              ____      CCC  AT   T
GAM98  GLRX           TTGGTGTAGGGGGCTGTAAGTTTT 1289 TG   TC_  C_   I
                              GTGTAG  GCTG AGTTT

                              IIIIII  IIII IIIII
                              CACATC  CGAC TCAAA
                              __     CCC  AT   I
GAM98  MEIS1          ATTGTTG-A-TGACTGCAGTTTT 1280 ____      TAGTC      I
                             TTGGTG  GCTGCAGTTT

                             IIIIII  IIIIIIIIII
                             AACTAC  TGACGTCAAA
                             TAAC    _____         I
GAM98  MEIS1          ATTGTTG-A-TGACTGCAGTTTT 1280 TA_   TAGTC
                             TTGGTG  GCTGCAGTTTT

                             IIIIII  IIIIIIIIII
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                        AACTAC    TGACGTCAAAA
                        AAC      _____
GAM98  SIGLEC9          GGTG-AGTCTCTGCAGTTT    1281    T    G     I
                        GGTG AGTC CTGCAGTT
                        |||| |||| ||||||||
                        CCAC TCAG GACGTCAA
                         _    A    A
GAM98  SOX11            TGGCCTAGCAGCTGCAGTT    1287    G    C     II
                        TGGT TAGT GCTGCAGT
                        |||| |||| ||||||||
                        ACCG ATCG CGACGTCA
                          G    T    AI
GAM98  SOX11            TGGCCTAGCAGCTGCAGTT    1287 TATTGGTG   C      T
                        TAGT GCTGCAGTT
                        |||| ||||||||||
                        ATCG CGACGTCAA
                        GG_____    T    T
GAM98  SP3             ATAGGTGAACT-GCTGCAGTT   1278 TATT   T  TC      T
                        GGTG AG  GCTGCAGTT
                        |||| ||  ||||||||||
                        CCAC TT  CGACGTCAA
                        AT__  _  GA      T
GAM98  SP3             ATAGGTGAACT-GCTGCAGTT   1278 TT_   T  TC      I
                        GGTG AG  GCTGCAGT
                        |||| ||  |||||||||
                        CCAC TT  CGACGTCA
                        TAT   _  GA      I
GAM98  SPAG8        TACTGGTGTTGAGAAGCTGCAGTT   1283        __  TC      TTI
                        TATTGGTGT AG  GCTGCAGTT
                        ||||||||| || ||||||||||
                        ATGACCACA TC  CGACGTCAA
                             AC TT        III
GAM98  SPAG8        TACTGGTGTTGAGAAGCTGCAGTT   1283 AT      __  TC      I
                        TGGTGT AG  GCTGCAGT
                        |||||| || |||||||||
                        ACCACA TC  CGACGTCA
                        __     AC TT       I
GAM98  THY1            TTGGTTTTATTG-TGCAGTTTT   1292 _    GTAGTCGC      I
                        TGGT    TGCAGTTT
                        ||||    ||||||||
                        ACCA    ACGTCAAA
                        A  AAATAAC_      I
GAM98  THY1            TTGGTTTTATTG-TGCAGTTTT   1292 TATT  GTAGTCGC
                        GGT    TGCAGTTTT
                        |||    |||||||||
                        CCA    ACGTCAAAA
                        ____   AAATAAC_
GAM98  TLR4            ATTGGTGTATTCAAAGCAGTT    1279 TA      G  CT      T
                        TTGGTGTA TCG  GCAGTTT
                        |||||||| |||  ||||||||
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                         AACCACAT AGT CGTCAAG
                          __      A  TT    I
GAM98  TLR4      ATTGGTGTATTCAAAGCAGTT   1279       G  CT   I
                         TTGGTGTA TCG GCAGT
                         ||||||| ||| |||||
                         AACCACAT AGT CGTCA
                                 A  TT   I
GAM98  TTID      TAATGGTGTAGTTG--GCTGTTTT  1284 T      C_  CAGI
                         TGGTGTAGT GCTG
                         ||||||||| ||||
                         ACCACATCA CGAC
                          T    AC  AAII
GAM98  TTID      TAATGGTGTAGTTG--GCTGTTTT  1284 TAT     C_  CAGTTTT
                          TGGTGTAGT GCTG
                         ||||||||| ||||
                         ACCACATCA CGAC
                         ATT      AC  AAAAIII
GAM99  CDH10       GACATGTACCTAACAGAAGCG   1300      __  CC III
                         GACATGTACC ACAG GC
                         |||||||||| |||| ||
                         CTGTACATGG TGTC CG
                           AT    TT CII
GAM99  CDH10       GACATGTACCTAACAGAAGCG   1300 ACGA    __  CC  C
                         CATGTACC ACAG GCG GC
                         |||||||| |||| ||| ||
                         GTACATGG TGTC CGC CG
                         ____       AT  TT  _
GAM99  LASS1     CACGTACAGCCGCCGCGCGC   1297     CACA     I
                         ATGTAC  GCCGCGCG
                         ||||||  ||||||||
                         TGCATG  CGGCGCGC
                          TCGG      I
GAM99  MADH7      ACG-CGTGCACACACAGCCGC   1295 ACA   _     GCG
                         ACG  TGTAC CACAGCCGC
                         |||  ||||| |||||||||
                         TGC  ACGTG GTGTCGGCG
                          GC_   T     III
GAM99  MADH7      ACG-CGTGCACACACAGCCGC   1295 ACA   _     I
                         CG  TGTAC CACAGCCG
                         ||  ||||| ||||||||
                         GC  ACGTG GTGTCGGC
                          GC_   T     I
GAM99  PACE4      GAGATTTACTACACAGCCGC   1299 ACGACATG __     CG
                         TAC CACAGCCGCG
                         ||| |||||||||
                         ATG GTGTCGGCGT
                         CTAA____  AT    CI
GAM99  PACE4      GAGATTTACTACACAGCCGC   1299 GACATG __      III
                         TAC CACAGCCG
                         ||| ||||||||
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                               ATG  GTGTCGGC
                            CTCTAA  AT      GII
GAM99  PKIB           CATG-ACTCCAGCCGCGCGC   1298 _  T  CA        I
                          ATG AC  CAGCCGCGCG
                          III II  IIIIIIIIII
                          TAC TG  GTCGGCGCGC
                            G  _  AG       I
GAM99  PKIB           CATG-ACTCCAGCCGCGCGC   1298 ACGACATGT  CA
                            AC  CAGCCGCGCG
                            II  IIIIIIIIII
                            TG  GTCGGCGCGC
                         _____  AG
GAM99  REQ            GGGGCTGGGCCCAAGGCAAGCAGA  1301 T  T  GC_  ___      TCGI
                         GG GC  GCCC  GCAAGCAGA
                         II II  IIII  IIIIIIIII
                         CC CG  CGGG  CGTTCGTCT
                         _  _  ACC  TTC      CIII
GAM99  RUNX1            TGGTTTG-GACAGCAAGCAGATC  1302   GCGC CC       G
                         TGGT  GC GCAAGCAGATC
                         IIII  II IIIIIIIIIII
                         ACCA  TG CGTTCGTCTAG
                          AACC  T_        I
GAM99  TFEB           CATGTACCAGGCACTGCCGC   1296        __ __   IIIG
                         CATGTACCA CA GCCG
                         IIIIIIIII II IIII
                         GTACATGGT GT CGGC
                          CC GA  GIII
GAM99  TFEB           CATGTACCAGGCACTGCCGC   1296 ACGA  T  CACA     G
                         CA GTAC  GCCGCGC
                         II IIII  IIIIIII
                         GT CGTG  CGGCGTG
                          ATG_ C  A___     G
GAM100 ADH5           TGGCAATGT-GAT-CTCGAAGTG  1313  G GGT  G     A
                         TGG AA  TGAT CTCGAAGTG
                         III II  IIII IIIIIIIII
                         ACC TT  ACTA GAGCTTCAC
                          G AC_  _      I
GAM100 CDH11            AAGATTGATGCTC-AAGAGA   1305 TGGGAAGG       AGTG
                            TTGATGCTCGA
                            IIIIIIIIIII
                            AACTACGAGTT
                            _____   CTCT
GAM100 CLN2            TGGGAAGGTGGACGAT-GAAATG   1314      T  CTC    A
                         TGGGAAGGT GATG  GAAGTG
                         IIIIIIIII IIII  IIIIII
                         ACCCTTCCA CTGC  CTTTAC
                           C  TA_  I
GAM100 CMAR            GAAGGTTGAGGC-CGCAGTGA   1307 TGGGAA    T  T  A
                         GGTTGA GC CG AGTG
                         IIIIII II II IIII
```

<pre>
                              CCAACT CG GC TCAC
                              _____    C _ G
GAM100 FUT4          TGGGAAGGTACAGGAGGCTCGA   1310      T___ T    AGTGA
                        TGGGAAGGT  GA GCTCGA
                        IIIIIIIII  II IIIIII
                        ACCCTTCCA  CT CGAGCT
                           TGTC  C     IIIAG
GAM100 IL10RA        GGAAGCTCTGATGCTCG-AGTG   1308 TGGG  G_      A A
                          AAG  TTGATGCTCGA GTG
                          III IIIIIIIIII III
                          TTC  GACTACGAGCT CAC
                          ____  GA    _  C
GAM100 NFRKB          GAAGGTTGACCCT-GATAGT    1306 TGGGAA    G C _  G
                          GGTTGAT CT GA AGT
                          IIIIIIII II II III
                          CCAACTG GA CT TCA
                          _____    G _ A G
GAM100 SKI          GGGAAGGTTG-TGGACAAAGTG    1309 TG     A CT    A
                        GGAAGGTTG TG CGAAGTG
                        IIIIIIIII II IIIIIII
                        CCTTCCAAC AC GTTTCAC
                          __     _ CT     G
GAM100 TNF          TGGGAAGGTTGGATGTTCG        1312       _ C AAGTG
                        TGGGAAGGTTG ATG TCG
                        IIIIIIIIIII III III
                        ACCCTTCCAAC TAC AGC
                            C  A  IIIAG
GAM100 VAX2          TGGGAAGGTGCTG-TGCTCG      1311       __ A    AAGTG
                        TGGGAAGGT TG TGCTCG
                        IIIIIIIII II IIIIII
                        ACCCTTCCA AC ACGAGC
                           CG _   IIIAG
GAM101 ANKRD3         TGAGCCAGCTTCACCTGGA      1321 _ C      II
                        TGA CTA CTTCACCTGG
                        III III IIIIIIIIII
                        ACT GGT GAAGTGGACC
                          C  C    TI
GAM101 BAZ2A         CTACAGCTGCACTTGTGGAACATCA 1319 TAC T  C__      I
                          CT CAC  TGGAACATC
                          II III  IIIIIIIII
                          GA GTG  ACCTTGTAG
                          C__ C AAC      I
GAM101 CPO          ACTA---TCACCTGGAGCA        1318 CCT      AC
                        ACTA  TCACCTGGA
                        IIII  IIIIIIIII
                        TGAT  AGTGGACCT
                           ___     CG
GAM101 DPP4          TGCCT-CTTTCACTAGGAACATCA  1326 GA_ ACC    CT      I
                        CT  TTCAC GGAACATC
                        II  IIIII IIIIIIII
</pre>

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                        GA   AAGTG  CCTTGTAG
                      ACG GA_    AT      I
GAM101 DUOX1        TGACTATGGCCACCTGGAACA   1324    CCT        I
                      GACTA  TCACCTGGAAC
                      |||||  ||||||||||
                      CTGAT  GGTGGACCTTG
                         ACC         I
GAM101 EIF4G2      TACCTTCACCGAGAAC-TCA    1320 _      T   ATCI
                       ACCTTCACC GGAAC
                       ||||||||| |||||
                       TGGAAGTGG TCTTG
                        A    C   AGII
GAM101 GNAS        TGACTTTGTCCACCTGGAAC    1323   ACC         I
                       GACT  TTCACCTGGAA
                       ||||  ||||||||||
                       CTGA  AGGTGGACCTT
                         AAC          I
GAM101 MGAM         TGATTAGCTTCAAGACCTGGAAC  1322 GACTAC  ___     I
                        CTTC  ACCTGGAA
                        ||||  ||||||||
                        GAAG  TGGACCTT
                      ATC___   TTC      I
GAM101 PCDH11Y       ACATGCACCTGGAAAACCA    1317 ACCTT      C  II
                        CACCTGGAA ATC
                        ||||||||| |||
                        GTGGACCTT TGG
                      TGTAC      T  TI
GAM101 SLC21A3      TGACTGACG-CACCTGGAAAATC  1325 _  _ CTT      CATI
                        GACT AC  CACCTGGAA
                        |||| ||  ||||||||||
                        CTGA TG  GTGGACCTT
                        A   C C__        TTAI
GAM102 ANKRD3       TGAGCCAGCTTCACCTGGA    1321  _ C        ACATC
                       TGA CTA CTTCACCTGGA
                       ||| ||| ||||||||||
                       ACT GGT GAAGTGGACCT
                         C  C       IIIAC
GAM102 BAZ2A        CTACAGCTGCACTTGTGGAACATCA 1319 TGACTAC T  C__       II
                        CT CAC  TGGAACATCA
                        || |||  ||||||||||
                        GA GTG  ACCTTGTAGT
                      GTC____  C  AAC       GT
GAM102 CPO        ACTA---TCACCTGGAGCA    1318 TGACTACCT      A
                        TCACCTGGA CA
                        ||||||||| ||
                        AGTGGACCT GT
                      AT_____         C
GAM102 DPP4       TGCCT-CTTTCACTAGGAACATCA  1326 TGA ACC    CT      I
                       CT  TTCAC  GGAACATCA
                       ||  |||||  ||||||||||
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                        GA   AAGTG  CCTTGTAGT
                       ACG  GA_    AT        I
GAM102 DUOX1          TGACTATGGCCACCTGGAACA   1324    CCT        TCA
                       TGACTA  TCACCTGGAACA
                       IIIIII  IIIIIIIIIIII
                       ACTGAT  GGTGGACCTTGT
                        ACC          III
GAM102 EIF4G2        TACCTTCACCGAGAAC-TCA    1320 TGACTACC    T  A
                       TTCACC GGAAC TC
                       IIIIII IIIII II
                       AAGTGG TCTTG AG
                       _____       C    _
GAM102 GNAS          TGACTTTGTCCACCTGGAAC    1323    ACC        ATC
                       TGACT  TTCACCTGGAAC
                       IIIII  IIIIIIIIIIII
                       ACTGA  AGGTGGACCTTG
                        AAC          III
GAM102 MGAM          TGATTAGCTTCAAGACCTGGAAC 1322  C C  ___       ATCAI
                       TGA TA CTTC  ACCTGGAAC
                       III II IIII  IIIIIIIII
                       ACT AT GAAG  TGGACCTTG
                        A  C  TTC    IIIAC
GAM102 SLC21A3       TGACTGACG-CACCTGGAAAATC  1325    _ CTT     C  A
                       TGACT AC  CACCTGGAA ATC
                       IIIII II  IIIIIIIII III
                       ACTGA TG  GTGGACCTT TAG
                        C  C__    T  I
GAM103 ACTB         CAAGGGACTTCCTGTAACAATGCAT 1345 AAGG       ____     C  I
                       GACTTCT   GCAAT CA
                       IIIIIII   IIIII II
                       CTGAAGG   TGTTA GT
                        ____       ACAT    C  I
GAM103 ACTB         CAAGGGACTTCCTGTAACAATGCAT 1345 TACA        ____      C  GII
                       AGGGACTTCT   GCAAT CAT
                       IIIIIIIIII   IIIII III
                       TCCCTGAAGG   TGTTA GTA
                        ____         ACAT   C  GAI
GAM103 COL9A1        CAAGTAGGACTTCTGTAATC    1343 CAA__        CAATIII
                       GGGACTTCTG
                       IIIIIIIIII
                       TCCTGAAGAC
                       GTTCA        ATTAGII
GAM103 COL9A1        CAAGTAGGACTTCTGTAATC    1343 TACAA      C   CAT
                       GGGACTTCTG AATC
                       IIIIIIIIII IIII
                       TCCTGAAGAC TTAG
                        TCA__      A  TAI
GAM103 HK1          AACGCACTGTCCTTGCAATCCA   1339 AAGGGA____   C     III
                       CTT TGCAATCC
                       III IIIIIIII
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```
                              GGA ACGTTAGG
                       TTGCGTGACA  _        TII
GAM103 HK1             AACGCACTGTCCTTGCAATCCA   1339 TACAAG G  _  __        TG
                          G ACT TCT  GCAATCCA
                          I III III  IIIIIIII
                          C TGA AGG  CGTTAGGT
                       _____G   C   AA      TG
GAM103 INHBB           ACATGGGCAACTTCTGCAA    1340 A  __        III
                          ACA GGG  ACTTCTGCA
                          III III  IIIIIIIII
                          TGT CCC  TGAAGACGT
                            A  GT        TII
GAM103 INHBB           ACATGGGCAACTTCTGCAA        1340 TACAA  __        TCCAT
                            GGG  ACTTCTGCAA
                            III  IIIIIIIIII
                            CCC  TGAAGACGTT
                       GTA__  GT        TIIIG
GAM103 KIF5C           AAGTGGATCTTCTGCAA-CCAT    1338 TACAAG  _     T  G
                            GGA CTTCTGCAA CCAT
                            III IIIIIIIII IIII
                            CCT GAAGACGTT GGTA
                          A_____ A      _  G
GAM103 KIF5C           AAGTGGATCTTCTGCAA-CCAT    1338 AG  _      T  I
                            GGA CTTCTGCAA CCA
                            III IIIIIIIII III
                            CCT GAAGACGTT GGT
                          CA  A       _  I
GAM103 NPTX2           ACAAGGGACATGGCCACTCCA    1342       TTCT AA_  I
                          CAAGGGAC  GC  TCC
                          IIIIIIII  II  III
                          GTTCCCTG  CG  AGG
                           TAC_ GTG  I
GAM103 NPTX2           ACAAGGGACATGGCCACTCCA    1342 TA      TTCT AA_   TG
                          CAAGGGAC  GC  TCCA
                          IIIIIIII  II  IIII
                          GTTCCCTG  CG  AGGT
                          __      TAC_ GTG  CI
GAM103 PCDHB1          ACAAGCGCGCTCTCTGCAATC    1341     GGA_ _        III
                          ACAAG   CT TCTGCAAT
                          IIIII   II IIIIIIIII
                          TGTTC   GA AGACGTTA
                          GCGC  G        GII
GAM103 PCDHB1          ACAAGCGCGCTCTCTGCAATC    1341 TA   GGA_ _        CATG
                          CAAG   CT TCTGCAATC
                          IIII   II IIIIIIIIII
                          GTTC   GA AGACGTTAG
                          __   GCGC  G        TIII
GAM103 RUNX1          CAAGGCAGAAATCTGCAATCC    1344   __ CT        III
                          CAAGG GA TCTGCAATC
                          IIIII II IIIIIIIII
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                        GTTCC  CT AGACGTTAG
                         GT  TT      GII
GAM103  RUNX1        CAAGGCAGAAATCTGCAATCC    1344 TACAAG  CT        ATG
                        GGA  TCTGCAATCC
                        III  IIIIIIIIII
                        TCT  AGACGTTAGG
                       TCCG__  TT      ATI
GAM103  TIAL1        TATAAGG-ACTTCTGTCACATC    1346 ACA         _ ATI
                        AGGGACTTCTG CA
                        IIIIIIIIIIII II
                        TTCCTGAAGAC GT
                        A__      A GTA
GAM103  TIAL1        TATAAGG-ACTTCTGTCACATC    1346 TACA        _ _  CATG
                        AGGGACTTCTG CA ATC
                        IIIIIIIIIIII II III
                        TTCCTGAAGAC GT TAG
                       ATA_       A G  IIIG
GAM104  AQP1         CCTCCGCCCGCCCCTGCCCCTGC   1369 __    CA        I
                        CTGCCC GCCCCTGCCTCTG
                        IIIIII IIIIIIIIIIIII
                        GGCGGG CGGGGACGGGGAC
                         GA       __        I
GAM104  AQP1         CCTCCGCCCGCCCCTGCCCCTGC   1369 AC    CA        I
                        CTGCCC GCCCCTGCCTCTGC
                        IIIIII IIIIIIIIIIIIII
                        GGCGGG CGGGGACGGGGACG
                         GA       __        G
GAM104  AQP6         GCCCCTGCCCCTGCCCCTG    1384    A       II
                        GCCCC GCCCCTGCCTCT
                        IIIII IIIIIIIIIII
                        CGGGG CGGGGACGGGGA
                            A       CI
GAM104  AQP6         GCCCCTGCCCCTGCCCCTG    1384 AC    A      C G
                        CTGCCCC GCCCCTGC TCT
                        IIIIIII IIIIIIII III
                        GACGGGG CGGGGACG AGG
                         __      A    _ I
GAM104  AQP6         GCTCC-GCCCCTGCCCCTGC   1388 ____    A      CTCTI
                        GCCCC GCCCCTGC
                        IIIII IIIIIIII
                        CGGGG CGGGGACG
                       GAGG    A      IIITC
GAM104  AQP6         GCTCC-GCCCCTGCCCCTGC   1388 ACCT    A         G
                        GCCCC GCCCCTGCCTCT
                        IIIII IIIIIIIIIIII
                        CGGGG CGGGGACGGGGA
                       G___    A      I
GAM104  AVPR2        CCTGGCCCCAGCCTGGTCCTTCCT  1358 _    ____  G IIIA
                        CCTG CCCCAGCC  CCT CC
                        IIII IIIIIIII   III II
```

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                                    GGAC GGGGTCGG   GGA GG
                                      C     ACCA  A  AIII
GAM104  AVPR2          CCTGGCCCCAGCCTGGTCCTTCCT  1358 ACCT       ____  G  CTGCI
                                    GCCCCAGCC   CCT CCT
                                    |||||||||   ||| |||
                                    CGGGGTCGG   GGA GGA
                                    GAC_        ACCA  A  AIIIC
GAM104  BLTR2          ACCTGCCCCA-CTCCTGGCCTC  1352       G C  _  TGC
                                    ACCTGCCCCA C CCTG CCTC
                                    ||||||||||| | |||| ||||
                                    TGGACGGGGT G GGAC GGAG
                                     _  A   C   III
GAM104  BLTR2          ACCTGCCCCA-CTCCTGGCCTC  1352       G C  _  I
                                    CCTGCCCCA C CCTG CCT
                                    |||||||| | |||| |||
                                    GGACGGGGT G GGAC GGA
                                     _  A   C   I
GAM104  BLTR2          CTTCCCTGCAGCC--TGCCTCT  1371 A_   CCC   CC    G
                                     CCTGC  AGCC  TGCCTCT
                                     |||||  ||||  |||||||
                                     GGACG  TCGG  ACGGAGA
                                     AG    ___   __     A
GAM104  BLTR2          CTTCCCTGCAGCC--TGCCTCT  1371 TGC  A  C_    I
                                      CCC GC  CCTGCCTC
                                      ||| ||  ||||||||
                                      GGG CG  GGACGGAG
                                      AA_  A TC     I
GAM104  CKAP1          CCCGCCCTGCCCCCTGCCTCTG  1367    CAG      I
                                     CTGCCC CCCCTGCCTCT
                                     |||||| |||||||||||
                                     GGCGGG GGGGACGGAGA
                                       ACG        I
GAM104  CKAP1          CCCGCCCTGCCCCCTGCCTCTG  1367 AC    CAG       C
                                     CTGCCC CCCCTGCCTCTG
                                     |||||| ||||||||||||
                                     GGCGGG GGGGACGGAGAC
                                     __    ACG      A
GAM104  COMT           GCCCCAGCCCCAGTGCCTC   1383        __   III
                                     GCCCCAGCCCC TGCCT
                                     ||||||||||| |||||
                                     CGGGGTCGGGG ACGGA
                                       TC   GII
GAM104  COMT           GCCCCAGCCCCAGTGCCTC   1383 ACCT    CCCC   TG
                                     GCCCCAG  TGCCTC
                                     |||||||  ||||||
                                     CGGGGTC  ACGGAG
                                     GT__    ____    TC
GAM104  CTSF           TGCCCCAGCCCAGTGCCCTCTGC  1390 ACCTGC      C_  _   I
                                     CCCAGCCC TGCC TCTGC
                                     |||||||| |||| |||||
```

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                          GGGTCGGG ACGG AGACG
                          _____     TC  G    A
GAM104 CTSF       TGCCCCAGCCCAGTGCCCTCTGC  1390 GC     C_  _   I
                          CCCAGCCC TGCC TCTG
                          |||||||| |||| ||||
                          GGGTCGGG ACGG AGAC
                              __    TC  G   I
GAM104 DVL1       CCTGCCCCCACCCTGCCTC    1365       AGC     I
                          CTGCCCC CCCTGCCT
                          ||||||| ||||||||
                          GACGGGG GGGACGGA
                             GGT      I
GAM104 DVL1       CCTGCCCCCACCCTGCCTC    1365 AC    AGC       G
                          CTGCCCC CCCTGCCTCT
                          ||||||| |||||||||
                          GACGGGG GGGACGGAGG
                           __    GGT       I
GAM104 EGR4       CCTGCCCCAG--CCTGTCTCTG  1368       CC C  I
                          CCTGCCCCAGCC TG CTC
                          ||||||||||| || |||
                          GGACGGGGTCGG AC GAG
                             __ A  A
GAM104 EGR4       CCTGCCCCAG--CCTGTCTCTG  1368 AC     CC C
                          CTGCCCCAGCC TG CTCTG
                          ||||||||||| || |||||
                          GACGGGGTCGG AC GAGAC
                           __     __ A
GAM104 EIF4G1     CCTGCCCCAGCTCCCACCCT    1362       C TG II
                          CCTGCCCCAGC CC CC
                          ||||||||||| || ||
                          GGACGGGGTCG GG GG
                           A GT GA
GAM104 EIF4G1     CCTGCCCCAGCTCCCACCCT    1362 AC     C TG  CTG
                          CTGCCCCAGC CC CCT
                          |||||||||| || |||
                          GACGGGGTCG GG GGG
                           __     A GT  AAI
GAM104 EIF4G1     GCCCCAAGCCATCCTGCCTCT   1382     _  __      III
                          GCCCCA GCC CCTGCCTC
                          |||||| ||| |||||||||
                          CGGGGT CGG GGACGGAG
                            T  TA    AII
GAM104 EIF4G1     GCCCCAAGCCATCCTGCCTCT   1382 ACCTGCCCC  __     GC
                          AGCC CCTGCCTCT
                          |||| |||||||||
                          TCGG GGACGGAGA
                          GT_____   TA    AG
GAM104 FOXE3      CCTCTCCCAGCCCCCTTACTCTG  1361 ACCTGC     GC_  CI
                          CCCAGCCCCT CTCTG
                          |||||||||| |||||
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                        GGGTCGGGGG  GAGAC
                        GAGA__         AAT    AI
GAM104  FOXE3           CCTCTCCCAGCCCCCTTACTCTG  1361 CTGC       GC_    I
                        CCCAGCCCCT  CTCT
                        ||||||||||  ||||
                        GGGTCGGGGG  GAGA
                        AGA_         AAT   I
GAM104  GIPR            ACTTGCTCCTGCAGCCCCTGCCACCGC1349 ___     CCC        T  I
                        CCTGC  AGCCCCTGCC  CTG
                        |||||  |||||||||| |||
                        GGACG  TCGGGGACGG  GGC
                        CGA      ___         T   I
GAM104  GIPR            ACTTGCTCCTGCAGCCCCTGCCACCGC1349 A_____      CCC       T   III
                        CCTGC  AGCCCCTGCC  CTGC
                        |||||  |||||||||| ||||
                        GGACG  TCGGGGACGG  GGCG
                        TGAACGA      ___         T   III
GAM104  H1F0            ACCGGGCTCTGCCTCTGCCTCTGC  1354   T_  CCCA  C         I
                        ACC  GC   GCC  CTGCCTCTGC
                        |||  ||   |||  ||||||||||
                        TGG  CG   CGG  GACGGAGACG
                        CC  AGA_  A          I
GAM104  H1F0            ACCGGGCTCTGCCTCTGCCTCTGC  1354 CCTGCCCCA  C        I
                        GCC  CTGCCTCTG
                        |||  |||||||||
                        CGG  GACGGAGAC
                        GGCCCGAGA  A          I
GAM104  H1F0            CCCAGCCCC-GCCGGTCTG       1356        T  TCTII
                        CCCAGCCCC  GCC
                        ||||||||| |||
                        GGGTCGGGG  CGG
                        _  CCAGA
GAM104  H1F0            CTGCCTCTGCCTCTGCCTCTGC    1380     CCA  C         I
                        TGCC  GCC  CTGCCTCTG
                        ||||  |||  |||||||||
                        ACGG  CGG  GACGGAGAC
                        AGA  A       I
GAM104  H1F0            CTGCCTCTGCCTCTGCCTCTGC    1380 ACCT  CCA  C
                        GCC  GCC  CTGCCTCTGC
                        |||  |||  ||||||||||
                        CGG  CGG  GACGGAGACG
                        ____  AGA  A
GAM104  H1F0            GCACCGGGCTCTGCCTCTGC      1385 ACCTGCCCCA  C       G
                        GCC  CTGCCTCT
                        |||  ||||||||
                        CGG  GACGGAGA
                        GCCCGAGA__  A    I
GAM104  H1F0            GCACCGGGCTCTGCCTCTGC      1385 C_  CA  CC          I
                        CC  GC  CTGCCTCTG
                        ||  ||  |||||||||
```

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                              GG  CG  DACGGAGAC
                              GT  CC  A_         I
GAM104 HD              ACCAGCCC--GCCCCTGCCCCCGC  1353  T   CA
                              ACC GCCC  GCCCCTGCCTCTGC
                              ||| |||| ||||||||||||
                              TGG CGGG  CGGGGACGGGGGCG
                               T    __
GAM104 HD              ACCAGCCC--GCCCCTGCCCCCGC  1353  T   CA          I
                              ACC GCCC  GCCCCTGCCTCT
                              ||| |||| |||||||||||
                              TGG CGGG  CGGGGACGGGGG
                               T   __        C
GAM104 KCNK4            CCGGCCCTCAGCCCCTGTCT      1360  T   _       CCII
                              CC GCCC CAGCCCCTG
                              || |||| |||||||||
                              GG CGGG GTCGGGGAC
                               C  A      AGAI
GAM104 KCNK4            CCGGCCCTCAGCCCCTGTCT      1360 ACCT   _      CC
                              GCCC CAGCCCCTG  TCTG
                              |||| ||||||||| ||||
                              CGGG GTCGGGGAC AGAC
                             GC__   A       __
GAM104 LZTR1           CTGCCCCAGCTCCTGCTCTCT      1375 ACCT    C   _  GC
                              GCCCCAGC CCTGC CTCT
                              |||||||| ||||| ||||
                              CGGGGTCG GGACG GAGA
                             ____       A  A  GA
GAM104 LZTR1           CTGCCCCAGCTCCTGCTCTCT      1375 T     C   _  I
                              GCCCCAGC CCTGC CTC
                              |||||||| ||||| |||
                              CGGGGTCG GGACG GAG
                             _      A   A  I
GAM104 MAPT           CTGCCC-AGCCCCTGCCTCGGC      1378 _   C       TGI
                              TGCCC AGCCCCTGCCTC
                              ||||| |||||||||||||
                              ACGGG TCGGGGACGGAG
                             G   _        CCI
GAM104 MAPT           CTGCCC-AGCCCCTGCCTCGGC      1378 ACCTGC             T
                              CCCAGCCCCTGCCTC GC
                              ||||||||||||||| ||
                              GGGTCGGGGACGGAG CG
                             C_____          C
GAM104 MECP2           CTGCCCCAG-CCCTGGTCCTC      1374           CTG_ II
                              CTGCCCCAGCCC  CCT
                              |||||||||||  |||
                              GACGGGGTCGGG  GGA
                                 ACCA  GI
GAM104 MECP2           CTGCCCCAG-CCCTGGTCCTC      1374 ACCT       CTG_
                              GCCCCAGCCC  CCTCTG
                              |||||||||  ||||||
```

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                          CGGGGTCGGG   GGAGGC
                               ACCA
GAM104 MMP2          GCCCCAGCCCCGCCGCCGC   1387          T  I
                        CCCCAGCCCCTGCC CTG
                        |||||||||||| |||
                        GGGGTCGGGGGCGG GGC
                             C  I
GAM104 MMP2          GCCCCAGCCCCGCCGCCGC   1387 ACCTGCCC        T
                          CAGCCCCTGCC CTG
                          |||||||||| |||
                          GTCGGGGGCGG GGC
                                   C
GAM104 MYO1E          ACCAGCCCCCAGCCCCTGAC-CTGC 1350  T   _     C T  I
                        ACC GCCCC AGCCCCTG C CTGC
                        ||| ||||| ||||||||| | ||||
                        TGG CGGGG TCGGGGAC G GACG
                         T   G    T_   I
GAM104 MYO1E          ACCAGCCCCCAGCCCCTGAC-CTGC 1350  T    _     _   CTGI
                        CC GCCCC AGCCCCTG CCT
                        || ||||| |||||||| |||
                        GG CGGGG TCGGGGAC GGA
                         T   G     T CIII
GAM104 NCOA6IP          CTGCCCCTGCCCCTGCCCCCGC   1379     A       I
                          TGCCCC GCCCCTGCCTCTG
                          |||||| ||||||||||||
                          ACGGGG CGGGGACGGGGGC
                             A      I
GAM104 NCOA6IP          CTGCCCCTGCCCCTGCCCCCGC   1379 ACCT   A
                            GCCCC GCCCCTGCCTCTGC
                            ||||| |||||||||||||
                            CGGGG CGGGGACGGGGGCG
                                A
GAM104 OFD1          CCTGCCCTCAGAACCCTGCCTCTG  1359 AC    _  C_      CI
                        CTGCCC CAG  CCCTGCCTCTG
                        |||||| |||  ||||||||||||
                        GACGGG GTC  GGGACGGAGAC
                         __    A TT       AI
GAM104 OFD1          CCTGCCCTCAGAACCCTGCCTCTG  1359 CT  _  C_      I
                        GCCC CAG  CCCTGCCTCT
                        |||| |||  |||||||||||
                        CGGG GTC  GGGACGGAGA
                         __    A TT       I
GAM104 PCDHGA1          CCTGCCCTAGCTCCCTGCCTC   1363 AC    C  _      GC
                        CTGCCC AGC CCCTGCCTCT
                        |||||| ||| |||||||||||
                        GACGGG TCG GGGACGGAGG
                         __    A A      II
GAM104 PCDHGA1          CCTGCCCTAGCTCCCTGCCTC   1363 C   C  _    I
                         TGCCC AGC CCCTGCCT
                         ||||| ||| |||||||||
```

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                              ACGGG TCG GGGACGGA
                               _   A   A     I
GAM104  PCDHGA10      CCTGCCCTAGCTCCCTGCCTC   1363 AC    C  _       GC
                         CTGCCC AGC CCCTGCCTCT
                         |||||| ||| ||||||||||
                         GACGGG TCG GGGACGGAGG
                           __    A   A      II
GAM104  PCDHGA10      CCTGCCCTAGCTCCCTGCCTC   1363 C    C  _      I
                          TGCCC AGC CCCTGCCT
                          ||||| ||| |||||||||
                          ACGGG TCG GGGACGGA
                           _   A   A     I
GAM104  PCDHGA11      CCTGCCCTAGCTCCCTGCCTC   1363 AC    C  _       GC
                         CTGCCC AGC CCCTGCCTCT
                         |||||| ||| ||||||||||
                         GACGGG TCG GGGACGGAGG
                           __    A   A      II
GAM104  PCDHGA11      CCTGCCCTAGCTCCCTGCCTC   1363 C    C  _      I
                          TGCCC AGC CCCTGCCT
                          ||||| ||| |||||||||
                          ACGGG TCG GGGACGGA
                            _   A   A     I
GAM104  PCDHGA12      CCTGCCCTAGCTCCCTGCCTC   1363 AC    C  _       GC
                         CTGCCC AGC CCCTGCCTCT
                         |||||| ||| ||||||||||
                         GACGGG TCG GGGACGGAGG
                           __    A   A      II
GAM104  PCDHGA12      CCTGCCCTAGCTCCCTGCCTC   1363 C    C  _      I
                          TGCCC AGC CCCTGCCT
                          ||||| ||| |||||||||
                          ACGGG TCG GGGACGGA
                            _   A   A     I
GAM104  PCDHGA2       CCTGCCCTAGCTCCCTGCCTC   1363 AC    C  _       GC
                         CTGCCC AGC CCCTGCCTCT
                         |||||| ||| ||||||||||
                         GACGGG TCG GGGACGGAGG
                           __    A   A      II
GAM104  PCDHGA2       CCTGCCCTAGCTCCCTGCCTC   1363 C    C  _      I
                          TGCCC AGC CCCTGCCT
                          ||||| ||| |||||||||
                          ACGGG TCG GGGACGGA
                            _   A   A     I
GAM104  PCDHGA3       CCTGCCCTAGCTCCCTGCCTC   1363 AC    C  _       GC
                         CTGCCC AGC CCCTGCCTCT
                         |||||| ||| ||||||||||
                         GACGGG TCG GGGACGGAGG
                           __    A   A      II
GAM104  PCDHGA3       CCTGCCCTAGCTCCCTGCCTC   1363 C    C  _      I
                          TGCCC AGC CCCTGCCT
                          ||||| ||| |||||||||
```

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                              ACGGG TCG GGGACGGA
                               _    A   A      I
GAM104  PCDHGA4         CCTGCCCTAGCTCCCTGCCTC    1363 AC     C    _        GC
                          CTGCCC AGC CCCTGCCTCT
                          ||||||  |||  |||||||||||
                          GACGGG TCG GGGACGGAGG
                           __     A   A       II
GAM104  PCDHGA4         CCTGCCCTAGCTCCCTGCCTC    1363 C     C    _      I
                           TGCCC AGC CCCTGCCT
                           |||||  |||  ||||||||
                          ACGGG TCG GGGACGGA
                           _    A   A      I
GAM104  PCDHGA5         CCTGCCCTAGCTCCCTGCCTC    1363 AC     C    _        GC
                          CTGCCC AGC CCCTGCCTCT
                          ||||||  |||  |||||||||||
                          GACGGG TCG GGGACGGAGG
                           __     A   A       II
GAM104  PCDHGA5         CCTGCCCTAGCTCCCTGCCTC    1363 C     C    _      I
                           TGCCC AGC CCCTGCCT
                           |||||  |||  ||||||||
                          ACGGG TCG GGGACGGA
                           _    A   A      I
GAM104  PCDHGA6         CCTGCCCTAGCTCCCTGCCTC    1363 AC     C    _        GC
                          CTGCCC AGC CCCTGCCTCT
                          ||||||  |||  |||||||||||
                          GACGGG TCG GGGACGGAGG
                           __     A   A       II
GAM104  PCDHGA6         CCTGCCCTAGCTCCCTGCCTC    1363 C     C    _      I
                           TGCCC AGC CCCTGCCT
                           |||||  |||  |||||||||
                          ACGGG TCG GGGACGGA
                           _    A   A      I
GAM104  PCDHGA7         CCTGCCCTAGCTCCCTGCCTC    1363 AC     C    _        GC
                          CTGCCC AGC CCCTGCCTCT
                          ||||||  |||  |||||||||||
                          GACGGG TCG GGGACGGAGG
                           __     A   A       II
GAM104  PCDHGA7         CCTGCCCTAGCTCCCTGCCTC    1363 C     C    _      I
                           TGCCC AGC CCCTGCCT
                           |||||  |||  |||||||||
                          ACGGG TCG GGGACGGA
                           _    A   A      I
GAM104  PCDHGA8         CCTGCCCTAGCTCCCTGCCTC    1363 AC     C    _        GC
                          CTGCCC AGC CCCTGCCTCT
                          ||||||  |||  |||||||||||
                          GACGGG TCG GGGACGGAGG
                           __     A   A       II
GAM104  PCDHGA8         CCTGCCCTAGCTCCCTGCCTC    1363 C     C    _      I
                           TGCCC AGC CCCTGCCT
                           |||||  |||  |||||||||
```

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                              ACGGG TCG GGGACGGA
                              _    A A     I
GAM104 PCDHGA9        CCTGCCCTAGCTCCCTGCCTC    1363 AC   C  _      GC
                         CTGCCC AGC CCCTGCCTCT
                         ||||||| ||| |||||||||||
                         GACGGG TCG GGGACGGAGG
                             __    A A     II
GAM104 PCDHGA9        CCTGCCCTAGCTCCCTGCCTC    1363 C    C  _      I
                           TGCCC AGC CCCTGCCT
                           ||||| ||| |||||||||
                           ACGGG TCG GGGACGGA
                           _    A A     I
GAM104 PCDHGB1        CCTGCCCTAGCTCCCTGCCTC    1363 AC   C  _      GC
                         CTGCCC AGC CCCTGCCTCT
                         ||||||| ||| |||||||||||
                         GACGGG TCG GGGACGGAGG
                             __    A A     II
GAM104 PCDHGB1        CCTGCCCTAGCTCCCTGCCTC    1363 C    C  _      I
                           TGCCC AGC CCCTGCCT
                           ||||| ||| |||||||||
                           ACGGG TCG GGGACGGA
                           _    A A     I
GAM104 PCDHGB2        CCTGCCCTAGCTCCCTGCCTC    1363 AC   C  _      GC
                          CTGCCC AGC CCCTGCCTCT
                          ||||||| ||| |||||||||||
                          GACGGG TCG GGGACGGAGG
                             __    A A     II
GAM104 PCDHGB2        CCTGCCCTAGCTCCCTGCCTC    1363 C    C  _      I
                          TGCCC AGC CCCTGCCT
                          ||||| ||| |||||||||
                          ACGGG TCG GGGACGGA
                          _    A A     I
GAM104 PCDHGB3        CCTGCCCTAGCTCCCTGCCTC    1363 AC   C  _      GC
                         CTGCCC AGC CCCTGCCTCT
                         ||||||| ||| |||||||||||
                         GACGGG TCG GGGACGGAGG
                             __    A A     II
GAM104 PCDHGB3        CCTGCCCTAGCTCCCTGCCTC    1363 C    C  _      I
                          TGCCC AGC CCCTGCCT
                          ||||| ||| |||||||||
                          ACGGG TCG GGGACGGA
                          _    A A     I
GAM104 PCDHGB4        CCTGCCCTAGCTCCCTGCCTC    1363 AC   C  _      GC
                          CTGCCC AGC CCCTGCCTCT
                          ||||||| ||| |||||||||||
                          GACGGG TCG GGGACGGAGG
                             __    A A     II
GAM104 PCDHGB4        CCTGCCCTAGCTCCCTGCCTC    1363 C    C  _      I
                          TGCCC AGC CCCTGCCT
                          ||||| ||| |||||||||
```

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                    ACGGG TCG GGGACGGA
                      _   A   A      I
GAM104  PCDHGB5     CCTGCCCTAGCTCCCTGCCTC     1363 AC    C   _      GC
                    CTGCCC AGC CCCTGCCTCT
                    ||||| ||| ||||||||||
                    GACGGG TCG GGGACGGAGG
                      __   A   A       II
GAM104  PCDHGB5     CCTGCCCTAGCTCCCTGCCTC     1363 C    C   _     I
                    TGCCC AGC CCCTGCCT
                    ||||| ||| |||||||||
                    ACGGG TCG GGGACGGA
                      _   A   A      I
GAM104  PCDHGB6     CCTGCCCTAGCTCCCTGCCTC     1363 AC    C   _      GC
                    CTGCCC AGC CCCTGCCTCT
                    ||||| ||| ||||||||||
                    GACGGG TCG GGGACGGAGG
                      __   A   A       II
GAM104  PCDHGB6     CCTGCCCTAGCTCCCTGCCTC     1363 C    C   _     I
                    TGCCC AGC CCCTGCCT
                    ||||| ||| |||||||||
                    ACGGG TCG GGGACGGA
                      _   A   A      I
GAM104  PCDHGB7     CCTGCCCTAGCTCCCTGCCTC     1363 AC    C   _      GC
                    CTGCCC AGC CCCTGCCTCT
                    ||||| ||| ||||||||||
                    GACGGG TCG GGGACGGAGG
                      __   A   A       II
GAM104  PCDHGB7     CCTGCCCTAGCTCCCTGCCTC     1363 C    C   _     I
                    TGCCC AGC CCCTGCCT
                    ||||| ||| |||||||||
                    ACGGG TCG GGGACGGA
                      _   A   A      I
GAM104  PCDHGC3     CCTGCCCTAGCTCCCTGCCTC     1363 AC    C   _      GC
                    CTGCCC AGC CCCTGCCTCT
                    ||||| ||| ||||||||||
                    GACGGG TCG GGGACGGAGG
                      __   A   A       II
GAM104  PCDHGC3     CCTGCCCTAGCTCCCTGCCTC     1363 C    C   _     I
                    TGCCC AGC CCCTGCCT
                    ||||| ||| |||||||||
                    ACGGG TCG GGGACGGA
                      _   A   A      I
GAM104  PCDHGC4     CCTGCCCTAGCTCCCTGCCTC     1363 AC    C   _      GC
                    CTGCCC AGC CCCTGCCTCT
                    ||||| ||| ||||||||||
                    GACGGG TCG GGGACGGAGG
                      __   A   A       II
GAM104  PCDHGC4     CCTGCCCTAGCTCCCTGCCTC     1363 C    C   _     I
                    TGCCC AGC CCCTGCCT
                    ||||| ||| |||||||||
```

```
                      ACGGG TCG GGGACGGA
                       _    A  A      I
GAM104  PCDHGC5        CCTGCCCTAGCTCCCTGCCTC    1363 AC    C  _       GC
                      CTGCCC AGC CCCTGCCTCT
                      |||||| ||| ||||||||||
                      GACGGG TCG GGGACGGAGG
                        __    A  A      II
GAM104  PCDHGC5        CCTGCCCTAGCTCCCTGCCTC    1363 C     C  _       I
                       TGCCC AGC CCCTGCCT
                       ||||| ||| ||||||||
                      ACGGG TCG GGGACGGA
                       _    A  A      I
GAM104  PODXL          CTTCCCCAGCCCCTCCCCCT     1377 ACCTG       G
                      CCCCAGCCCCT CCTCTG
                      ||||||||||| ||||||
                      GGGGTCGGGGA GGGGAT
                      A____        G
GAM104  PODXL          CTTCCCCAGCCCCTCCCCCT     1377 TG        G  I
                      CCCCAGCCCCT CCTC
                      ||||||||||| ||||
                      GGGGTCGGGGA GGGG
                      AA         G  I
GAM104  PPP2CA         ACCCGCCCCAGCCGGCTGCCGCT  1351          C_   T GCI
                      ACCTGCCCCAGCC CTGCC CT
                      ||||||||||||| |||||| ||
                      TGGGCGGGGTCGG GACGG GA
                        CC     C  III
GAM104  PPP2CA         ACCCGCCCCAGCCGGCTGCCGCT  1351 C        C_   TCI
                      CTGCCCCAGCC CTGCC
                      ||||||||||| |||||
                      GGCGGGGTCGG GACGG
                      _         CC   CGI
GAM104  PRX           CCCAGCCCCCTCAGCCTCTGC      1355          ___    III
                      CCCAGCCCCT GCCTCTG
                      |||||||||| |||||||
                      GGGTCGGGGG CGGAGAC
                       AGT      GII
GAM104  PRX           CCCAGCCCCCTCAGCCTCTGC      1355 ACCTG _    C    CT
                      CCC CAGCC CTGCCT GC
                      ||| ||||| |||||| ||
                      GGG GTCGG GACGGA CG
                      G____      A  A   AT
GAM104  PRX           CCT-CCCCAGCCCCTTTGGCCTCAGC 1364 ACCTG        ___   T II
                      CCCCAGCCCCT GCCTC GC
                      |||||||||| ||||| ||
                      GGGGTCGGGGA CGGAG CG
                      GA___        AAC  T GI
GAM104  PRX           CCT-CCCCAGCCCCTTTGGCCTCAGC 1364 G           ___     TGI
                      CCCCAGCCCCT GCCTC
                      |||||||||| |||||
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                              GGGGTCGGGGA  CGGAG
                               _        AAC    III
GAM104 RARG              GCCACAGCCCCTGCCCATGC     1386 ACCTGCCC        C
                              CAGCCCCTGCCT TG
                              |||||||||||| ||
                              GTCGGGGACGGG AC
                              _____          T
GAM104 RARG              GCCACAGCCCCTGCCCATGC     1386 C _        CTGI
                              CC CAGCCCCTGCCT
                              || ||||||||||||
                              GG GTCGGGGACGGG
                              _ T      TACI
GAM104 ROCK2            CCGGGCCCACCGCCTGCCTCT     1366 ACCT  CA  _       C
                              GCCC  GCC CCTGCCTCTG
                              ||||  ||| |||||||||
                              CGGG  TGG GGACGGAGAT
                          GCC_  __  C     I
GAM104 ROCK2            CCGGGCCCACCGCCTGCCTCT     1366 CT_  CA  _     I
                              GCCC  GCC CCTGCCTC
                              ||||  ||| ||||||||
                              CGGG  TGG GGACGGAG
                          GCC   __  C     I
GAM104 RYR3           TGCCCCAGCCTCCGGCGCCTCTGC  1389 ACCTGC    _ __      I
                              CCCAGCC CC TGCCTCTGC
                              ||||||| || |||||||||
                              GGGTCGG GG GCGGAGACG
                              _____      A CC      A
GAM104 RYR3           TGCCCCAGCCTCCGGCGCCTCTGC  1389 GCC     _ __     I
                              CCAGCC CC TGCCTCTG
                              |||||| || ||||||||
                              GGTCGG GG GCGGAGAC
                              ___     A CC     I
GAM104 SFN          CCCCAGCCCCAGGTGGCCTCAGC     1357      T____  TGIIIG
                              CCCCAGCCCC   GCCTC
                              ||||||||||   |||||
                              GGGGTCGGGG   CGGAG
                              TCCAC   TCGIII
GAM104 SFN          CCCCAGCCCCAGGTGGCCTCAGC     1357 ACCT     CC__  GC_   I
                              GCCCCAG  CCT CTCTGC
                              |||||||  ||| ||||||
                              CGGGGTC  GGA GAGACG
                              ____    CACC GTC    I
GAM104 SLC6A9          CTGACGCATCCCCTGCCTCT     1376 ACCT CCCAG        G
                              GC  CCCCTGCCTCT
                              ||  ||||||||||
                              CG  GGGGACGGAGA
                          CTG_ TA___      G
GAM104 SLC6A9          CTGACGCATCCCCTGCCTCT     1376 T___ CCCAG        I
                              GC  CCCCTGCCTC
                              ||  |||||||||
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                              CG    GGGGACGGAG
                            ACTG  TA___          I
GAM104  TEM5        CTGCCCCAGTTCCACCTGCCCTCT  1372 ACCT      __ _   _  GCI
                            GCCCCAG  CC CCTGCC TCT
                            ||||||| || |||||| |||
                            CGGGGTC  GG GGACGG AGA
                              ____      AA  T    G  GGI
GAM104  TEM5        CTGCCCCAGTTCCACCTGCCCTCT  1372 TGCC  __ _      CI
                            CCAG  CC CCTGCCT
                            |||| || ||||||||
                            GGTC  GG GGACGGG
                              ____     AA  T     AG
GAM104  TFAP4       CTGCCCCGGCTCCCTCCAGCC     1373    A _  GCIIIG
                            CTGCCCC GC CCCT
                            ||||||| || ||||
                            GACGGGG CG GGGA
                               C  A  GGTCGG
GAM104  TFAP4       CTGCCCCGGCTCCCTCCAGCC     1373 ACCT    A _  ___    TGC
                            GCCCC GC CCCT  GCCTC
                            ||||| || ||||  |||||
                            CGGGG CG GGGA  CGGGG
                              ____     C  A  GGT   III
GAM104  TRPV4       CCTGCCCCAGGCCC-G--TCTGC  1370 AC      C  TGCC
                            CTGCCCCAG CCC   TCTG
                            |||||||||| |||   ||||
                            GACGGGGTC GGG   AGAC
                              __       C  C___
GAM104  TRPV4       CCTGCCCCAGGCCC-G--TCTGC  1370           _ __  CTCI
                            CCTGCCCCAG CCC  CTGC
                            |||||||||| ||| ||||
                            GGACGGGGTC GGG  GACG
                               C  CA   IIIC
GAM104  VAV1        CTGTCACAGCCCCTGGCTCCGC    1381 ACCTGCCC      C
                            CAGCCCCTG CTCTGC
                            |||||||||| ||||||
                            GTCGGGGAC GAGGCG
                            CAGT____        C
GAM104  VAV1        CTGTCACAGCCCCTGGCTCCGC    1381 TGCCC    C  I
                            CAGCCCCTG CTCTG
                            |||||||||| |||||
                            GTCGGGGAC GAGGC
                            ACAGT      C  I
GAM105  ACVR1B      ACTTCTGGTTCTTCCGGGCCAC    1399        _____    IIIG
                            ACTTCTGG  CCGGGCCA
                            |||||||| |||||||||
                            TGAAGACC  GGCCCGGT
                             AAGAA    GIII
GAM105  ACVR1B      ACTTCTGGTTCTTCCGGGCCAC    1399 TAACAAC  GG     GG
                            TTCT CCGGGCCAC
                            |||| |||||||||
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                      AAGA  GGCCCGGTG
                   ACC____  A_      GA
GAM105 ATP6V0C        ACAGCTCCGCGCAGGGCCACGG    1398 CAAC    _ C     I
                      TTCTG GC GGGCCACG
                      |||||  ||  |||||||||
                      GAGGC CG CCCGGTGC
                   GTC_   G T      I
GAM105 ATP6V0C        ACAGCTCCGCGCAGGGCCACGG    1398 TAACAAC    _ C
                      TTCTG GC GGGCCACGG
                      |||||  ||  ||||||||||
                      GAGGC CG CCCGGTGCC
                   TC_____    G T
GAM105 ATSV        AACTGCTCCCACGGGCCACGG    1397 A__     GGC      I
                      CTTCT  CGGGCCACG
                      |||||  ||||||||||
                      GAGGG  GCCCGGTGC
                   GAC    T__      I
GAM105 ATSV        AACTGCTCCCACGGGCCACGG    1397 TAACAA    GGC
                      CTTCT  CGGGCCACGG
                      |||||  |||||||||||
                      GAGGG  GCCCGGTGCC
                   C_____    T__
GAM105 DGSI        AACAGCTTCTGGCCCAGGCC    1395    A       _  II
                      AACA CTTCTGGCC GGGC
                      |||| |||||||||| ||||
                      TTGT GAAGACCGG TCCG
                      C      G  GI
GAM105 DGSI        AACAGCTTCTGGCCCAGGCC    1395 TA A      _  ACG
                      ACA CTTCTGGCC GGGCC
                      ||| |||||||||| |||||
                      TGT GAAGACCGG TCCGG
                   __   C      G  AII
GAM105 INHBB       CAACTTCGAGACGTGGCCGGGCCA 1400        _____        IIIT
                      CAACTTC   TGGCCGGGCC  G
                      |||||||   |||||||||| |
                      GTTGAAG   ACCGGCCCGG  C
                      CTCTGC        TIII
GAM105 LFG         AACATCCACTGCAGCCGGGCCA   1394 ACAA T  __      I
                      CT CTG GCCGGGCC
                      || ||| |||||||||
                      GG GAC CGGCCCGG
                   TA__ T GT      I
GAM105 LFG         AACATCCACTGCAGCCGGGCCA   1394 TA A T  __      CGG
                      ACA CT CTG GCCGGGCCA
                      ||| || ||| |||||||||
                      TGT GG GAC CGGCCCGGT
                   __   A T GT      CII
GAM105 LYZ         TAAGAACTGAATGTGGCCGGGC   1402 C  TC___       CACGG
                      TAA AACT  TGGCCGGGC
                      ||| ||||   ||||||||||
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                                ATT TTGA   ACCGGCCCG
                                C   CTTAC      IIIGG
GAM105  LYZ             TAAGAACTGAATGTGGCCGGGC  1402  C  TC___       III
                                TAA AACT    TGGCCGGG
                                III IIII   IIIIIIIII
                                ATT TTGA   ACCGGCCC
                                C   CTTAC     GII
GAM105  PPID         AACATTTTACTTGGCCGGG-CACGG  1393 ACA___  TC     C  I
                                   ACT  TGGCCGGGC ACG
                                   III IIIIIIIIII III
                                   TGA  ACCGGCCCG TGC
                                GTAAAA  __     _   I
GAM105  PPID         AACATTTTACTTGGCCGGG-CACGG  1393 TAACA__  TC     C  I
                                   ACT  TGGCCGGGC ACGG
                                   III IIIIIIIIII IIII
                                   TGA  ACCGGCCCG TGCC
                                TGTAAAA  __     _   A
GAM105  RAD1          AACAACTTCTCGGCGGATCGCCA   1396 ACA     _  C  ___  I
                                   ACTTCT GGC GG  GCC
                                   IIIIII III II   III
                                   TGAAGA CCG CC  CGG
                                   ___   G _ TAG  I
GAM105  RAD1          AACAACTTCTCGGCGGATCGCCA   1396 TA      _  C  ___  CGGI
                                  ACAACTTCT GGC GG  GCCA
                                  IIIIIIIII III II  IIII
                                  TGTTGAAGA CCG CC  CGGT
                                  __       G _ TAG  TIII
GAM105  TBX1          CAACTGCCGGCCGGGCCGCGG     1401    T      A  I
                                   AACT CTGGCCGGGCC CG
                                   IIII IIIIIIIIIII II
                                   TTGA GGCCGGCCCGG GC
                                   C       C  I
GAM105  TBX1          CAACTGCCGGCCGGGCCGCGG     1401 TAACAA  T      A
                                   CT CTGGCCGGGCC CGG
                                   II IIIIIIIIIII III
                                   GA GGCCGGCCCGG GCC
                                   _____  C      C
GAM106  BRCA1          TGTCC-AACACCCACTCTCGGGTC  1410  G  G  T  G     I
                                   TG CC AAC CTCG TCTCGGGTC
                                   II II III IIII IIIIIIIII
                                   AC GG TTG GGGT AGAGCCCAG
                                   A _ T  G     I
GAM106  BRCA1          TGTCC-AACACCCACTCTCGGGTC  1410 GG_ G  T  G     I
                                   CC AAC CTCG TCTCGGGT
                                   II III IIII IIIIIIIII
                                   GG TTG GGGT AGAGCCCA
                                   ACA _ T  G     I
GAM106  CAPNS1          GGCCGCAACTCTCGG-GTCGG    1408  _      _  TCGI
                                   GCCG AACTCTCGG TC
                                   IIII IIIIIIIIII II
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                        CGGC TTGAGAGCC AG
                         G        C CIII
GAM106 CAPNS1           GGCCGCAACTCTCGG-GTCGG    1408 TG   _        TC    T
                        GCCG AACTCTCGG TCGGG
                        |||| ||||||||| |||||
                        CGGC TTGAGAGCC AGCCT
                        __   G        C_   I
GAM106 GAS7          CCCAACT---GGTCTCGGG      1406  G   CTC
                        CC AACT  GGTCTCGG
                        || ||||  ||||||||
                        GG TTGA  CCAGAGCC
                          G   ___
GAM106 GAS7          CCCAACT---GGTCTCGGG      1406 TGGCCGAACTCTC
                                GGTCTCGG
                                ||||||||
                                CCAGAGCC
                        TTGA_____
GAM106 SH3BP2      GAACT----GTCTCGGGTC    1407    CTCG
                        GAACT  GTCTCGGGT
                        |||||  |||||||||
                        CTTGA  CAGAGCCCA
                          _____
GAM106 TBX1           GGGCGA---CGCGGTCTCGGG    1409 _  C ACTCT        I
                        GGC GA   CGGTCTCG
                        ||| ||   ||||||||
                        CCG CT   GCCAGAGC
                        C  _ GC___       C
GAM106 TBX1           GGGCGA---CGCGGTCTCGGG    1409 T  C ACTCT
                        GGC GA   CGGTCTCGGG
                        ||| ||   ||||||||||
                        CCG CT   GCCAGAGCCC
                        _  _  GC___
GAM106 TNFRSF6B       CCGAACATCTTAGGGTCTCGGG    1405      _  C__      III
                        CCGAAC TCT  GGTCTCGG
                        |||||| |||  ||||||||
                        GGCTTG AGA  CCAGAGCC
                          T  ATC       CII
GAM106 TNFRSF6B       CCGAACATCTTAGGGTCTCGGG    1405 TGGCCG  _  C__       C
                        AAC TCT  GGTCTCGGGT
                        ||| |||  ||||||||||
                        TTG AGA  CCAGAGCCCG
                        _____  T  ATC       T
GAM107 ATRN          CTGAGGCCGGAGAAAGCTGT     1417 AGTTCTGA      T  _
                        GGCCGGAG AA CTGT
                        |||||||| || ||||
                        CCGGCCTC TT GACA
                        _____      T C
GAM107 AVPR2        GTTCTGAGGGCCTGGAGGTGA-TGTG 1419 AG        _  _   TAAC    II
                        TTCTGAGG CC GGAG   TGTG
                        |||||||| || ||||   ||||
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                        AAGACTCC GG CCTC   ACAC
                        __      C  A  CACT  GI
GAM107 BGN              AGCTCTGAGGCCAAGGGAACATGTG 1416        AGT _ II
                        AGTTCTGAGGCCGG  AAC TGTG
                        |||||||||||  ||| ||||
                        TCGAGACTCCGGTT  TTG ACAC
                              CCC  T  II
GAM107 BRCA2            AGTTCTTTTTGGCCGGAGTAAGCTG 1414      GA___        _ TGII
                        AGTTCT   GGCCGGAGTAA CTG
                        ||||||   |||||||||| |||
                        TCAAGA   CCGGCCTCATT GAC
                         AAAAA        C  IIIG
GAM107 CFTR            TTCTGAGGCAGAGGTAACTGT   1425 AGTT    C GA     G
                        CTGAGGC G GTAACTGT
                        ||||||| | |||||||||
                        GACTCCG C CATTGACA
                        ____       T TC     A
GAM107 DGCR2           AGTTCTGAGGCCTGGCAGGAA   1415         _ _ TAACTGTG
                        AGTTCTGAGGCC GG AG
                        |||||||||||| || ||
                        TCAAGACTCCGG CC TC
                          A  G  CTTIIIGT
GAM107 ECH1           GTTCGGA---CGGAGTAAC      1420    TGA C
                        GTTC  GG CGGAGTAA
                        ||||  || ||||||||
                        CAAG  CC GCCTCATT
                          ___  T
GAM107 ECH1           GTTCGGA---CGGAGTAAC      1420 GAGTTCTGA C
                          GG CGGAGTAAC
                          || |||||||||
                          CC GCCTCATTG
                        AG_____ T
GAM107 ECH1           GTTCGGA---CGGAGTAAC-GTG   1422 AGTTCTGA C      _
                          GG CGGAGTAAC TGT
                          || ||||||||| |||
                          CC GCCTCATTG ACG
                        AAG_____ T    C
GAM107 EZH1           TTCTGAGGCCAGAGAAACAGT    1426 AGTT        T  T G
                        CTGAGGCCGGAG AAC GT
                        ||||||||||| ||| ||
                        GACTCCGGTCTC TTG CA
                        ___         T  T G
GAM107 MX2           AGTATCTTAGGACACTGTAACTGTG 1413 _ G  C GA      II
                        AGT TCT AGG CG  GTAACTGTG
                        ||| ||| ||| ||  |||||||||
                        TCA AGA TCC GT  CATTGACAC
                         T  A  T GA      II
GAM107 PODXL          TTCTGAGGCGCACAGT--CTGTG   1424 AGTT    _ G  AA
                        CTGAGGC CG AGT  CTGTG
                        ||||||| || |||  |||||
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                        GACTCCG GT TCA  GACAC
                        ____        C G  __
GAM107 PTER             CTG-GGTCTGAGTAACTGT     1418 AGTTCTGAGGCCG
                            GAGTAACTG
                            |||||||||
                            CTCATTGAC
                        CAGA_____
GAM107 PTP4A2           TTCTGAGGCC--AGTCTCGGTG   1427 AGTT       AGTAAC
                            CTGAGGCCGG    TGT
                            |||||||||| |||
                            GACTCCGGTC    ACA
                        ____          AGAGCC
GAM107 SOX15            GTTCTGAGGCC-TACTGACTG    1421 _       GGAGTA  I
                            TTCTGAGGCC    ACT
                            |||||||||  |||
                            AAGACTCCGG    TGA
                        C       ATGAC_  I
GAM107 SOX15            GTTCTGAGGCC-TACTGACTG    1421 AG      GGAGTA   T
                            TTCTGAGGCC    ACTG
                            ||||||||||    ||||
                            AAGACTCCGG    TGAC
                            __        ATGAC_  C
GAM107 SOX15            GTTCTGAGGCC-TACTGACTG    1421 GAGT      GGAGTA
                            TCTGAGGCC     ACTG
                            |||||||||     ||||
                            AGACTCCGG     TGAC
                        ____          ATGAC_
GAM107 TMOD            GTTCTGAGG--GGA-AAATTGTG   1423 AG      CC  T C
                            TTCTGAGG GGAG AA TGT
                            |||||||| |||| || |||
                            AAGACTCC CCTT TT ACA
                            __      __   _ A
GAM108 ATF7           AGGGCTGAGTCTGAAGTAGTTAC    1431 GAG       T TAI
                            CTGAGTCTGG GT
                            |||||||||| ||
                            GACTCAGACT CA
                            ___       T TCA
GAM108 CERD4           AGTGCTGCCAGTCTGGTGT       1430 AGA  __      III
                            GCTG AGTCTGGTG
                            |||| |||||||||
                            CGAC TCAGACCAC
                        TCA  GG      AII
GAM108 CERD4           AGTGCTGCCAGTCTGGTGT       1430 TGTCAGA G      TA
                            GCT AGTCTGGTGT
                            ||| ||||||||||
                            CGG TCAGACCACA
                        GA____  _      CC
GAM108 COL19A1         TGTACAGAGCTGAGGCAGG       1438 _       TCT TGTTA
                            TGT CAGAGCTGAG  GG
                            ||| |||||||||  ||
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                         ACA GTCTCGACTC  CC
                         T       CGT IIICA
GAM108 COL19A1       TGTACAGAGCTGAGGCAGG      1438 _       TCTGII
                         TGT CAGAGCTGAG
                         III IIIIIIIIII
                         ACA GTCTCGACTC
                         T       CGTCCI
GAM108 CSF1R         TCAGAGCTGGGCCGAGCTGTT    1437 TGTC    A  T _  AC
                          AGAGCTG GTC GG TGTT
                          IIIIIII III II IIII
                          TCTCGAC CGG TC ACAA
                          ___     C  C  G  CT
GAM108 CSF1R         TCAGAGCTGGGCCGAGCTGTT    1437 C     A  T GTI
                          AGAGCTG GTC GGT
                          IIIIIII III III
                          TCTCGAC CGG TCG
                          _       C  C  ACA
GAM108 CTGF          TGTCAGAGCTGAGTCTGCTGTT   1442         G  AC
                         TGTCAGAGCTGAGTCTG TGTT
                         IIIIIIIIIIIIIIII IIII
                         ACAGTCTCGACTCAGAC ACAA
                              G    II
GAM108 CTGF          TGTCAGAGCTGAGTCTGCTGTT   1442         G  I
                          GTCAGAGCTGAGTCTG TGT
                          IIIIIIIIIIIIIIII III
                          CAGTCTCGACTCAGAC ACA
                             G   I
GAM108 CTLA1         GTCAGAGCT--GT-TGGTGTT     1436       AGTC   I
                         GTCAGAGCTG   TGGTG
                         IIIIIIIIII   IIIII
                         CAGTCTCGAC   ACCAC
                            A___    A
GAM108 CTLA1         GTCAGAGCT--GT-TGGTGTT     1436 TG      AGTC
                         TCAGAGCTG   TGGTGTT
                         IIIIIIIII   IIIIIII
                         AGTCTCGAC   ACCACAA
                         __       A___
GAM108 EHF           TGCCTGAGCTGAGTTTTCTGTT   1441 A   ___   GTGTTAC
                         TGTC GAGCTGAG  TCTG
                         IIII IIIIIIII  IIII
                         ACGG CTCGACTC  AGAC
                         A    AAA  AAIIICA
GAM108 EHF           TGCCTGAGCTGAGTTTTCTGTT   1441 A   ___   GTGTI
                         GTC GAGCTGAG  TCTG
                         III IIIIIIII  IIII
                         CGG CTCGACTC  AGAC
                         A   AAA  AIIIT
GAM108 EMP3          GTCAGAGCTGGAGTC-GGAGT    1434         _  T TGI
                         TCAGAGCTG AGTC GG
                         IIIIIIIII IIII II
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                        AGTCTCGAC TCAG CC
                         C  _ TCI
GAM108 EMP3             GTCAGAGCTGGAGTC-GGAGT   1434 TG     _  T T A
                        TCAGAGCTG AGTC GG GTT
                        |||||||||| |||| || |||
                        AGTCTCGAC TCAG CC CAG
                           __       C  _ T  I
GAM108 GOLGA5          CAGAGCTGAG-CT--TGTTA    1432       TC GTGTI
                      CAGAGCTGAG  TG
                      |||||||||| ||
                      GTCTCGACTC  AC
                          GA  AATII
GAM108 GOLGA5          CAGAGCTGAG-CT--TGTTA    1432 TGTCAG    T  GG
                         AGCTGAG CT  TGTT
                         ||||||| || ||||
                         TCGACTC GA  ACAA

                        _____     _  __
GAM108 KCNJ6           TGTCAGAGCTGCTGTATGG     1439      A_ C  TGTTA
                      TGTCAGAGCTG  GT TGG
                      |||||||||||  || |||
                      ACAGTCTCGAC  CA ACC
                         GA  T  IIICA
GAM108 KCNJ6           TGTCAGAGCTGCTGTATGG     1439      AGT  II
                      TGTCAGAGCTG   CTG
                      |||||||||||   |||
                      ACAGTCTCGAC   GAC
                           ___   AT
GAM108 MAK            GTCAGAGCTGAGTCAGTGGT     1435         __  III
                     GTCAGAGCTGAGTC TGG
                     |||||||||||||| |||
                     CAGTCTCGACTCAG ACC
                          TC  AII
GAM108 MAK            GTCAGAGCTGAGTCAGTGGT     1435 TG       __  GTTA
                     TCAGAGCTGAGTC TGGT
                     ||||||||||||| ||||
                     AGTCTCGACTCAG ACCA
                         __        TC  GIII
GAM108 SLC25A14       TGTCAGAGC-GAG-CTCGTG     1440     T  T G  TT
                     TGTCAGAGC GAG CT GTG
                     ||||||||| ||| || |||
                     ACAGTCTCG CTC GA CAC
                          _ _ G  II
GAM108 SLC25A14       TGTCAGAGC-GAG-CTCGTG     1440 _     T  T G  I
                      GTCAGAGC GAG CT GT
                      |||||||| ||| || ||
                      CAGTCTCG CTC GA CA
                         A   _ _ G  I
GAM108 TNP2          GTCAGATTAAGCTGAGTCT       1433     ____      IIIA
                     GTCAGA  GCTGAGTC
                     ||||||  ||||||||
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                            CAGTCT   CGACTCAG
                             AATT      AIII
GAM108  TNP2        GTCAGATTAAGCTGAGTCT    1433 TG   ____       GGTGTT
                        TCAGA   GCTGAGTCT
                        |||||   |||||||||
                        AGTCT   CGACTCAGA
                         __     AATT      IIICAT
GAM109  AIM1        GGATGAGTTAAAATAATTCA    1459  G  A       TTC
                        GGA GAG TAAAATAATTCA
                        ||| ||| |||||||||||
                        CCT CTC ATTTTATTAAGT
                          A   A       |||
GAM109  AIM1        GGATGAGTTAAAATAATTCA    1459 GAG  A       I
                          GAG TAAAATAATTC
                          ||| |||||||||||
                          CTC ATTTTATTAAG
                          CTA  A        I
GAM109  CD2AP        AGGAGA--AAATAATTCATT   1448 _   TA       I
                         GGAGA AAATAATTCAT
                         ||||| |||||||||||
                         CCTCT TTTATTAAGTA
                           T    __       I
GAM109  CD2AP        AGGAGA--AAATAATTCATT   1448 GGAG   TA
                          GAGA AAATAATTCATT
                          |||| ||||||||||||
                          CTCT TTTATTAAGTAA

                         ____   __
GAM109  COL4A6      GGAGGTAAAGATAACAATAATTCA 1457    ___   _       TTCTI
                        GGAGG  AGATAA AATAATTCA
                        |||||  |||||| |||||||||
                        CCTCC  TCTATT TTATTAAGT
                         ATT      G      IIITC
GAM109  COL4A6      GGAGGTAAAGATAACAATAATTCA 1457 GA       _    I
                        GGAGATAA AATAATTC
                        |||||||| |||||||||
                        TTTCTATT TTATTAAG
                          A_     G      I
GAM109  CPO        AGCAAATAAAATAATACATTC    1450  G       T  I
                         G AGATAAAATAAT CATT
                         | ||||||||||| ||||
                         C TTTATTTTATTA GTAA
                          G       T  I
GAM109  CPO        AGCAAATAAAATAATACATTC    1450 GGAGG      T  T
                          AGATAAAATAAT CATTC
                          |||||||||||| |||||
                          TTTATTTTATTA GTAAG
                          G___      T  T
GAM109  DGKI       AGTAGATAAAATAATATATT     1449 AGG       TCAI
                         AGATAAAATAAT
                         ||||||||||||
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                          TCTATTTTATTA
                          A__        TATA
GAM109 DGKI       AGTAGATAAAATAATATATT    1449 GGAGG        TC  C
                          AGATAAAATAAT ATT
                          |||||||||||| |||
                          TCTATTTTATTA TAA
                          A____        TA  T
GAM109 EPS8      GGATGGGGATAAAATAATT-AGTCT  1456  _  A       CAT  I
                          GGA GG GATAAAATAATT  TCT
                          ||| || |||||||||||  |||
                          CCT CC CTATTTTATTAA  AGA
                           A  C       TC_  I
GAM109 EPS8      GGATGGGGATAAAATAATT-AGTCT  1456 A  A        CATI
                           GG GATAAAATAATT
                           || |||||||||||
                           CC CTATTTTATTAA
                           A  C        TCAI
GAM109 KLRC1      GAGCAAATAACATAATTCATT     1454  G    A       I
                           AG AGATAA ATAATTCAT
                           || |||||| |||||||||
                           TC TTTATT TATTAAGTA
                            G    G      I
GAM109 KLRC1      GAGCAAATAACATAATTCATT     1454 GG  G    A        CT
                           AG AGATAA ATAATTCATT
                           || |||||| ||||||||||
                           TC TTTATT TATTAAGTAA
                           __ G    G       AI
GAM109 KLRC2      GAGCAAATAACATAATTCATT     1454  G    A       I
                           AG AGATAA ATAATTCAT
                           || |||||| |||||||||
                           TC TTTATT TATTAAGTA
                            G    G      I
GAM109 KLRC2      GAGCAAATAACATAATTCATT     1454 GG  G    A        CT
                           AG AGATAA ATAATTCATT
                           || |||||| ||||||||||
                           TC TTTATT TATTAAGTAA
                           __ G    G       AI
GAM109 NDUFA6     GAGA-AAAATAATTCAATC       1452    T      TTI
                           GAGA AAAATAATTCA
                           |||| ||||||||||||
                           CTCT TTTTATTAAGT
                            _        TAG
GAM109 NDUFA6     GAGA-AAAATAATTCAATC       1452 GGAGGAGAT        T
                           AAAATAATTCA T
                           ||||||||||| |
                           TTTTATTAAGT A
                           _____        T
GAM109 OPHN1     AGGAGATAAAAGAGTTTAT        1447          TAATTCAII
                           AGGAGATAAAA
                           |||||||||||
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                                TCCTCTATTTT
                                 CTCAAATAI
GAM109  PLAG1        GAGAAGATAAAC--ATTCATTCT  1455        ATA      I
                         GAGGAGATAAA  ATTCATT
                         |||||||||| |||||||
                         CTCTTCTATTT  TAAGTAA
                                G__       G
GAM109  PLAG1        GAGAAGATAAAC--ATTCATTCT  1455 GG       ATA
                          AGGAGATAAA  ATTCATTCT
                          ||||||||| |||||||||
                          TCTTCTATTT  TAAGTAAGA
                          __        G__
GAM109  PSMD9        GGAGAGGAAAAAATAATTCA       1458   GA  T     TTC
                         GGAG  GA AAAATAATTCA
                         |||| || ||||||||||
                         CCTC  CT TTTTATTAAGT
                          TC  T       III
GAM109  PSMD9        GGAGAGGAAAAAATAATTCA       1458 __     TA      I
                         GAGGAGA  AAATAATTC
                         ||||||| |||||||||
                         CTCCTTT  TTTATTAAG
                         CT    __      I
GAM109  PTP4A2       AGGAGATTTCAAAATAATTCAATC  1446 GAGA_       TTI
                            TAAAATAATTCA
                            ||||||||||||
                            GTTTTATTAAGT
                         CTAAA         TII
GAM109  PTP4A2       AGGAGATTTCAAAATAATTCAATC  1446 GGAG    ___      T  I
                          GAGAT  AAAATAATTCA TCT
                          ||||| ||||||||||| |||
                          CTCTA  TTTTATTAAGT AGG
                          ____    AAG      T  A
GAM109  PYCS         AGGACGACAAAATAATTCAT       1445 GGAGGA           TC
                            GATAAAATAATTCAT
                            |||||||||||||||
                            CTGTTTTATTAAGTA
                         CTG___         TG
GAM109  PYCS         AGGACGACAAAATAATTCAT       1445  _         II
                          AGGA GATAAAATAATTCA
                          |||| ||||||||||||||
                          TCCT CTGTTTTATTAAGT
                           G       AI
GAM109  RAB1A        GGAGG--ATAAAATAGTTGAATCT  1461    GA     ATTCAT
                          GGAGGA TAAAATA     TCT
                          |||||| |||||||     |||
                          CCTCCT ATTTTAT     AGA
                          __       CAACTT
GAM109  RAB1A        GGAGG--ATAAAATAGTTGAATCT  1461    GA     ATTCATTI
                          GGAGGA TAAAATA
                          |||||| |||||||
```

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                        CCTCCT  ATTTTAT
                          __      CAACTTAG
GAM109 SPRR2C           GAAGACATCAAAATAATTCTTT   1453   G _       ATI
                         GGA AT AAAATAATTC
                         ||| || |||||||||||
                         TCT TA TTTTATTAAG
                          G  G       AII
GAM109 SPRR2C           GAAGACATCAAAATAATTCTTT   1453 GG   G _       ATTCT
                         AGGA AT AAAATAATTC
                         |||| || |||||||||||
                         TTCT TA TTTTATTAAG
                          __  G  G       AAACI
GAM109 SPTA1            GAGAGAGAGAGAAATAATTCA    1451   _  TA      TTCT
                         GGAG GAGA  AAATAATTCA
                         |||| |||| ||||||||||
                         TCTC CTCT  TTTATTAAGT
                          T   C_       TIII
GAM109 SPTA1            GAGAGAGAGAGAAATAATTCA    1451 __  _  TA        III
                          GAG GAGA  AAATAATTC
                          ||| |||| |||||||||
                          CTC CTCT  TTTATTAAG
                          CT  T  C_       TII
GAM109 STK38            GGAGGAGATAAATCAATGGATT   1460        A   TCATTCT
                         GGAGGAGATAAA TAAT
                         ||||||||||| ||||
                         CCTCCTCTATTT GTTA
                              A  CCTAII
GAM109 STK38            GGAGGAGATAAATCAATGGATT   1460        A   TCATI
                         GAGGAGATAAA TAAT
                         ||||||||||| ||||
                         CTCCTCTATTT GTTA
                             A   CCTAI
GAM110 ADCY6           CAGGGAAAGGGGTAAAAGG       1480 TGCAACAGGGGAT
                           GGGTAAAAGG
                           ||||||||||
                           CCCATTTTCC
                         TTTC_____
GAM110 EGFL5           CAGGGTTGTAGGGGTAAAAG      1479 TGCAACAGGGGAT      G
                            GGGTAAAAG
                            |||||||||
                            CCCATTTTC
                         AACATC_____       A
GAM110 GCSH           AACACTAGAGCCTAGTCTAA      1466      CCCA   II
                          AACACTAGA  GCCTA
                          ||||||||| |||||
                          TTGTGATCT  CGGAT
                          ____       CA
GAM110 GCSH           AACACTAGAGCCTAGTCTAA      1466 TA      _ C C  CTG
                          ACACTAGA CC AG CTAA
                          |||||||| || || ||||
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                         TGTGATCT GG TC GATT
                         __      C A A  TII
GAM110 GJB3        AACATCAGCCCCAGCCTAAC    1467   C  A       I
                         ACA TAG CCCAGCCTAA
                         III III IIIIIIIIII
                         TGT GTC GGGTCGGATT
                              A   G       I
GAM110 GJB3        AACATCAGCCCCAGCCTAAC    1467 TA  C  A        G
                          ACA TAG CCCAGCCTAACT
                          III III IIIIIIIIIII
                          TGT GTC GGGTCGGATTGG
                          __  A   G        I
GAM110 GPRK7       ACAGGGACATGATGGTAAAAGG   1473 TGCAACA  G  __      G
                           GGG ATG GGTAAAAGG
                           III III IIIIIIIII
                           CCT TAC CCATTTCC
                           _____ G  TA      G
GAM110 HPCAL1       CACTAGACCATGCC---CTGT    1478      CA   AACI
                           CACTAGACC GCCT
                           IIIIIIIII IIII
                           GTGATCTGG CGGG
                              TA   ACAI
GAM110 HPCAL1       CACTAGACCATGCC---CTGT    1478 TAACAC   CA   AACT
                           TAGACC GCCT
                           IIIIII IIII
                           ATCTGG CGGG
                           _____    TA   ACAC
GAM110 IL13RA1     CACCGGACCCAGCCCAGACTGT   1476 A TA         _  I
                         C GACCCAGCCTA ACTG
                         I IIIIIIIIIII IIII
                         G CTGGGTCGGGT TGAC
                         _ GC         C  I
GAM110 IL13RA1     CACCGGACCCAGCCCAGACTGT   1476 TAACACTA        _
                            GACCCAGCCTA ACTGT
                            IIIIIIIIIII IIIII
                            CTGGGTCGGGT TGACA
                         GC_____         C
GAM110 LAMC1       TAACACTAGTTCCAAGACTAACT  1481      AC  C_   GTI
                           TAACACTAG CCAG CTAACT
                           IIIIIIIII IIII IIIIII
                           ATTGTGATC GGTT GATTGA
                              AA   CT    III
GAM110 LAMC1       TAACACTAGTTCCAAGACTAACT  1481 A    AC  C_   I
                           ACACTAG CCAG CTAAC
                           IIIIIII IIII IIIII
                           TGTGATC GGTT GATTG
                           _   AA   CT   I
GAM110 LMO2        TGAAACAGGGGA--GTTAAAA    1485 C      TGGG   GG
                           TG AACAGGGGA  TAAAA
                           II IIIIIIIII   IIIII
```

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                        AC TTGTCCCCT   ATTTT
                     T        CA__      II
GAM110 MFAP2         AACATGGGGATGGGGAAAA    1465 TGCAACA        T
                        GGGGATGGG AAAAGG
                        ||||||||| ||||||
                        CCCCTACCC TTTTTT
                     TA_____          C
GAM110 NEDD4L        TGCAACAGGTCATTGGTAA    1484    GG G    AAGG
                        TGCAACAGG  AT GGTAA
                        ||||||||| || |||||
                        ACGTTGTCC  TA CCATT
                          AG A    IIIG
GAM110 NOC4          CAC-AG-CCCAGCCTACCTG    1477  T A      ACI
                        CAC AG CCCAGCCTA
                        ||| || ||||||||||
                        GTG TC GGGTCGGAT
                         _ _        GGA
GAM110 NOC4          CAC-AG-CCCAGCCTACCTG    1477 TAACACT A      A
                        AG CCCAGCCTA CT
                        || |||||||||| ||
                        TC GGGTCGGAT GA
                        _____ _         G
GAM110 PDE4B         CAACAGGGGAAGGAAGTAAAA    1475 TGCA    T __    GGG
                        ACAGGGGA GG  GTAAAA
                        |||||||| ||  ||||||
                        TGTCCCCT CC  CATTTT
                        ____         T TT    ACI
GAM110 PMP22         AACAGCCTAGACCCAGCCAAGCT   1464 AACA        TAI
                        CTAGACCCAGCC
                        ||||||||||||
                        GATCTGGGTCGG
                     G___        TTC
GAM110 PMP22         AACAGCCTAGACCCAGCCAAGCT   1464 TAACA        TAA GTI
                        CTAGACCCAGCC  CT
                        ||||||||||||  ||
                        GATCTGGGTCGG  GA
                     TGTCG        TTC GII
GAM110 PON1          TGCAACAGGAGAATTGAAAAAG    1486        TG_ T   GG
                        TGCAACAGGGA  GG AAAAG
                        |||||||||||  || |||||
                        ACGTTGTCCTCT  CT TTTTC
                           TAA _    II
GAM110 PXF           AAGAGAGGA--GGTAAAAGGG    1470 TGCAAC    TG
                        AGGGGA  GGTAAAAGG
                        ||||||  |||||||||
                        TCTCCT  CCATTTTCC
                        _____  __
GAM110 SIX2          ACAAGAGA-GGGTAAAAGG    1474 TGCAACAG  T
                        GGGA GGGTAAAAG
                        |||| |||||||||
```

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                        CTCT CCCATTTTC
                        _____  _
GAM110  SLC25A13      AACAAGAGATGGACGTAAAAGGG   1469 TGCAAC       I
                         AGGGGATGG GTAAAAGGG
                         ||||||||| |||||||||
                         TTCTCTACC CATTTTCCC
                                  TG     T
                         _____
GAM110  SLC29A1       ACAGGGTGCATGATGGGTAAAA   1472 __  ACAGGG        GG
                         TGCA    GATGGGTAAAAG
                         ||||    |||||||||||
                         ACGT    CTACCCATTTT
                         CC  A_____        GA
GAM110  TIMP3         TGGAACGAGGGGA-GGGTAAAAG  1483  C  _   T     GG
                         TG AAC AGGGGA GGGTAAAAG
                         || ||| |||||| |||||||||
                         AC TTG TCCCCT CCCATTTTC
                         C  C   _      ||
GAM110  TRPS1         ACAGGCAGGGCTGGGTAAAA    1471 TGCAA   GA       G
                         CAGGG TGGGTAAAAG
                         ||||| ||||||||||
                         GTCCC ACCCATTTT
                         C____ G_       G
GAM110  UNG          TAACA--AGACCCAGCTTA      1482    CT      CTAACT
                         TAACA AGACCCAGC
                         ||||| |||||||||
                         ATTGT TCTGGGTCG
                           __       AATIII
GAM110  UNG          TAACA--AGACCCAGCTTA      1482    CT      CTI
                         TAACA AGACCCAGC
                         ||||| |||||||||
                         ATTGT TCTGGGTCG
                           __      AAT
GAM110  ZNF264       AACAATGGAATGGGTAAAGAGG   1468 TGCAACAG        AG
                         GGGATGGGTAAA GG
                         |||||||||||| ||
                         CCTTACCCATTT CC
                         TTA_____           CT
GAM111  EGR2         CTTGTCTTTTTGCTGT-CCCCAC  1490 TCTG  C      GA
                         GTC TTTTGCTGT CCCAC
                         ||| |||||||||| |||||
                         CAG AAAACGACA GGGTG
                         AA__ A      G_
GAM111  EGR2         CTTGTCTTTTTGCTGT-CCCCAC  1490 TG_  C      GA  I
                         GTC TTTTGCTGT CCCA
                         ||| |||||||||| ||||
                         CAG AAAACGACA GGGT
                         GAA  A      G_  I
GAM111  EIF4EBP2     TTTTGCTGTGTACC          1493  T      CCI
                         TCC TTTGCTGTGA
                         ||| |||||||||
```

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                        AGG GAACGACACT
                            C       CGI
GAM111  EIF4EBP2        TTTTGCTGTGTACC        1493 TCTGG   T      GACCC
                            TCC TTTGCTGT
                            III IIIIIIII
                            AGG GAACGACA
                        AAAAG   C      IIICA
GAM111  FMN2            GTGACCCAC            1491        II
                            GTGACCCA
                            IIIIIIII
                            CACTGGGT
                                GI
GAM111  KLRC4           TGTTCATTTTGCTGTTGACC    1492  G  C       _   II
                            TG TC TTTTGCTGT GAC
                            II II IIIIIIIII III
                            AC AG AAAACGACA CTG
                            A  T       A  GI
GAM111  KLRC4           TGTTCATTTTGCTGTTGACC    1492 TCTGG  C      _   CA
                            TC TTTTGCTGT GACC
                            II IIIIIIIII IIII
                            AG AAAACGACA CTGG
                        A____  T       A  TT
GAM111  PLAB            TTTTGCTGTGTACC          1493   T       CCI
                            TCC TTTGCTGTGA
                            III IIIIIIIIII
                            AGG GAACGACACT
                                C       CGI
GAM111  PLAB            TTTTGCTGTGTACC          1493 TCTGG  T      GACCC
                            TCC TTTGCTGT
                            III IIIIIIII
                            AGG GAACGACA
                        AAAAG   C      IIICA
GAM111  PSCDBP          CTGGTGCACCTGCTG          1489       ACII
                            TTTTGCTGTG
                            IIIIIIIIII
                            AAAACGACAC
                            ATGG
GAM112  DDX11           TGGCCTCTCTCCTGGCCACAGGC  1508     _  GA    TGI
                            TGGCCTCTC CCTGG ACGGGC
                            IIIIIIIII IIIII  IIIIII
                            ACCGGAGAG GGACC  TGTCCG
                                A  GG    III
GAM112  EHD2            TGCCCTCTCC-TGGGAACG      1510 G   C     GGC
                            TG CCTCTCC TGGGAACG
                            II IIIIIII IIIIIIII
                            AC GGAGAGG ACCCTTGC
                                G  _    III
GAM112  GNA11           CCCCTCCCTGGGAA-GGCCT     1498 TGGCCT        AC
                            CTCCCTGGGA GGGCT
                            IIIIIIIIII IIIII
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                        GAGGGACCCT TCCGG
                        _____     __
GAM112 HSF4        CCTCTCCCTGCGCCGGGGC    1497 TGGCCT    GGAAC
                        CTCCCTG   GGGCT
                        |||||||   |||||
                        GAGGGAC   CCCGG
                        _____    GCGGC
GAM112 ISG20       GCCTCTAGTCCCTGCGGAACGGGCTG 1499 TGGC  ___   _       II
                        CTC  TCCCTG GGAACGGGCTG
                        |||  |||||| |||||||||||
                        GAG  AGGGAC CCTTGCCCGAC
                        ____   ATC  G       CT
GAM112 ITGB1       GGCCTCTCCC-G----CGGGCTG  1506 TG      TGGGAA
                        GCCTCTCCC   CGGGC
                        |||||||||   |||||
                        CGGAGAGGG   GCCCG
                        __         C_____
GAM112 KHK         GCCTCTCCCTGTGGGGAAC      1502 TGGC     ___    GGCT
                        CTCTCCCT GGGAACG
                        |||||||| |||||||
                        GAGAGGGA CCCTTGT
                        ____      CAC    GIII
GAM112 LAMA4       CCTCTCCCTGGCCGTTCGGGACTG 1496 TGGCCT     GAA__  _ I
                        CTCCCTGG   CGGG CTG
                        ||||||||   |||| |||
                        GAGGGACC   GCCC GAC
                        _____      GGCAA  T  C
GAM112 MAFG        TGGCCTCTCCCAGG--CTGGGCTG 1514          T  AAC
                        TGGCCTCTCCC GGG  GGGCTG
                        ||||||||||| |||  ||||||
                        ACCGGAGAGGG TCC  CCCGAC
                        _  GA_
GAM112 MAP3K14     TGGCAATC-CCCTGGGAAC-GGCTG 1507   C_ T       G  I
                        TGGC  TC CCCTGGGAACGG CTG
                        ||||  || ||||||||||| |||
                        ACCG  AG GGGACCCTTGCC GAC
                        TT _        _  I
GAM112 MMP19       TGCCCTCTCCCTG----CAGGCTG 1513 G       GGAA
                        TG CCTCTCCCTG   CGGGCT
                        || |||||||||   ||||||
                        AC GGAGAGGGAC   GTCCGA
                        G          ____
GAM112 NR1D1       GCCTTTCCCTGGGACAGAGGGCT  1503 TGGC C       AC__   GI
                        CT TCCCTGGGA  GGGCT
                        || |||||||||  |||||
                        GA AGGGACCCT  CCCGA
                        ____   A     GTCT   GA
GAM112 PLD2        TGACCTCTCCCTG---ACGGG    1511            GGA   C
                        TGGCCTCTCCCTG ACGGG
                        ||||||||||||| |||||
```

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                         ACTGGAGAGGGAC  TGCCC
                                 ___        I
GAM112 RS1           GCCTCTCCC-AGGAAGGGGC     1504 TGGC      T    C
                         CTCTCCC GGGAA GGGCT
                         ||||||| ||||| |||||
                         GAGAGGG TCCTT CCCGG
                            ___        _      C
GAM112 SLC7A8          TGGCCTCTCCTCTCTGAAGGGGC  1509        _ GG  C  TGI
                       TGGCCTCTCC CT  GAA GGGC
                       |||||||||| || ||| ||||
                       ACCGGAGAGG GA  CTT CCCG
                          A  GA  C   III
GAM112 SNL           GCCTCTCCCACGTGGGAGAGGGGCTG 1500 TGGC     ___    AC_    II
                         CTCTCCC  TGGGA  GGGCTG
                         |||||||  |||||  ||||||
                         GAGAGGG  ACCCT  CCCGAC
                           ___        TGC   CTC    AA
GAM112 SOLH         TGGCAGCTCCCTGGG--CGGG      1512   CT      AA   CT
                       TGGC CTCCCTGGG CGGG
                       |||| ||||||||| ||||
                       ACCG GAGGGACCC GCCC
                          TC      __   II
GAM112 STAT1         GCCTCTCCC---GAGCGCGCTG   1505 TGGC     T  AA  G
                         CTCTCCC GGG  CG GCT
                         ||||||| ||| || |||
                         GAGAGGG CTC  GC CGA
                         ___     _  __   G
GAM112 WHSC1         GCCTCTCCCGAGTGGCGACGGCGCTG 1501 TGGC     ___   GA  _   II
                         CTCTCCC  TGG  ACGG GCTG
                         |||||||  |||  |||| ||||
                         GAGAGGG  ACC  TGCC CGAC
                         ___      CTC  GC  G   TC
GAM113 ABCD1         AGGGCGAGGG-TTACGCAGG     1518 TAG   ___ _    TTAGTAGG
                         GAGGG  CG AGGGC
                         |||||  || |||||
                         CTCCC  GC TCCCG
                         G__    AAT G    CGIIITGG
GAM113 CAPON         TAGGAGGGCGGCAGGG--GAGGAGGT 1523       __   CTT  T   I
                         TAGGAGGGCG AGGG  AG AGGT
                         |||||||||| |||| || ||||
                         ATCCTCCCGC TCCC  TC TCCA
                            CG  C__  C   I
GAM113 DISC1         TAGCATGGCAAGGGCTTAGCATGGT 1524 TA AG_          _  II
                         GG  GGCGAGGGCTTAGTA GGT
                         ||  |||||||||||||| |||
                         TC  CCGTTCCCGAATCGT CCA
                         A_  GTA         A  II
GAM113 GAS41         AGGAGGGCGAG---TTACTTGG    1517 TA       G_  AGTAGG
                         GGAGGGCGAG GCTT
                         |||||||||| ||||
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                              CCTCCCGCTC TGAA
                              __        AA   CCCIII
GAM113  HOXC5         GAGGGCGAGG--TTAGAGGGT   1519 TAGGAG     GC   TA
                             GGCGAGG TTAG GG
                             |||||| |||| ||
                             CCGCTCC AATC CC
                             _____     __  TC
GAM113  NR3C2         GGACGAGCGAGGGCTCAG-AGG   1520 TAGGA          T
                            GGGCGAGGGCTTAG AGGT
                            ||||||||||||| ||||
                            CTCGCTCCCGAGTC TCCG
                      TG___          _
GAM113  OTP          GGCGGGCGAGGGGGGGTCGTAGG   1521 TAGGA      CTTA_
                            GGGCGAGGG  GTAGGT
                            |||||||||  ||||||
                            CCCGCTCCC  CATCCG
                      G____           CCCAG
GAM113  SIAT7D        GGGCGAGGGCAGGACGTAGGT   1522 TAGG   G   TTA
                             AGGGC AGGGC  GTAGGT
                             ||||| |||||  ||||||
                             TCCCG TCCTG  CATCCA

                             ____   _   ____
GAM114  ADCY6         GGCGCCTGTAATCCCAGCT-ACT   1565 G A__         CACI
                             GC  TGATCCCAGCT
                             ||  ||||||||||
                             CG  ATTAGGGTCGA
                             G GAC        TIII
GAM114  ADCY6         GGCGCCTGTAATCCCAGCT-ACT   1565 TAGGG A__      C G
                             GC  TGATCCCAGCT ACT
                             ||  |||||||||| |||
                             CG  ATTAGGGTCGA TGA
                             G____ GAC      _ G
GAM114  AQP6        AGGCGCCTGTAATCCCAGCT-ACT   1531 GG A__      CAI
                             GC  TGATCCCAGCT
                             ||  ||||||||||
                             CG  ATTAGGGTCGA
                             G_ GAC        TII
GAM114  AQP6        AGGCGCCTGTAATCCCAGCT-ACT   1531 TA G A__      C GI
                            GG GC  TGATCCCAGCT ACT
                            || ||  |||||||||| |||
                            CC CG  ATTAGGGTCGA TGA
                            __ G GAC      _ AI
GAM114  AQP6        AGGCGCCTGTAATCCCAGCT-ACT   1531 TA G A__      C GI
                            GG GC  TGATCCCAGCT ACT
                            || ||  |||||||||| |||
                            CC CG  ATTAGGGTCGA TGA
                            __ G GAC      _ GI
GAM114  ARCN1       ATGATCCCAGTGCCTGACTG   1551        ___ C III
                            ATGATCCCAG  CT ACT
                            ||||||||||  || |||
```

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                               TACTAGGGTC  GA TGA
                                  ACG  C  CII
GAM114 ATP1A2        GGCACGATCTCAGCTCACTG    1555      C      I
                        GCATGATC CAGCTCACT
                        |||||||| |||||||||
                        CGTGCTAG GTCGAGTGA
                               A      I
GAM114 ATP1A2        GGCACGATCTCAGCTCACTG    1555 TAGGGGCAT   C
                            GATC CAGCTCACT
                            |||| |||||||||
                            CTAG GTCGAGTGA
                        G_____     A
GAM114 AXUD1         AGTGTGCACAT-GGCACCTGT    1549        GA    CC
                        AGTGTGCACGTGG ACCTGT
                        ||||||||||||| ||||||
                        TCACACGTGTACC TGGACA
                               G_     II
GAM114 BLTR2         AGTAGGC-CTTGGGAACCT    1548  T ACG     GTC
                        AGTG GC  TGGGAACCT
                        |||| ||  |||||||||
                        TCAT CG  ACCCTTGGA
                            C GA_      III
GAM114 C1orf1        AGGGGCATGATCTCAACTCACTG  1534        C      I
                        GGGGCATGATC CAGCTCACT
                        |||||||||| |||||||||
                        CCCCGTACTAG GTTGAGTGA
                               A      I
GAM114 C1orf1        AGGGGCATGATCTCAACTCACTG  1534 TA      C      I
                        GGGGCATGATC CAGCTCACTG
                        |||||||||| |||||||||||
                        CCCCGTACTAG GTTGAGTGAC
                        __      A      C
GAM114 CIT           TGAGCACGTGGGCGCTTGGGTCCC  1574 AGTGT     AACCT__  I
                        GCACGTGGG    GTCCC
                        |||||||||    |||||
                        CGTGCACCC    CAGGG
                        T____        GCGAACC    G
GAM114 CPT2          AGTGGTGTGATCTCAGCTCACTG    1545 GG CA   C      I
                        GG TGATC CAGCTCACT
                        || ||||| |||||||||
                        CC ACTAG GTCGAGTGA
                        CA AC   A      I
GAM114 CPT2          AGTGGTGTGATCTCAGCTCACTG    1545 TAGG CA   C       I
                        GG TGATC CAGCTCACTG
                        || ||||| |||||||||||
                        CC ACTAG GTCGAGTGAC
                        CA__ AC  A       G
GAM114 DDOST         GGCGTGATCTCAGCTCACTG    1561 A  C      I
                        GC TGATC CAGCTCACT
                        || ||||| |||||||||
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                              CG ACTAG GTCGAGTGA
                                 C     A        I
GAM114 DDOST          GGCGTGATCTCAGCTCACTG    1561 TAGGGGCA    C
                              TGATC CAGCTCACT
                              ||||| |||||||||
                              ACTAG GTCGAGTGA
                              _____        A
GAM114 DGKI        AGTGGTGTGATCTCAGCTCACTG    1545 GG  CA    C        I
                              GG  TGATC CAGCTCACT
                              ||  ||||| |||||||||
                              CC  ACTAG GTCGAGTGA
                              CA AC   A        I
GAM114 DGKI        AGTGGTGTGATCTCAGCTCACTG    1545 TAGG  CA    C        I
                              GG  TGATC CAGCTCACTG
                              ||  ||||| ||||||||||
                              CC  ACTAG GTCGAGTGAC
                              CA__ AC   A         G
GAM114 FGFR1         AGTGGCGTGATCTCAGCTCACTG    1544 GG  A    C      I
                              GGC TGATC CAGCTCACT
                              ||| ||||| |||||||||
                              CCG ACTAG GTCGAGTGA
                              CA  C   A      I
GAM114 FGFR1         AGTGGCGTGATCTCAGCTCACTG    1544 TAGG  A    C        I
                              GGC TGATC CAGCTCACTG
                              ||| ||||| ||||||||||
                              CCG ACTAG GTCGAGTGAC
                              CA__  C   A         G
GAM114 FGFR2          GGCATGATCTCGGCTCACTG    1560       CCA    I
                              GCATGATC GCTCACT
                              |||||||| |||||||
                              CGTACTAG CGAGTGA
                                 AGC       I
GAM114 FOLR1         AGGGTTCCCGTTC-AACCTGTCCC  1550 T GCA  GGG       I
                              AG GT  CGT  AACCTGTCCC
                              || ||  |||  ||||||||||
                              TC CA  GCA  TTGGACAGGG
                               C AGG  AG_       I
GAM114 GALNT7        GGCATGATCTCAGCTCACTG    1557      C   I
                              GCATGATC CAGCTCACT
                              |||||||| |||||||||
                              CGTACTAG GTCGAGTGA
                                 A       I
GAM114 GALNT7        GGCATGATCTCAGCTCACTG    1557 TAGGGGCA    C
                              TGATC CAGCTCACT
                              ||||| |||||||||
                              ACTAG GTCGAGTGA
                              _____        A
GAM114 HDAC4        GTGGGCACGTGGGCACGCTG    1568 AG  T     A _  CC
                              TG GCACGTGGG AC CTGT
                              || ||||||||| || ||||
```

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                          AC CGTGCACCC TG GACG
                          __  C      G C  II
GAM114 HIP1         GGCGTGATCTCAGCTCACTG    1561 A   C      I
                        GC TGATC CAGCTCACT
                        II IIIII IIIIIIIII
                        CG ACTAG GTCGAGTGA
                           C    A         I
GAM114 HIP1         GGCGTGATCTCAGCTCACTG    1561 TAGGGGCA   C
                           TGATC CAGCTCACT
                           IIIII IIIIIIIII
                           ACTAG GTCGAGTGA
                        _____        A
GAM114 HR         TGAGCACCTGGTCTACCTGTCCC  1573 AGTGT  G  GA_     I
                       GCAC TGG  ACCTGTCCC
                       IIII III  IIIIIIIII
                       CGTG ACC  TGGACAGGG
                       T____  G  AGA      G
GAM114 HYAL4        GGGCATGATGGCATGCTC-CTG  1562    CC _  A I
                       GGCATGAT CA GCTC CT
                       IIIIIIII II IIII II
                       CCGTACTA GT CGAG GA
                           CC A   _ I
GAM114 IGF1        GGTGCCTGTAATCCCAGCT-ACT  1566 G A__      CACI
                        GC  TGATCCCAGCT
                        II  IIIIIIIIIII
                        CG  ATTAGGGTCGA
                        A GAC         TIII
GAM114 IGF1        GGTGCCTGTAATCCCAGCT-ACT  1566 TAGGG A__      C
                        GC  TGATCCCAGCT ACTG
                        II  IIIIIIIIIII IIII
                        CG  ATTAGGGTCGA TGAC
                        A____  GAC         _
GAM114 IL10      AGGGGCATGATATCAGCTCACTG    1533      CC     I
                       GGGGCATGAT CAGCTCACT
                       IIIIIIIIII IIIIIIIII
                       CCCCGTACTA GTCGAGTGA
                          TA       I
GAM114 IL10      AGGGGCATGATATCAGCTCACTG    1533 TA      CC     I
                       GGGGCATGAT CAGCTCACTG
                       IIIIIIIIII IIIIIIIIII
                       CCCCGTACTA GTCGAGTGAC
                          __     TA    G
GAM114 IPP       AGTGGCATGATCGTAGCTCACT     1532 GG      CC     I
                       GGCATGATC AGCTCAC
                       IIIIIIIII IIIIIII
                       CCGTACTAG TCGAGTG
                       CA     CA    I
GAM114 IPP       AGTGGCATGATCGTAGCTCACT     1532 TAGG      CC
                       GGCATGATC AGCTCACTG
                       IIIIIIIII IIIIIIIII
```

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                          CCGTACTAG TCGAGTGAT
                          CA__      CA
GAM114 IRAK4          AGTGGCACGATCTCAGCTCACTG  1537 GG       C        I
                          GGCATGATC CAGCTCACT
                          ||||||||| |||||||||
                          CCGTGCTAG GTCGAGTGA
                          CA        A        I
GAM114 IRAK4          AGTGGCACGATCTCAGCTCACTG  1537 TAGG      C        I
                          GGCATGATC CAGCTCACTG
                          ||||||||| ||||||||||
                          CCGTGCTAG GTCGAGTGAC
                          CA__      A        G
GAM114 JRK          AGGTGCCAAG-TCCCAGCTCA    1527 G ATGA       I
                          GG GC   TCCCAGCTC
                          || ||   |||||||||
                          CC CG   AGGGTCGAG
                           A GTTC         I
GAM114 JRK          AGGTGCCAAG-TCCCAGCTCA    1527 TA G ATGA      CT
                          GG GC   TCCCAGCTCA
                          || ||   ||||||||||
                          CC CG   AGGGTCGAGT
                          __ A GTTC        TI
GAM114 KAI1       GCACGATCTCAGCTCACTG      1552       C        II
                          GCATGATC CAGCTCACT
                          |||||||| |||||||||
                          CGTGCTAG GTCGAGTGA
                                A       CI
GAM114 KCNJ5        AGTGGCATGATCTTGGCTCACTG  1543 GG       CCA    I
                          GGCATGATC GCTCACT
                          ||||||||| |||||||
                          CCGTACTAG CGAGTGA
                          CA       AAC     I
GAM114 KCNJ5        AGTGGCATGATCTTGGCTCACTG  1543 TAGG      CCA      I
                          GGCATGATC GCTCACTG
                          ||||||||| ||||||||
                          CCGTACTAG CGAGTGAC
                          CA__      AAC      G
GAM114 KLK5       GGGGGATTTGCTCCCAGCTCA    1563 _  CA_ A       III
                          GGGG  TG TCCCAGCTC
                          ||||  || |||||||||
                          CCCC  AC AGGGTCGAG
                          C  TAA G       TII
GAM114 KLK5       GGGGGATTTGCTCCCAGCTCA    1563 TA  CA A      CTG
                          GGGG  TG TCCCAGCTCA
                          ||||  || ||||||||||
                          CCCT  AC AGGGTCGAGT
                          __  AA G       CGI
GAM114 MBD4          AGTGGCATGATCATGGCTCACTG  1540 GG       CCA    I
                          GGCATGATC GCTCACT
                          ||||||||| |||||||
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                        CCGTACTAG  CGAGTGA
                        CA      TAC      I
GAM114 MBD4             AGTGGCATGATCATGGCTCACTG  1540 TAGG      CCA      I
                            GGCATGATC  GCTCACTG
                            |||||||||  ||||||||
                            CCGTACTAG  CGAGTGAC
                        CA__      TAC      G
GAM114 MEF2A            AGGCGCCTGTAATCCCAGCT-ACT  1531 GG  A__        CAI
                           GC  TGATCCCAGCT
                           ||  ||||||||||
                           CG  ATTAGGGTCGA
                        G_  GAC        TII
GAM114 MEF2A            AGGCGCCTGTAATCCCAGCT-ACT  1531 TA G  A__        C  GI
                           GG GC   TGATCCCAGCT ACT
                           || ||  |||||||||| |||
                           CC CG  ATTAGGGTCGA TGA
                        __ G GAC          _ GI
GAM114 MEFV             GGCGCCTGTAATCCCAGCT-ACT  1565 G  A__        CACI
                           GC  TGATCCCAGCT
                           ||  ||||||||||
                           CG  ATTAGGGTCGA
                        G  GAC        TIII
GAM114 MEFV             GGCGCCTGTAATCCCAGCT-ACT  1565 TAGGG  A__        C  G
                           GC  TGATCCCAGCT ACT
                           ||  |||||||||| |||
                           CG  ATTAGGGTCGA TGA
                        G____  GAC        _  A
GAM114 MERTK           TGGACGTCCCGAACCTGTCC      1571 AGTGTGCA  GG_
                           CGT  GAACCTGTCC
                           |||  ||||||||||
                           GCA  CTTGGACAGG
                        _____  GGG
GAM114 MRPL49          GGCGCCTGTAATCCCAGCT-ACT  1565 G  A__        CACI
                           GC  TGATCCCAGCT
                           ||  ||||||||||
                           CG  ATTAGGGTCGA
                        G  GAC        TIII
GAM114 MRPL49          GGCGCCTGTAATCCCAGCT-ACT  1565 TAGGG  A__        C  G
                           GC  TGATCCCAGCT ACT
                           ||  |||||||||| |||
                           CG  ATTAGGGTCGA TGA
                        G____  GAC        _  G
GAM114 MYCL2           AGGCGCCTGCGATCCCAGCT-ACT  1530 GG  AT__        CAI
                           GC  GATCCCAGCT
                           ||  ||||||||||
                           CG  CTAGGGTCGA
                        G_  GACG        TII
GAM114 MYCL2           AGGCGCCTGCGATCCCAGCT-ACT  1530 TA G  AT__        C  GI
                           GG GC   GATCCCAGCT ACT
                           || ||  |||||||||| |||
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                        CC CG   CTAGGGTCGA TGA
                        __ G  GACG        _  GI
GAM114 NCALD            GGCAAGAATTCAGCTCACT     1554   T TCC      II
                        GGCA GA   CAGCTCAC
                        IIII II  IIIIIIIII
                        CCGT CT  GTCGAGTG
                          T  TAA        AI
GAM114 NPHS1            AGTGGCGTGATCTCAGCTCACTG   1544 GG  A   C      I
                        GGC TGATC CAGCTCACT
                        III IIIII IIIIIIIII
                        CCG ACTAG GTCGAGTGA
                          CA  C   A      I
GAM114 NPHS1            AGTGGCGTGATCTCAGCTCACTG   1544 TAGG  A   C       I
                        GGC TGATC CAGCTCACTG
                        III IIIII IIIIIIIIII
                        CCG ACTAG GTCGAGTGAC
                          CA__   C   A      G
GAM114 PAICS           AGTGGCATGATCCAGGCTCACTG   1541 GG        CA     I
                        GGCATGATCC GCTCACT
                        IIIIIIIIII IIIIIII
                        CCGTACTAGG CGAGTGA
                        CA        TC     I
GAM114 PAICS           AGTGGCATGATCCAGGCTCACTG   1541 TAGG       CA     I
                        GGCATGATCC GCTCACTG
                        IIIIIIIIII IIIIIIII
                        CCGTACTAGG CGAGTGAC
                        CA__       TC      G
GAM114 PHEMX          AGGGGCCTCAGACCGCAGCTCACTG 1528 GG  AT__  C     I
                        GGC  GATC CAGCTCACT
                        III  IIII IIIIIIIII
                        CCG  CTGG GTCGAGTGA
                        __  GAGT  C      I
GAM114 PHEMX          AGGGGCCTCAGACCGCAGCTCACTG 1528 TA   AT__  C      II
                        GGGGC  GATC CAGCTCACTG
                        IIIII  IIII IIIIIIIIII
                        CCCCG   CTGG GTCGAGTGAC
                        __  GAGT  C     GI
GAM114 PLOD3          TACGCGCCTGGATCCCAGCTC     1569 AGGG  AT_       I
                        GC  GATCCCAGCT
                        II  IIIIIIIIII
                        CG  CTAGGGTCGA
                        GCG_ GAC        I
GAM114 PLOD3          TACGCGCCTGGATCCCAGCTC     1569 TAGGG  AT_       ACTG
                        GC  GATCCCAGCTC
                        II  IIIIIIIIIII
                        CG  CTAGGGTCGAG
                        ATGCG GAC         IIIG
GAM114 PMSCL1         GTTCACA-GGAAACCTGTCC      1567 AGTGTG   T
                        CACG GGGAACCTGTCC
                        IIII IIIIIIIIIIII
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                          GTGT CCTTTGGACAGG
                          _____  _
GAM114 PSMB2      AGTGGCATGATCTCGGCTCACTG  1542 GG      CCA      I
                          GGCATGATC  GCTCACT
                          |||||||||  |||||||
                          CCGTACTAG  CGAGTGA
                          CA      AGC     I
GAM114 PSMB2      AGTGGCATGATCTCGGCTCACTG  1542 TAGG     CCA      I
                          GGCATGATC  GCTCACTG
                          |||||||||  ||||||||
                          CCGTACTAG  CGAGTGAC
                          CA__     AGC       G
GAM114 PSMD5      AGTGGCAAGATCTCAGCTCACTG  1535 GG   T  C      I
                          GGCA GATC CAGCTCACT
                          |||| |||| |||||||||
                          CCGT CTAG GTCGAGTGA
                          CA   T  A       I
GAM114 PSMD5      AGTGGCAAGATCTCAGCTCACTG  1535 TAGG  T  C      I
                          GGCA GATC CAGCTCACTG
                          |||| |||| ||||||||||
                          CCGT CTAG GTCGAGTGAC
                          CA__    T  A       G
GAM114 PTGFRN     AGTGCTGCTGGTAGGAACCTGT  1546  _ AC       CCC
                          AGTG TGC GTGGGAACCTGT
                          |||| ||| ||||||||||||
                          TCAC ACG CATCCTTGGACA
                          G  AC           III
GAM114 RANBP3     AGTGTGGGCGTCACGTGGGAACGTGGCC1547      _____       C T CIII
                          AGTGTG   CACGTGGGAAC TG CC
                          ||||||   ||||||||||| || ||
                          TCACAC   GTGCACCCTTG AC GG
                          CCGCA        C C IIIC
GAM114 SIP        AGTGGCATCATCATAGCTCACTG  1538 GG   G  CC     I
                          GGCAT ATC AGCTCACT
                          ||||| ||| ||||||||
                          CCGTA TAG TCGAGTGA
                          CA   G TA       I
GAM114 SIP        AGTGGCATCATCATAGCTCACTG  1538 TAGG   G  CC     I
                          GGCAT ATC AGCTCACTG
                          ||||| ||| |||||||||
                          CCGTA TAG TCGAGTGAC
                          CA__    G TA       G
GAM114 SLC1A4     TGTATGTGA-AACCTGTCC     1572 AGTGTGCAC  G
                          GTGG AACCTGTC
                          |||| ||||||||
                          CACT TTGGACAG
                          A_____    _
GAM114 SLC2A6     GGCATGATCTCAGCTCATTG   1558      C    CTI
                          GCATGATC CAGCTCA
                          |||||||| |||||||
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                            CGTACTAG GTCGAGT
                                A     AAI
GAM114 SLC2A6       GGCATGATCTCAGCTCATTG     1558 TAGGGGCA   C    CT
                       TGATC CAGCTCA
                       ||||| |||||||
                       ACTAG GTCGAGT
                       _____     A    AA
GAM114 SMAC         GGCGCCTGCAATCCCAGCT-ACT   1564 G AT__        CACI
                       GC   GATCCCAGCT
                       ||   ||||||||||
                       CG   TTAGGGTCGA
                       G   GACG        TIII
GAM114 SMAC         GGCGCCTGCAATCCCAGCT-ACT   1564 TAGGG AT__       C  G
                         GC   GATCCCAGCT ACT
                         ||   |||||||||| |||
                         CG   TTAGGGTCGA TGA
                         G____ GACG        _  G
GAM114 SUDD        GCATGATCTCAGCTCACTG        1553       C    II
                       GCATGATC CAGCTCACT
                       |||||||| |||||||||
                       CGTACTAG GTCGAGTGA
                           A      CI
GAM114 SWAP70      GGCATGATCTCAGCTCGCTG        1559       C   A I
                       GCATGATC CAGCTC CT
                       |||||||| |||||| ||
                       CGTACTAG GTCGAG GA
                           A     C I
GAM114 SWAP70      GGCATGATCTCAGCTCGCTG        1559 TAGGGGCA   C    A
                         TGATC CAGCTC CT
                         ||||| |||||| ||
                         ACTAG GTCGAG GA
                         _____     A    C
GAM114 TBX1       AGTGGCATGATCATAGCTTACTG      1539 GG        CC   C  I
                       GGCATGATC AGCT ACT
                       ||||||||| |||| |||
                       CCGTACTAG TCGA TGA
                       CA       TA  A  I
GAM114 TBX1       AGTGGCATGATCATAGCTTACTG      1539 TAGG        CC   C  I
                       GGCATGATC AGCT ACTG
                       ||||||||| |||| ||||
                       CCGTACTAG TCGA TGAC
                       CA__        TA  A  G
GAM114 TNFSF10    TAGTGGCATGATCTCACCACACTG     1570 G       CCA  _   I
                       TAG GGCATGATC  GCT CACTG
                       ||| |||||||||  ||| |||||
                       ATC CCGTACTAG  TGG GTGAC
                          A     AG_  T  I
GAM114 TNFSF10    TAGTGGCATGATCTCACCACACTG     1570 AGG       CCA  _   I
                       GGCATGATC  GCT CACT
                       |||||||||  ||| ||||
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                          CCGTACTAG  TGG GTGA
                          TCA        AG_ T  I
GAM114 TPMT               AGTGGCACGATCTCAGCTCACTG   1537 GG       C      I
                          GGCATGATC CAGCTCACT
                          ||||||||| ||||||||||
                          CCGTGCTAG GTCGAGTGA
                          CA        A    I
GAM114 TPMT               AGTGGCACGATCTCAGCTCACTG   1537 TAGG      C      I
                          GGCATGATC CAGCTCACTG
                          ||||||||| |||||||||||
                          CCGTGCTAG GTCGAGTGAC
                          CA__      A        G
GAM114 TRAF5              GGCGCCTGTAATCCCAGCT-ACT    1565 G A__         CACI
                          GC  TGATCCCAGCT
                          ||  ||||||||||||
                          CG  ATTAGGGTCGA
                          G  GAC        TIII
GAM114 TRAF5              GGCGCCTGTAATCCCAGCT-ACT    1565 TAGGG A__       C  G
                          GC  TGATCCCAGCT ACT
                          ||  |||||||||||| |||
                          CG  ATTAGGGTCGA TGA
                          G____     GAC        _  G
GAM114 UBE2B              GGCATAATCACAGCTCACTG      1556        C      I
                          GCATGATC CAGCTCACT
                          |||||||| |||||||||
                          CGTATTAG GTCGAGTGA
                                    T      I
GAM114 UBE2G2             AGTGGCGTGATCTCAGCTCACTG   1544 GG A   C      I
                          GGC TGATC CAGCTCACT
                          ||| ||||| |||||||||
                          CCG ACTAG GTCGAGTGA
                          CA  C   A      I
GAM114 UBE2G2             AGTGGCGTGATCTCAGCTCACTG   1544 TAGG  A   C      I
                          GGC TGATC CAGCTCACTG
                          ||| ||||| |||||||||||
                          CCG ACTAG GTCGAGTGAC
                          CA__  C   A        G
GAM114 VDR                GGCACGATCTCAGCTCACTG      1555       C      I
                          GCATGATC CAGCTCACT
                          |||||||| |||||||||
                          CGTGCTAG GTCGAGTGA
                          A        I
GAM114 VDR                GGCACGATCTCAGCTCACTG      1555 TAGGGGCAT   C
                          GATC CAGCTCACT
                          |||| |||||||||
                          CTAG GTCGAGTGA
                          G_____    A
GAM114 VHL                AGTGGCACCATCTCAGCTCACTG   1536 GG    G  C      I
                          GGCAT ATC CAGCTCACT
                          ||||| ||| |||||||||
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                                    CCGTG TAG GTCGAGTGA
                                    CA    G   A        I
GAM114  VHL          AGTGGCACCATCTCAGCTCACTG  1536 TAGG   G   C        I
                                    GGCAT ATC CAGCTCACTG
                                    IIIIII III IIIIIIIIII
                                    CCGTG TAG GTCGAGTGAC
                                    CA__  G   A        G
GAM114  VHL          AGGCGCCTGTAATCCCAGCTCA   1529 GGG  A__         I
                                    GC  TGATCCCAGCTC
                                    II  IIIIIIIIIIII
                                    CG  ATTAGGGTCGAG
                                    G__ GAC        I
GAM114  VHL          AGGCGCCTGTAATCCCAGCTCA   1529 TA G A__          CTG
                                    GG GC  TGATCCCAGCTCA
                                    II II  IIIIIIIIIIII
                                    CC CG  ATTAGGGTCGAGT
                                    __ G  GAC          CII
GAM114  ZNF133       AGGCGCCTGTAATCCCAGCT-ACT  1531 GG  A__         CAI
                                    GC  TGATCCCAGCT
                                    II  IIIIIIIIIII
                                    CG  ATTAGGGTCGA
                                    G_  GAC        TII
GAM114  ZNF133       AGGCGCCTGTAATCCCAGCT-ACT  1531 TA G A__          C GI
                                    GG GC  TGATCCCAGCT ACT
                                    II II  IIIIIIIIIII III
                                    CC CG  ATTAGGGTCGA TGA
                                    __ G  GAC          _ GI
GAM114  ZNF14        AGTGGCGTGATCTCAGCTCACTG   1544 GG  A   C        I
                                    GGC TGATC CAGCTCACT
                                    III IIIII IIIIIIIII
                                    CCG ACTAG GTCGAGTGA
                                    CA  C   A        I
GAM114  ZNF14        AGTGGCGTGATCTCAGCTCACTG   1544 TAGG  A   C        I
                                    GGC TGATC CAGCTCACTG
                                    III IIIII IIIIIIIIII
                                    CCG ACTAG GTCGAGTGAC
                                    CA__ C   A        G
GAM115  ACADSB      TCTAAATAAATTTTCATCAGTTTT   1586 CAC   GCTG       I
                                    TCT TAAGT ATCAGTTTT
                                    III IIIII IIIIIIIII
                                    AGA ATTTA TAGTCAAAA
                                    TTT AAAG        I
GAM115  BCL2L2      TCTAGCTAAG--CTGATCAGT      1585 CA GT       TT
                                    TCT CTAA GCTGATCAGT
                                    III IIII IIIIIIIIII
                                    AGA GATT CGACTAGTCA
                                    TC  __        II
GAM115  CD28        TCACTAAGTACATGGTAAGTT      1580 TCTC     _ ATC TT
                                    ACTAAGTGC TG  AGTT
                                    IIIIIIIII II IIII
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                           TGATTCATG AC  TCAA
                           ____      T CAT   CC
GAM115 CD79A         TCACTAAGTGGCCCTGA-CAG    1579 TCTC     ___  T TTT
                           ACTAAGTG  CTGA CAG
                           |||||||| |||| |||
                           TGATTCAC  GACT GTC
                              ____     CGG  _  TAI
GAM115 CYP7A1          TCTCACTAA--GCTGTCCAG    1584    GT  A  TT
                           TCTCACTAA GCTG TCAG
                           ||||||||| |||| ||||
                           AGAGTGATT CGAC GGTC
                              __  A  II
GAM115 EIF4G2         TCTCTCAAAA--CTGATCAGTTTT 1587 __   CTAAGT
                           TCTCA    GCTGATCAGTTTT
                           |||||    |||||||||||||
                           AGAGT    TGACTAGTCAAAA
                           AG    TT____
GAM115 FGF7       CAC-AAGTCCAGCTTGATCAGTTTT 1577 TCTCA  A GC       I
                           CTA GT  TGATCAGTTTT
                           ||| ||  ||||||||||
                           GGT CG  ACTAGTCAAAA
                          TTCA_  _ A_          A
GAM115 FOLH1          TCTCACTAATGCCTCGCTTATCAG  1583       _ ___  G   TTTTI
                           TCTCACTAA GT  GCT ATCAG
                           ||||||||| ||  ||| |||||
                           AGAGTGATT CG  CGA TAGTC
                            A  GAG  A    IIITT
GAM115 LANCL1          TCTTACTGTAAGTGCTGAT     1581   C  __      CAGTTT
                           TCT ACT AAGTGCTGAT
                           ||| ||| ||||||||||
                           AGA TGA TTCACGACTA
                            A  CA        IIITTT
GAM115 NRIP1          TCTGACCACAGTGCTGATCA     1582  C  _       GTTT
                           TCT ACTA AGTGCTGATCA
                           ||| |||| ||||||||||||
                           AGA TGGT TCACGACTAGT
                            C   G       IIIT
GAM115 SNX6          CTCACTAAGAGC--ATCAG       1578 TC    T TG   TT
                           TCACTAAG GC ATCAG
                           |||||||| || |||||
                           AGTGATTC CG TAGTC
                             __    T __  TI
GAM115 TGFBR2          TCTTCCTAAG--C--ATCAGTTTT  1588  CA    GCTG
                           TCT CTAAGT  ATCAGTTT
                           ||| |||||| |||||||||
                           AGA GATTCG  TAGTCAAA
                            AG    ____
GAM116 AADAC          TAAAGTATACAAG-AATGTAATATTT 1609       _ TAAG  ATTTII
                           TAAAGTATA AGG  GTAA
                           ||||||||| |||   ||||
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                        ATTTCATAT TTC   CATT
                          G   TTA_    ATAAAI
GAM116 ATP8A2           AAG-ATCAGGTAAGGTGAA     1602 TAAAGTATA      AAAT
                          AGGTAAGGT
                          ||||||||
                          TCCATTCCA
                        CTAG_____        CTTC
GAM116 BACH1           AAAAAATAAGGTAATGTTATTTT  1600 TAAAGTAT        ATTTI
                         AAGGTAAGGTAA
                         ||||||||||||
                         TTTTATTCCATT
                        T_____          ACAAT
GAM116 BCAT1            TAAAG-ACAATATAAGGTAAAT    1611    T   G       TT
                         TAAAG ATAA GTAAGGTAAAT
                         ||||| |||| ||||||||||
                         ATTTC TGTT TATTCCATTTA
                          _   A      ||
GAM116 CAV1            AAATAAAAGGTAAGGAAAA     1595 TAA   T_     T TT
                         AGTA  AAGGTAAGG AAA
                         ||||  ||||||||| |||
                         TTAT  TTCCATTCC TTT
                         ___    TT      T TI
GAM116 COG5           TAAAGTATAAGTGCTAAAGAGGTAAAT1610      _ A____      TTIII
                         TAAAGTATAAG GT   AGGTAAAT
                         |||||||||| ||   ||||||||
                         ATTTCATATTC CG   TCCATTTA
                          A ATTTC     ||ITT
GAM116 COL19A1         AAAGTATCTG--AAGGTAAAT     1598 TA    AAGGT      T
                          AAGTAT   AAGGTAAAT
                          ||||||   |||||||||
                          TTCATA   TTCCATTTA
                          __    GAC__        T
GAM116 COL4A4          TAAAGTATATGGAAAAATAGATT  1612      A  T    AATTTI
                         TAAAGTATA GG AAGGTA
                         ||||||||| || ||||||
                         ATTTCATAT CC TTTTAT
                          A  T    CTAAII
GAM116 EGR3           AGTATAAGGTACTATAAAT      1605 TAAAGT      AG
                          ATAAGGTA GTAAATT
                          |||||||| |||||||
                          TATTCCAT TATTTAG
                         _____      GA
GAM116 EPB72          TAGAGAATGAG-TAAGGTAAGTTT  1615 TAAAGTATAA       ATTTI
                          GGTAAGGTAA
                          ||||||||||
                          TCATTCCATT
                        ATCTCTTAC_       CAAAI
GAM116 FGF5           TAAAGTATAA-ATTAGTTCAATTT  1613        GTA GTA   I
                          TAAAGTATAAG AG AATTT
                          |||||||||| || |||||
```

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                              ATTTCATATTT  TC  TTAAA
                                 AA_  AAG    I
GAM116 GPR23          AAAGTATAACAGGGAGGATAAAT  1591 TA      _  TA  _   TTI
                              AAGTATAA GG  AGG TAAAT
                              |||||||| || ||| |||||
                              TTCATATT TC  TCC ATTTA
                                 __     G  CC  T   TII
GAM116 KERA        TAAAGTATAACAAAAAG-ATATTT  1614        GGT_    AATTTI
                              TAAAGTATAA   AAGGTA
                              |||||||||   ||||||
                              ATTTCATATT  TTCTAT
                                 GTTT     AAAIII
GAM116 MYCN          TAAAGTATACAGGCAGTGTAA      1608       _   AG  ATTT
                              TAAAGTATA AGGTA  GTAA
                              ||||||||| ||||| ||||
                              ATTTCATAT TCCGT  CATT
                                G   CA   IIIT
GAM116 OSR1          AAACTCTAAGGTAAGCGGTAA      1594 TAAAGTA      __    ATTT
                              TAAGGTAA  GGTAA
                              |||||||| |||||
                              ATTCCATT  CCATT
                              TTGAG__       CG   CIII
GAM116 OSR1       AAG-AGAAAATAAGGTAAA       1601 TAAAGTAT          T
                              AAGGTAAGGTAAA
                              |||||||||||||
                              TTTTATTCCATTT
                       CTC_____           T
GAM116 PPP3R1        AAAATGTAAT-TAAGGTAAAT    1596 TAAA  TAAGG        T
                              GTA    TAAGGTAAAT
                              |||    ||||||||||
                              CAT    ATTCCATTTA
                       TTTA  TA___        T
GAM116 PTPN12        AGTATAAGG-CAGGTAGAT     1604 TAAAGT      A   AAT
                              ATAAGGTA GGTA
                              |||||||| ||||
                              TATTCCGT CCAT
                       _____        _   CTA
GAM116 RFXAP         AAGTATAA-GAAAAATAATTTT   1603 TAAA      T   ATTT
                              GTATAAGG AAGGTAA
                              |||||||| |||||||
                              CATATTCT TTTTATT
                          ____       _    AAAA
GAM116 RFXAP         AAAGTATAAGAAAAAGGTA     1592 TA         T_    AATT
                              AAGTATAAGG AAGGTA
                              |||||||||| ||||||
                              TTCATATTCT TTCCAT
                                __        TT   AIII
GAM116 SPF30       AAAATATAAGGATAAAAAGGTAAAT  1593 TA       T____     TTII
                              AAGTATAAGG   AAGGTAAAT
                              ||||||||||   |||||||||
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                          TTTATATTCC    TTCCATTTA
                           __      TATTT    CIII
GAM116 SPO11       TAAAGTATAAAGGCAAAGGAAAAT  1607      _   T  TTTI
                          TAAAGTATAA GGTAAGG AAA
                          IIIIIIIII IIIIII III
                          ATTTCATATT CCGTTTC TTT
                            T    C  TAII
GAM116 TCTEL1      AAAGTATAAAGTATGGAAAATT   1599 TA       A  T   T
                          AAGTATAAGGTA GG AAATT
                          IIIIIIIIIII II IIIII
                          TTCATATTTCAT CC TTTAA
                          __        A  T   T
GAM116 USP7        AAAGTATAACTGAAGG-AAAT    1597 TA     GGT  T  T
                          AAGTATAA  AAGG AAAT
                          IIIIIIII  IIII IIII
                          TTCATATT  TTCC TTTA
                          __      GAC   _  T
GAM116 ZNF24       GTAAAAGGAAATAAGGGTAAATTT  1606 TAAAGTATA    _   I
                          AGGTAAGG TAAATTT
                          IIIIIIII IIIIIII
                          TTTATTCC ATTTAAA
                        TTCC_____     C    A
GAM117 AHR         GACAATTTATACACATTGAAATGGG 1631 ACAACAG    C   I
                          ACACATTGA ATGG
                          IIIIIIIII IIII
                          TGTGTAACT TACC
                        TTAAATA      T  I
GAM117 AHR         GACAATTTATACACATTGAAATGGG 1631 TG   CAG__     C   II
                          ACAA   ACACATTGA ATGGG
                          IIII   IIIIIIIII IIIII
                          TGTT   TGTGTAACT TACCC
                          __   AAATA     T  AI
GAM117 AKAP13      ACAACAGAC-C-TTTACATG   1623        ACATTG  I
                          ACAACAGAC   ACA
                          IIIIIIIII   III
                          TGTTGTCTG   TGT
                           GAAA__  A
GAM117 AKAP13      ACAACAGAC-C-TTTACATG   1623        ACATTG  I
                          ACAACAGAC   ACA
                          IIIIIIIII   III
                          TGTTGTCTG   TGT
                           GAAA__  A
GAM117 AKAP13      ACAACAGAC-C-TTTACATG   1623 TGAC     ACATTG
                            AACAGAC    ACATG
                            IIIIIII    IIIII
                            TTGTCTG    TGTAC
                          ____      GAAA__
GAM117 AKAP13      ACAACAGAC-C-TTTACATG   1623 TGAC     ACATTG
                            AACAGAC    ACATG
                            IIIIIII    IIIII
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                       TTGTCTG     TGTAC
                  ____       GAAA__
GAM117 ARHGEF7        TGA-AACAGACACAGTTATAT    1639   C        TTGACATGG
                     TGA AACAGACACA
                     ||| |||||||||
                     ACT TTGTCTGTGT
                       _         CAATATA||
GAM117 ARHGEF7        TGA-AACAGACACAGTTATAT    1639 _ C        TTGACA|
                      GA AACAGACACA
                      || |||||||||
                      CT TTGTCTGTGT
                       A _        CAATAT|
GAM117 BCAR1        ACAGC-GACTC-TTGACATGGG    1625 TGACAACA  ACA
                        GAC  TTGACATGG
                        ||| |||||||||
                        CTG  AACTGTACC
                     TCG_____  AG_
GAM117 BCAR1        ACAGC-GACTC-TTGACATGGG    1625 CA   AC A_       |
                      ACAG AC TTGACATGG
                      |||| || |||||||||
                      TGTC TG AACTGTACC
                       __  GC AG        |
GAM117 CACNA1C      ACATGAGAAGCATTGACAT       1622  AC  CA       ||
                        ACA AGA CATTGACA
                        ||| ||| |||||||||
                        TGT TCT GTAACTGT
                         AC  TC      A|
GAM117 CACNA1C      ACATGAGAAGCATTGACAT       1622 TGACAAC  CA      GG
                          AGA  CATTGACAT
                          ||| |||||||||
                          TCT GTAACTGTA
                     TAC____  TC      AC
GAM117 CBS         TGACAACAGAATC--TGTCATGGG 1642          CACA  A
                    TGACAACAGA    TTG CATGGG
                    ||||||||||    ||| ||||||
                    ACTGTTGTCT    GAC GTACCC
                         TA__  A
GAM117 CBS         TGACAACAGAATC--TGTCATGGG 1642 _        CACA  A  |
                       GACAACAGA    TTG CATGG
                       |||||||||    ||| |||||
                       CTGTTGTCT    GAC GTACC
                       A    TA__  A  |
GAM117 CD3Z        TGACAACAGAAGCCAAATTTACA  1636        CA_ TTG__  TGGG|
                     TGACAACAGA CA   ACA
                     |||||||||| ||   |||
                     ACTGTTGTCT GT   TGT
                         TCG TTAAA ||IGG
GAM117 CDKN2C        GACACACAGACACACATACAT    1630 _ A      TG   |
                      ACA CAGACACAT ACA
                      ||| ||||||||| |||
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                              TGT GTCTGTGTG TGT
                               G  _       TA  I
GAM117 CDKN2C           GACACACAGACACACATACAT   1630 TG  _        TG  GGG
                             ACA ACAGACACAT ACAT
                             ||| |||||||||| ||||
                             TGT TGTCTGTGTG TGTA
                              __  G       TA  AII
GAM117 DIAPH2           GAAAACAGATACATTGACA   1633  C   C      II
                             GA AACAGA ACATTGAC
                             || |||||| |||||||||
                             CT TTGTCT TGTAACTG
                              T      A       TI
GAM117 DIAPH2           GAAAACAGATACATTGACA   1633 TGAC   C       TGG
                               AACAGA ACATTGACA
                               |||||| |||||||||
                               TTGTCT TGTAACTGT
                              TT__    A       TII
GAM117 EMX2           TGACAAAATATTGACATTGACAT  1638    CAGAC__      GGGI
                           TGACAA    ACATTGACAT
                           ||||||    ||||||||||
                           ACTGTT    TGTAACTGTA
                              TTATAAC      IIIG
GAM117 ETF1           GACATCAGGTTACACATTGACA   1632  A  ___         III
                           GACA CAG  ACACATTGAC
                           |||| |||  ||||||||||
                           CTGT GTC  TGTGTAACTG
                            A   CAA        TII
GAM117 ETF1           GACATCAGGTTACACATTGACA   1632 TG A  ___        TGGG
                           ACA CAG  ACACATTGACA
                           ||| |||  ||||||||||
                           TGT GTC  TGTGTAACTGT
                            __  A   CAA        CIII
GAM117 IL11RA         ACAGACACATGGTCACACATGG   1626        TG____    IIIC
                           ACAGACACAT    ACATG
                           ||||||||||    |||||
                           TGTCTGTGTA    TGTAC
                              CCAGTG    CIII
GAM117 IL11RA         ACAGACACATGGTCACACATGG   1626 TG  ACAG_   T   GG
                             ACA    ACACAT GACATG
                             |||    |||||| ||||||
                             TGT    TGTGTA CTGTGT
                            G_ ACCAG     C    II
GAM117 IL17BR         TGACACCTGCTAC-TTGACATGG  1641    ACAGAC A      G
                           TGACA    AC TTGACATGG
                           |||||    || |||||||||
                           ACTGT    TG AACTGTACC
                             GGACGA  _      I
GAM117 IL17BR         TGACACCTGCTAC-TTGACATGG  1641 _  ACAGAC A      I
                             GACA   AC TTGACATG
                             ||||   || ||||||||
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                      CTGT    TG AACTGTAC
                   A   GGACGA _        I
GAM117 KDR         GACA-CAGACACATT--CTTGGG  1635   A       GACATI
                   GACA CAGACACATT
                   IIII IIIIIIIIII
                   CTGT GTCTGTGTAA
                       _       GAACCC
GAM117 KDR         GACA-CAGACACATT--CTTGGG  1635 TG  A      GACA
                   ACA CAGACACATT   TGG
                   III IIIIIIIIII   III
                   TGT GTCTGTGTAA   ACC
                     __ _       GA__
GAM117 LRAT        AATACACACTGACATGGG      1619 ACAG          I
                       ACACATTGACATGG
                       IIIIIIIIIIIII
                       TGTGTGACTGTACC
                   TATG          I
GAM117 LRAT        AATACACACTGACATGGG       1619 TGACAACAG
                         ACACATTGACATGG
                         IIIIIIIIIIIII
                         TGTGTGACTGTACC
                   G_____
GAM117 MEN1        ACAGACACA--GGCTTGGG    1627       TTGACATGGI
                   ACAGACACA
                   IIIIIIIII
                   TGTCTGTGT
                       CCGAACCCII
GAM117 NCALD       ACCACAGACACACTTGCCCATG   1621 CA       GA__  I
                       ACAGACACATT   CAT
                       IIIIIIIIII    III
                       TGTCTGTGTGA   GTA
                     __       ACGG  I
GAM117 NCALD       ACCACAGACACACTTGCCCATG   1621 TGACA      GA__  GG
                       ACAGACACATT   CATG
                       IIIIIIIIII    IIII
                       TGTCTGTGTGA   GTAC
                   G____       ACGG  AG
GAM117 PNUTL1      AACAGACACAATGACCTGGG   1618     T  A I
                   ACAGACACA TGAC TGG
                   IIIIIIIII IIII III
                   TGTCTGTGT ACTG ACC
                       T  G  I
GAM117 PNUTL1      AACAGACACAATGACCTGGG   1618 TGACAACA   T  A
                       GACACA TGAC TGG
                       IIIIII IIII III
                       CTGTGT ACTG ACC
                   _____      T  G
GAM117 PTGFRN      ACAGACACATT--CTTGGG    1628       GACA  I
                   ACAGACACATT   TGG
                   IIIIIIIIII    III
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                    TGTCTGTGTAA  ACC
                      GA__   C
GAM117 SDC2        GACAACAGATAAATTAACA    1634      CAC    II
                     GACAACAGA ATTGAC
                     ||||||||| ||||||
                     CTGTTGTCT TAATTG
                        ATT    TI
GAM117 SDC2        GACAACAGATAAATTAACA    1634 TG    CAC     TGG
                      ACAACAGA ATTGACA
                      ||||||||| |||||||
                      TGTTGTCT TAATTGT
                      __     ATT    TII
GAM117 SLC29A1      GACACACAGACACATACACA    1629  _       TGACII
                     GACA ACAGACACAT
                     |||| |||||||||||
                     CTGT TGTCTGTGTA
                       G      TGTGTI
GAM117 SLC29A1      GACACACAGACACATACACA    1629 TG  _      TG
                      ACA ACAGACACAT ACATGG
                      ||| |||||||||| ||||||
                      TGT TGTCTGTGTA TGTGTC
                      __    G        __
GAM117 SMP1        TGACAA-ATACTTACATTGACA    1637     CAG __      TGGG
                      TGACAA  AC ACATTGACA
                      ||||||  || |||||||||
                      ACTGTT  TG TGTAACTGT
                       TA_  AA     IIIG
GAM117 SMP1        TGACAA-ATACTTACATTGACA    1637 G   CAG __       I
                       ACAA  AC ACATTGAC
                       ||||  || |||||||||
                       TGTT  TG TGTAACTG
                       _    TA_ AA      I
GAM117 SUV39H1       ACAGACAGACACATAGATCTGG    1620 CA       T CA I
                       ACAGACACAT GA  TG
                       |||||||||| ||  ||
                       TGTCTGTGTA CT  AC
                      TC       T AG  I
GAM117 SUV39H1       ACAGACAGACACATAGATCTGG    1620 TGACA      T CA  G
                        ACAGACACAT GA  TGG
                        |||||||||| ||  |||
                        TGTCTGTGTA CT  ACC
                      TC___        T AG  G
GAM117 UPF3A        TGCCAAAA-ATACATTGACAT    1640 GA_  C  C      I
                       CAA AGA ACATTGACA
                       ||| ||| |||||||||
                       GTT TTT TGTAACTGT
                      ACG _  A    I
GAM117 UPF3A        TGCCAAAA-ATACATTGACAT    1640 TGA  C  C      GG
                       CAA AGA ACATTGACAT
                       ||| ||| ||||||||||
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                      GTT TTT TGTAACTGTA
                      ACG  _  A        II
GAM117 ZNF255         ACAATAGATG--TTGACATGGG  1624 _  C  CACA        I
                      CAA AGA    TTGACATGG
                      III III   IIIIIIIII
                      GTT TCT    AACTGTACC
                       T  A  AC__         I
GAM117 ZNF255         ACAATAGATG--TTGACATGGG   1624 TGACAAC  CACA
                          AGA    TTGACATGG
                          III   IIIIIIIII
                          TCT    AACTGTACC
                      TTA____  AC__
GAM118 AHR            GACAATTTATACACATTGAAATGGG 1631 TG  CAG__       C   II
                      ACAA    ACACATTGA ATGGG
                      IIII    IIIIIIIII IIIII
                      TGTT    TGTGTAACT TACCC
                      __  AAATA    T  AI
GAM118 AKAP13         ACAACAGAC-C-TTTACATG    1623 TGAC     ACATTG
                      AACAGAC    ACATG
                      IIIIIII    IIIII
                      TTGTCTG    TGTAC
                      ____    GAAA__
GAM118 AKAP13         ACAACAGAC-C-TTTACATG    1623 TGAC     ACATTG
                      AACAGAC    ACATG
                      IIIIIII    IIIII
                      TTGTCTG    TGTAC
                      ____    GAAA__
GAM118 ARHGEF7        TGA-AACAGACACAGTTATAT    1639  C      TTGACATGG
                      TGA AACAGACACA
                      III IIIIIIIIII
                      ACT TTGTCTGTGT
                       _     CAATATAII
GAM118 BCAR1         ACAGC-GACTC-TTGACATGGG   1625 TGACAACA  ACA
                        GAC  TTGACATGG
                        III  IIIIIIIII
                        CTG  AACTGTACC
                      TCG____  AG_
GAM118 CACNA1C        ACATGAGAAGCATTGACAT     1622 TGACAAC  CA    GG
                      AGA  CATTGACAT
                      III  IIIIIIIII
                      TCT  GTAACTGTA
                      TAC____  TC    AC
GAM118 CBS           TGACAACAGAATC--TGTCATGGG 1642        CACA  A
                      TGACAACAGA   TTG CATGGG
                      IIIIIIIIII   III IIIIII
                      ACTGTTGTCT   GAC GTACCC
                            TA__  A
GAM118 CD3Z          TGACAACAGAAGCCAAATTTACA  1636       CA_ TTG__  TGGGI
                      TGACAACAGA  CA   ACA
                      IIIIIIIIII  II   III
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                      ACTGTTGTCT  GT    TGT
                        TCG  TTAAA  IIIGG
GAM118 CDKN2C         GACACACAGACACACATACAT    1630 TG  _       TG  GGG
                        ACA ACAGACACAT ACAT
                        ||| |||||||||| ||||
                        TGT TGTCTGTGTG TGTA
                        __  G     TA  AII
GAM118 DIAPH2         GAAAACAGATACATTGACA    1633 TGAC   C       TGG
                           AACAGA ACATTGACA
                           |||||| |||||||||
                           TTGTCT TGTAACTGT
                         TT__  A      TII
GAM118 EMX2          TGACAAAATATTGACATTGACAT  1638      CAGAC__      GGGI
                        TGACAA     ACATTGACAT
                        ||||||     ||||||||||
                        ACTGTT     TGTAACTGTA
                          TTATAAC        IIIG
GAM118 ETF1          GACATCAGGTTACACATTGACA  1632 TG  A ___      TGGG
                        ACA CAG  ACACATTGACA
                        ||| |||  |||||||||||
                        TGT GTC  TGTGTAACTGT
                         __  A  CAA       CIII
GAM118 IL11RA        ACAGACACATGGTCACACATGG  1626 TG  ACAG_    T    GG
                        ACA    ACACAT GACATG
                        |||    |||||| ||||||
                        TGT    TGTGTA CTGTGT
                        G_ ACCAG    C   II
GAM118 IL17BR        TGACACCTGCTAC-TTGACATGG  1641     ACAGAC A      G
                        TGACA    AC TTGACATGG
                        |||||    || |||||||||
                        ACTGT    TG AACTGTACC
                          GGACGA  _      I
GAM118 KDR          GACA-CAGACACATT--CTTGGG  1635 TG  A      GACA
                        ACA CAGACACATT  TGG
                        ||| ||||||||||  |||
                        TGT GTCTGTGTAA  ACC
                        __  _       GA__
GAM118 LRAT         AATACACACACTGACATGGG     1619 TGACAACAG
                           ACACATTGACATGG
                           ||||||||||||||
                           TGTGTGACTGTACC
                        G_____
GAM118 NCALD        ACCACAGACACACTTGCCCATG   1621 TGACA      GA__ GG
                        ACAGACACATT  CATG
                        |||||||||||  ||||
                        TGTCTGTGTGA  GTAC
                        G____     ACGG  AG
GAM118 PNUTL1       AACAGACACAATGACCTGGG     1618 TGACAACA    T  A
                        GACACA TGAC TGG
                        |||||| |||| |||
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                      CTGTGT ACTG ACC
                      _____    T  G
GAM118 SDC2       GACAACAGATAAATTAACA    1634 TG    CAC    TGG
                      ACAACAGA ATTGACA
                      |||||||| |||||||
                      TGTTGTCT TAATTGT
                        __      ATT    TII
GAM118 SLC29A1    GACACACAGACACATACACA   1629 TG _       TG
                      ACA ACAGACACAT ACATGG
                      ||| |||||||||| ||||||
                      TGT TGTCTGTGTA TGTGTC
                        __    G        __
GAM118 SMP1       TGACAA-ATACTTACATTGACA  1637   CAG __       TGGG
                      TGACAA  AC ACATTGACA
                      ||||||  || |||||||||
                      ACTGTT  TG TGTAACTGT
                        TA_  AA       IIIG
GAM118 SUV39H1    ACAGACAGACACATAGATCTGG  1620 TGACA      T  CA  G
                      ACAGACACAT GA TGG
                      |||||||||| || |||
                      TGTCTGTGTA CT  ACC
                      TC___         T AG  G
GAM118 UPF3A      TGCCAAAA-ATACATTGACAT   1640 TGA  C  C      GG
                      CAA AGA ACATTGACAT
                      ||| ||| ||||||||||
                      GTT TTT TGTAACTGTA
                      ACG  _  A      II
GAM118 ZNF255     ACAATAGATG--TTGACATGGG   1624 TGACAAC  CACA
                      AGA   TTGACATGG
                      |||   |||||||||
                      TCT   AACTGTACC
                      TTA____    AC__
GAM119 BLTR2      ACAACAGACAGTGAGAGAGTTG  1677 AA      T _T   C I
                      CAACAGACA TG G GAGGG TG
                      ||||||||| || | ||||| ||
                      GTTGTCTGT AC C CTCTC AC
                        __       C T T   A A
GAM119 EPHB1      AAGAAAAGAATGTCATTGGTGAGG  1670 AACAACAGA____       GCTGI
                      CATTGGTGAGG
                      |||||||||||
                      GTAACCACTCC
                      TTCTTTTCTTACA         IIIGT
GAM119 EPHB2      AACAACAGATGCTGGAGAGG    1673      CA  T  GCT
                      AACAACAGA TTGG GAGG
                      ||||||||| |||| ||||
                      TTGTTGTCT GACC CTCC
                         AC  T  III
GAM119 EPHB4      AACAGACA-TGATGATGGGC    1676 AACAAC   T  _
                      AGACAT GGTGA GGGCT
                      |||||| ||||| |||||
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                        TCTGTA CTACT CCCGG
                        _____       _    A
GAM119 LHX3             CAACAGACATCTGTGGGTGC   1682 AACA       G  A _ T
                        ACAGACATT GTG GG GC
                        ||||||||| ||| || ||
                        TGTCTGTAG CAC CC CG
                        ____        A  _ A T
GAM119 MMP15            CAGACAGGGTGTGTGAGGGCTG   1683 AACAACAGACAT _
                             TG GTGAGGGCTG
                             || ||||||||||
                             AC CACTCCCGAC
                        TCCC_____ A
GAM119 PIK3R3           AACAACAGATCATTCTTTAGG   1671     _  GGTG  GCTG
                        AACAACAGA CATT   AGG
                        ||||||||| ||||   |||
                        TTGTTGTCT GTAA   TCC
                         A   GAAA  |||G
GAM119 PLXNA1           ACACGCATGCGGTGAGGGCTG    1680 AACAACAGA  _
                           CAT TGGTGAGGGCTG
                           ||| |||||||||||||
                           GTA GCCACTCCCGAC
                        C_____   C
GAM119 PPP1R2           AACAGAGCAGACATTGGTGA   1669  A__       GGGCT
                        AACA  CAGACATTGGTGA
                        ||||  ||||||||||||||
                        TTGT  GTCTGTAACCACT
                         CTC         |||GT
GAM119 RBBP2            AACAGCAGACATTGGGGTCAGGGCTG 1672  A     __ G    ||
                        AACA CAGACATT  GGT AGGGCTG
                        |||| |||||||| ||| |||||||
                        TTGT GTCTGTAA  CCA TCCCGAC
                         C   CC  G    ||
GAM119 SLC26A4          CAACAGACACCTTGGTCGAAGG   1681 AACA      __  _  CTG
                        ACAGACAT TGGT GAGGG
                        |||||||| |||| |||||
                        TGTCTGTG ACCA CTTCC
                        ____       GA  G   CTI
GAM119 SPOCK            ACACACACTTTGTGAGGGCTG    1679 AACAACAG   G_
                          ACATT GTGAGGGCTG
                          ||||| |||||||||||
                          TGTGA CACTCCCGAC
                        _____   AA
GAM119 SRY              AACATAAGAAA---GTGAGGGCTG 1675 AAC  GACATT
                        AACA    GGTGAGGGCTG
                        ||||    |||||||||||
                        TTGT    TCACTCCCGAC
                        ___  ATTCTT
GAM119 TBX6             AACAACAGAC--TGGTGTGGCCTG 1674       AT  A G
                        AACAACAGAC TGGTG GG CTG
                        |||||||||| ||||| || |||
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                              TTGTTGTCTG  ACCAC CC GAC
                                  __       A  G
GAM119  VANGL2          ACAAAAGTTGTTGGTGAGG    1678 AA  C  ACA       GCT
                              CAA AG  TTGGTGAGG
                              ||| ||  |||||||||
                              GTT TC  AACCACTCC
                              __   T  AAC       AII
GAM120  DRD1            TGAAAATACATG-TCTTCTCGC   1697  T  ATG        I
                              GA GATA  GTCTTCTCG
                              || ||||  |||||||||
                              CT TTAT  CAGAAGAGC
                                T  GTA        I
GAM120  DRD1            TGAAAATACATG-TCTTCTCGC   1697 TGTGAT  ATG        C
                                 GATA  GTCTTCTCGC
                                 ||||  ||||||||||
                                 TTAT  CAGAAGAGCG
                              TT____  GTA        A
GAM120  FGF12           TGATGATAAATGGT-TCCTGGC   1696      _  C  CGI
                              GATGATAA TGGT TTCT
                              |||||||| |||| ||||
                              CTACTATT ACCA AGGA
                                 T  _  CCI
GAM120  FGF12           TGATGATAAATGGT-TCCTGGC   1696 T    TA  C  C C
                              GTGATGA ATGGT TTCT GC
                              ||||||| ||||| |||| ||
                              TACTATT TACCA AGGA CG
                                _   __  _    C A
GAM120  GRB14           ATGATAATG---TTTTCGCC   1686 _       GTCTTC
                              TGATAATG    TCGC
                              ||||||||    ||||
                              ACTATTAC    AGCG
                                T   AAA___
GAM120  HRH1           TGTAAT--TGAAGGTCTTCTC   1698      GATAAT      GC
                              TGTGAT   GGTCTTCTC
                              ||||||   |||||||||
                              ACATTA   CCAGAAGAG
                               ACTT__       II
GAM120  HRH1           TGTAAT--TGAAGGTCTTCTC   1698 _   GATAAT      I
                              GTGAT   GGTCTTCT
                              |||||   ||||||||
                              CATTA   CCAGAAGA
                              A   ACTT__       I
GAM120  HUNK           GATAATGCTGCCTTCTCGCC   1688      __        III
                              GATAATG GTCTTCTCGC
                              ||||||| ||||||||||
                              CTATTAC CGGAAGAGCG
                                 GA      GII
GAM120  IKBKAP          TGAGTGGAAATGGTCTTCTC   1693 _ AT        II
                              TGA TG AATGGTCTTCT
                              ||| || ||||||||||
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                         ACT AC  TTACCAGAAGA
                          C  CT         GI
GAM120  IKBKAP           TGAGTGGAAATGGTCTTCTC    1693 T  AT  T         GC
                          GTG  GA AATGGTCTTCTC
                          ||| ||  ||||||||||||
                          CAC  CT TTACCAGAAGAG
                          T  __  _          AC
GAM120  MAOB             GTGAGGACTAAATGGTCTT    1690   T  __       |||
                          GTGA GAT AATGGTCT
                          |||| ||| ||||||||
                          CACT CTG TTACCAGA
                           C  AT       A||
GAM120  MAOB             GTGAGGACTAAATGGTCTT    1690 TG  T  __       CTCGC
                          TGA GAT AATGGTCTT
                          ||| ||| |||||||||
                          ACT CTG TTACCAGAA
                          __  C  AT      A|||C
GAM120  NLGN1            TGATAATGGTGTACCTGCC    1695       CTT TC  ||
                          TGATAATGGT  C  GC
                          ||||||||||  |  ||
                          ACTATTACCA  G  CG
                          CAT GA  GI
GAM120  PLA2G5           GTGATGATAA---TCTGATCGC    1692        __      TTCTI
                          GTGATGATAA TGGTC
                          |||||||||| |||||
                          CACTACTATT ACTAG
                           AG    CGIII
GAM120  PLA2G5           GTGATGATAA---TCTGATCGC    1692 TG     ATG   TC
                          TGATGATA GTCT TCGC
                          |||||||| |||| ||||
                          ACTACTAT TAGA AGCG
                          __   ___      CT
GAM120  SPAM1            GTGATGATAGTCATGGTTTTTTC    1691 TG      ___    C C  CCI
                          TGATGATA ATGGT TT TCG
                          |||||||| ||||| || |||
                          ACTACTAT  TACCA AA AGT
                          __     CAG   A A  |||
GAM120  SYNGR1           GATAATGGTGCTACTTCTC    1687         ____    IIIG
                          GATAATGGT  CTTCT
                          |||||||||  |||||
                          CTATTACCA  GAAGA
                           CGAT   GIII
GAM120  TMSB4Y           TGAGAAAGCCCTTCTCGCC    1694  TAAT  _      II
                          TGA  GGTC TTCTCGC
                          |||  |||| ||||||||
                          ACT  TCGG AAGAGCG
                          CTT_ G   GI
GAM120  YY1              GTGGTCGAGAAGGGTCTTCTC    1689 TGA  T T     I
                          TGA AA GGTCTTCT
                          ||| || |||||||
```

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                         GCT TT CCAGAAGA
                         CCA   C  C        I
GAM120 YY1          GTGGTCGAGAAGGGTCTTCTC   1689 TGTGA  T  T      GCC
                         TGA AA GGTCTTCTC
                         ||| || |||||||||
                         GCT TT CCAGAAGAG
                         ACCA_   C  C      AII
GAM121 LAMB3            GTGATCCCCAGAAAGGACC   1701 GTTATA  TG      II
                         CC GAAAGGAC
                         || |||||||||
                         GG CTTTCCTG
                         CACTAG GT       GI
GAM121 LAMB3            GTGATCCCCAGAAAGGACC   1701 TGTTATA TG      GTG
                         CC GAAAGGACC
                         || |||||||||
                         GG CTTTCCTGG
                         ACTAG__ GT      AII
GAM122 APPL          TGTTATAGAACTTCTTTTGAAA   1711      ___ A      AGACT
                         TGTTATAGA TT TTTGGAA
                         ||||||||| || |||||||
                         ACAATATCT AG AAACTTT
                              TGA  A      IIITC
GAM122 CD53          ATAGTTTTTTTCTGGAAAGACT   1704 TGTTATAGATTA
                              TTTGGAAAGACT
                              ||||||||||||
                              AGACCTTTCTGA
                         AAAAAA_____
GAM122 DIAPH2          TGTGATAGTACCTTATTTGGAAA   1710  T  A___       GACTI
                         TGT ATAG   TTATTTGGAAA
                         ||| ||||   |||||||||||
                         ACA TATC   AATAAACCTTT
                              C  ATGG        IIITC
GAM122 FVT1          TGTTCAA-ATTATTTGGAAA   1714  A           GAC
                         TGTT TAGATTATTTGGAAA
                         |||| |||||||||||||||
                         ACAA GTTTAATAAACCTTT
                              _             |||
GAM122 HRMT1L1        ATAATTTATTTGG-AAGAC   1706 TGTTATAGA      A
                              TTATTTGGAA GA
                              |||||||||| ||
                              AATAAACCTT CT
                         A_____        _
GAM122 JAK2          TTATAGATTAACTATGGAAA   1717 TGTT     TT__     C
                         ATAGATTA  TGGAAAGA
                         ||||||||  ||||||||
                         TATCTAAT  ACCTTTTT
                         ____        TGAT    I
GAM122 NDUFAB1        TTATAGATTTATTTTCAAAGA   1716 TGTT    _  GG   CT
                         ATAGATT ATTT AAAGA
                         ||||||| |||| |||||
```

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                          TATCTAA TAAA  TTTCT
                           ____    A  AG    CA
GAM122 NRCAM              TGTTATAGATTTTCATATTTGGA 1712        _____       AAGACTI
                         TGTTATAGAT    TATTTGGA
                         |||||||||    ||||||||
                         ACAATATCTA   ATAAACCT
                           AAAGT       IIITCAG
GAM122 POLK          TTATAGATT-TGTGGAAAG     1720 TGTT    ATT    A
                         ATAGATT  TGGAAAG
                         |||||||  |||||||
                         TATCTAA  ACCTTTC
                          ____    AC_       A
GAM122 RCN2          ATGGAGTATTTAGGAAAGACT    1705 TGTTATAGAT    _
                         TATTT GGAAAGACT
                         ||||| |||||||||
                         ATAAA CCTTTCTGA
                         TC_____      T
GAM122 RFXAP        TTAAATGTTATTTGGAAAGA    1721 TGTTATAGA         C
                         TTATTTGGAAAGA
                         |||||||||||||
                         AATAAACCTTTCT
                         TTTAC____        A
GAM122 ROS1         TGCTATATGAATTATTTGG    1709     __      AAAGAC
                         TGTTATA GATTATTTGG
                         ||||||| ||||||||||
                         ACGATAT TTAATAAACC
                           AC      IIITCA
GAM122 SCN3A        TTATTAGATTACTTTTTGGAAAG  1715 TGTTA      ___      ACTI
                         TAGATTAT TTGGAAAG
                         |||||||| ||||||||
                         ATCTAATG AACCTTTC
                         TA___      AAA      GTII
GAM122 SLC1A2       GTTATAAAGCATTATTTGGCAAAGAC 1707 _  TAT  _      _   TII
                         TGT  AG ATTATTTGG AAAGAC
                         |||  || ||||||||| ||||||
                         ATA  TC TAATAAACC TTTCTG
                         A  TT_ G      G    TII
GAM122 SULT1C1      TTATATCTTACTTTGGAAAGA     1719 TGTT  GA     _     CT
                         ATA  TTATTT GGAAAGA
                         |||  |||||| |||||||
                         TAT  AATGAA CCTTTCT
                           ____    AG    A    TA
GAM122 TEX15        TAAAAAATATTTGGAAAAACT     1708 TGTTAT  T
                         AGA TATTTGGAAAGACT
                         ||| |||||||||||||
                         TTT ATAAACCTTTTTGA
                         _____      T
GAM122 ZNF192       TTAAAGGTTAATTTTGGAAAG    1718 TGTTATAGATTA      A
                         TTTGGAAAG CT
                         ||||||||| ||
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```
                              AAACCTTTC GG
                          TTTCCAATTA__       _
GAM122  ZNF192            TGTTCCAAAT-ATTTGGAA      1713   ATA  T      AGA
                          TGTT  GA TATTTGGAA
                          |||| || |||||||||
                          ACAA  TT ATAAACCTT
                            GG_  T      |||
GAM123  ASS               AGGCCCCAGCTCC-TCATTG      1727 TTAG        AA   G
                          GCCCCAGCTCC CATTG
                          |||||||||||| |||||
                          CGGGGTCGAGG GTAAC
                            ____          A_   A
GAM123  C10orf2           TTAGGCCCCAGCTC--ACAT       1732           _ ACATTG
                          TTAGGCCCCAGCTC CA
                          |||||||||||||| ||
                          AATCCGGGGTCGAG GT
                            T A|||GG
GAM123  C5               TTCGGCCCCAG--CAAACATT     1733 TTA      TCC    GG
                          GGCCCCAGC  AACATT
                          ||||||||| ||||||
                          CCGGGGTCG  TTGTAA
                          AAG       T__    ||
GAM123  DAG1             AGCCCTCACCTGGAACATTGGG     1729 TTAGG   _ G  CC
                          CCC CA CT AACATTGGG
                          ||| || || |||||||||
                          GGG GT GA TTGTAACCC
                          _____    A  G  CC
GAM123  ED1              AGGCCTGCTGCTCCAACATTG      1724 TTAG   CCA_        GG
                          GCC  GCTCCAACATTG
                          |||  |||||||||||
                          CGG  CGAGGTTGTAAC
                          _____   ACGA       AC
GAM123  EFNB1            AGGCCCCAGC-CCAAGACTGGG     1730 TTAG     T  C
                          GCCCCAGC CCAA ATTGGG
                          |||||||| |||| ||||||
                          CGGGGTCG GGTT TGACCC
                          ____     _  C
GAM123  FUS1             TAGGCCCCAG-GCAAAC-TTGG     1731 TT     CTC  CA
                          AGGCCCCAG CAA TTGG
                          ||||||||| ||| ||||
                          TCCGGGGTC GTT AACC
                            C__  TG
GAM123  KCNK5            AGGCCCCAG-GCCCACATAGG      1728 TTAG    CT  A  T
                          GCCCCAG CCA CAT GG
                          ||||||| ||| ||| ||
                          CGGGGTC GGT GTA CC
                          ____    CG  _  T
GAM123  MLC1             AGGCAC-AGACTAGCCAACATTGG  1725 TTAG CC  _  __      GI
                          GC CAG CT CCAACATTGG
                          || ||| || |||||||||
```

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                              CG  GTC GA  GGTTGTAACC
                         ____ T_ T TC       GG
GAM123 MVK               AGGCCCCAGCACCTGAGCATTGG   1726 TTAG    T AA__     I
                              GCCCCAGC CC   CATTGGG
                              ||||||| ||   |||||||
                              CGGGGTCG GG   GTAACCT
                         ____      T ACTC      G
GAM124 BTG1              AGATCTCAA--T-AGCTGCA    1738 TTAG    ACTC
                              ATCTCAA   AGCTGCA
                              ||||||| |||||||
                              TAGAGTT   TCGACGT
                         ____      A___
GAM124 DAB1              AGAAATGACACTCTGAGCTGCACA  1736 TTA_ CTCAA   __      I
                              GAT   ACTC AGCTGCACA
                              |||   |||| |||||||||
                              CTG   TGAG TCGACGTGT
                         TTTA _____ AC      A
GAM124 HYAL1            AGAT-TCCACCCCAGCTGCAC    1739 TTAGATC AAA
                              TC  CTCAGCTGCAC
                              ||  |||||||||||
                              AG  GGGTCGACGTG
                         TA_____ GTG
GAM124 RPH3AL          CTCAAAGCTGTCAGCTGCA     1740 TTAGATCTCAAAC      C
                                  TCAGCTGCA
                                  |||||||||
                                  AGTCGACGT
                         CGAC_____      C
GAM124 TAF11            AGCTCGGAAACCCGAGCTGCACA   1737 TTAGAT  __   _      I
                              CTC  AAACTC AGCTGCACA
                              |||  |||||| |||||||||
                              GAG  TTTGGG TCGACGTGT
                         _____ CC   C      C
GAM125 AR              GGCTGGCAGCGCTGGGCCGA     1769 CAACAGGAT CA
                              GC  CGCTGGGCCG
                              ||  |||||||||
                              CG  GCGACCCGGC
                         _____ TC
GAM125 BCL9             ACTGCAGTGCTCATCCTGGAGG   1748  _    A      II
                              ACT CGGTGT CGTCCTGGAGG
                              ||| |||||| |||||||||||
                              TGA GTCACG GTAGGACCTCC
                              C    A      II
GAM125 BCL9             ACTGCAGTGCTCATCCTGGAGG   1748 CT    A      I
                              CGGTGT CGTCCTGGAG
                              |||||| |||||||||||
                              GTCACG GTAGGACCTC
                              AC     A      I
GAM125 CARD10           CACCAGGGT-CCACGCTGG     1757 CAA   ATG      GCC
                              CAGG  CCACGCTGG
                              ||||  |||||||||
```

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                          GTCC  GGTGCGACC
                          GTG   CA_        III
GAM125 CEBPD              AGGCTGTCACCTCGCTGGGCC    1751 CAACAGGAT  A      GA
                              GCC CGCTGGGCC
                              III IIIIIIIII
                              TGG GCGACCCGG
                              ACAG_____  A      GT
GAM125 CSH2              ACAGGATGCCACGC-GGGC     1746 CAAC        T
                            AGGATGCCACGC GGGCC
                            IIIIIIIIIIII IIIII
                            TCCTACGGTGCG CCCGG
                            ____       _
GAM125 CSH2              ACAGGATGCCACGC-GGGC     1746 CAAC        T    C
                            AGGATGCCACGC GGGC
                            IIIIIIIIIIII IIII
                            TCCTACGGTGCG CCCG
                            ____       _  T
GAM125 CSHL1             ACAGGATGCCACGC-GGGCC    1747 CAAC        T
                            AGGATGCCACGC GGGCC
                            IIIIIIIIIIII IIIII
                            TCCTACGGTGCG CCCGG
                            ____        _
GAM125 CSHL1             ACAGGATGCCACGC-GGGCC    1747 CAAC        T    G
                            AGGATGCCACGC GGGCC
                            IIIIIIIIIIII IIIII
                            TCCTACGGTGCG CCCGG
                            ____        _  G
GAM125 ESR1             CAACCAGG--GCCACGCTGGG     1753 CAA_  AT       CCG
                            CAGG  GCCACGCTGGG
                            IIII  IIIIIIIIIII
                            GTCC  CGGTGCGACCC
                            GTTG  __         III
GAM125 FNTB             CAGGACCCAGCACGCTGGGC      1762 CAA_  GATGC      CG
                            CAG    CACGCTGGGC
                            III    IIIIIIIIII
                            GTC    GTGCGACCCG
                            CTGG  _____       CC
GAM125 GH1              ACAGGGATGCCAC-CCGGGC      1744 CAACA      G    CG
                            GGATGCCAC CTGGGC
                            IIIIIIIII IIIIII
                            CCTACGGTG GGCCCG
                            TC___      _    TC
GAM125 GH1              ACAGGGATGCCAC-CCGGGC      1744 CAACA      G    CG
                            GGATGCCAC CTGGGC
                            IIIIIIIII IIIIII
                            CCTACGGTG GGCCCG
                            TC___      _    TC
GAM125 GH2              ACAGGGATGCCAC-CCGGGC      1744 CAACA      G    CG
                            GGATGCCAC CTGGGC
                            IIIIIIIII IIIIII
```

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                        CCTACGGTG GGCCG
                    TC___       _   TC
GAM125 HIP12        ACAGGATGCCTGACCCTCGTCC   1745 CAAC       __ G _GG A
                        AGGATGCC AC CT G CCG
                        ||||||||| || || | |||
                        TCCTACGG TG GA C GGT
                          ____       AC G G AG  |
GAM125 HIVEP3       CAAGAG-ATGCCACGCTGG     1756 CAACA         GCC
                        GGATGCCACGCTGG
                        |||||||||||||
                        TCTACGGTGCGACC
                    GTTC_           |||
GAM125 HUNK         CAACAGGATG-AACACAGGGCC   1758      CC  T   GA
                        CAACAGGATG ACGC GGGCC
                        |||||||||| |||| |||||
                        GTTGTCCTAC TGTG CCCGG
                          T_  T   ||
GAM125 IRS2         GGACGCGCTCGCTGGGCCG      1768 CAACAGGAT CA
                          GC CGCTGGGCCG
                          || |||||||||
                          CG GCGACCCGGC
                    G_____ A_
GAM125 JPH2         CAGGATGCCA-GCAGAGGCTGA   1764 CAACAG   C T_  C
                        GATGCCA GC GGGC GA
                        ||||||| || |||| ||
                        CTACGGT CG TCCG CT
                    _____      _ TC  A
GAM125 MTMR1        CAGGGTCTCCACGCTGGGC      1761 CAACA ATG       CG
                        GG  CCACGCTGGGC
                        ||  |||||||||||
                        CC  GGTGCGACCCG
                    _____ AGA       AC
GAM125 NUCB1        CTGGGCCTAGGTCCTGGAG      1766 ACTC G C     G
                        GGT TA GTCCTGGAG
                        ||| || |||||||||
                        CCG AT CAGGACCTC
                    AC__  G C    A
GAM125 NUCB1        CTGGGCCTAGGTCCTGGAG      1766 CTC G C      ||
                        GGT TA GTCCTGGA
                        ||| || ||||||||
                        CCG AT CAGGACCT
                    GAC  G C    C|
GAM125 OTX1         CAACAGGATCGGGACCACGGAGGGC 1754      ____   CT  CGA||
                        CAACAGGAT  GCCACG GGGC
                        |||||||||  |||||| ||||
                        GTTGTCCTA  TGGTGC CCCG
                        GCCC    CT  |||AG
GAM125 PACE4        CAGGGTTCGCCA-GCTGGGCCG   1759 CAACAGGA    C     A
                        TGCCA GCTGGGCCG
                        ||||| ||||||||
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                          GCGGT CGACCCGGC
                      CCAA____   _        C
GAM125 PROS1          CAATCAGGA-GCCACGCTG    1752 CAA_   T      GGCC
                          CAGGA GCCACGCTG
                          ||||| |||||||||
                          GTCCT CGGTGCGAC
                      GTTA    _      IIIA
GAM125 RNH            CAGGATGCCAGGATCCTGGACC   1763 CAACAG     CG___     GA
                          GATGCCA   CTGGGCC
                          |||||||   |||||||
                          CTACGGT   GACCTGG
                      _____       CCTAG    GC
GAM125 SORL1          CAGGAGAGCCG-GCTGGGCCG    1760 CAACA  T  AC
                          GGA GCC  GCTGGGCCG
                          ||| |||  |||||||||
                          TCT CGG  CGACCCGGC
                      C____  _  C_
GAM125 SPK           AACTGTGATGCCACGCT---CCGA  1743 CAACAG       GGG
                          GATGCCACGCT  CCGA
                          |||||||||||  ||||
                          CTACGGTGCGA  GGCT
                      TGACA_        ___
GAM125 STXBP1        CAGGTGGGCGCGCTGGGCC     1765 CAACA  AT CA
                          GG  GC  CGCTGGGCCG
                          ||  ||  ||||||||||
                          CC  CG  GCGACCCGGT
                      CA___  __  C_
GAM125 SURF6         ACTCAGAGGGTGTCCTGGAG     1749      TGTAC    GI
                          ACTCGG   GTCCTGGAG
                          ||||||   |||||||||
                          TGAGTC   CAGGACCTC
                          TCCCA         II
GAM125 SURF6         ACTCAGAGGGTGTCCTGGAG     1749      TGTAC    I
                          CTCGG   GTCCTGGA
                          |||||   ||||||||
                          GAGTC   CAGGACCT
                          TCCCA        I
GAM125 UBASH3A       ACTCGGTGTACATGCTGCAGG    1750          C G I
                          ACTCGGTGTACGT CTG AGG
                          ||||||||||||| ||| |||
                          TGAGCCACATGTA GAC TCC
                              C  G  I
GAM125 UBASH3A       ACTCGGTGTACATGCTGCAGG    1750          C G I
                          CTCGGTGTACGT CTG AG
                          |||||||||||| ||| ||
                          GAGCCACATGTA GAC TC
                              C  G  I
GAM125 WIF1          CTCCCTCTA-GTCCTGGAGG     1767 A__   GGTGTAC
                          CTC     GTCCTGGAGG
                          |||     ||||||||||
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                            GAG     CAGGACCTCC
                            AGG  AT_____
GAM125  WIF1        CTCCCTCTA-GTCCTGGAGG     1767 TCGGTGTAC      I
                            GTCCTGGAG
                            |||||||||
                            CAGGACCTC
                            GAGGGAGAT      I
GAM125  ZNF14       CACCATGTTGACCACGCTGGTCTCGA 1755 CAA  GGA _     GC_ II
                            CA  TG CCACGCTGG  CGA
                            ||  || ||||||||| |||
                            GT  AC GGTGCGACC  GCT
                            GTG ACA  T      AGA  II
GAM126  ABL1        GGCCCAGTCTGGGGCTATTTG     1773  A _ __       III
                            GGC CA TC  GGGCTATTT
                            ||| || ||  |||||||||
                            CCG GT AG  CCCGATAAA
                             G  C  AC       CII
GAM126  ABL1        GGCCCAGTCTGGGGCTATTTG     1773 TG  A _ __       AACAC
                            GC CA TC  GGGCTATTTG
                            || || ||  ||||||||||
                            CG GT AG  CCCGATAAAC
                            __ G  C  AC      CIIIC
GAM126  BCL11A      GGCAGAGTCAAGTGCTATTTGAACAC 1774 GCA_  TCGG        I
                            CA   GCTATTTGAACA
                            ||   ||||||||||||
                            GT   CGATAAACTTGT
                            CTCA TCA_         I
GAM126  BCL11A      GGCAGAGTCAAGTGCTATTTGAACAC 1774 TG  CA_ __        II
                            GCA  TCG G GCTATTTGAACAC
                            |||  ||| | ||||||||||||||
                            CGT  AGT C CGATAAACTTGTG
                            __  CTC  T A      GI
GAM126  LARS2       CACATATTGGTTATTTGAACA     1772 A  CG_  C      I
                            CAT  GG TATTTGAAC
                            |||  || ||||||||
                            GTA  CC ATAAACTTG
                            _  TAA  A       I
GAM126  LARS2       CACATATTGGTTATTTGAACA     1772 TGGCACATC  GC      C
                            GG  TATTTGAACA
                            ||  |||||||||
                            CC  ATAAACTTGT
                            TATAA____  A_       A
GAM126  LPL         TGGCACATCAGGAACAATTT     1777          CTATTIII
                            TGGCACATCGGG
                            ||||||||||||
                            ACCGTGTAGTCC
                             TTGTTAAA
GAM126  LPL         TGGCACATCAGGAACAATTT     1777          CTATTTG
                            TGGCACATCGGG    AACA
                            ||||||||||||    ||||
```

```
                    ACCGTGTAGTCC    TTGT
                              _____
GAM126 RNF26        GGCCCTTCTG--TATTTGAAC    1776 TG  ACA  GGGC      A
                          GC  TC   TATTTGAAC
                          || ||  |||||||||
                          CG  AG   ATAAACTTG
                          __ GGA  AC__        G
GAM126 SLC20A1      TGGAACC-CGGGCTATTTTACACA 1778  C  A       GA  I
                          TGG AC TCGGGCTATTT ACAC
                          ||| || |||||||||| ||||
                          ACC TG GGCCCGATAAA TGTG
                           T _      A_  T
GAM126 SLC20A1      TGGAACC-CGGGCTATTTTACACA 1778  C  A       GAACI
                          GG AC TCGGGCTATTT
                          || || |||||||||||
                          CC TG GGCCCGATAAA
                           T _       ATGTG
GAM126 SLC4A7       TGCCAAATTTTGCAATTTGAACAC 1779 G  A  TCGG__  T      I
                          GC CA   GC ATTTGAACA
                          || ||    || |||||||||
                          CG GT    CG TAAACTTGT
                          _  _   TTAAAA  T      I
GAM126 SLC4A7       TGCCAAATTTTGCAATTTGAACAC 1779 TG  A  TCGG__  T      I
                          GC CA   GC ATTTGAACAC
                          || ||    || ||||||||||
                          CG GT    CG TAAACTTGTG
                          A_  _  TTAAAA  T      I
GAM126 TRPM1        GGCACTTCCTAGGCTATTTG     1775    A __      III
                          GGCAC TC GGGCTATTT
                          ||||| || |||||||||
                          CCGTG AG TCCGATAAA
                            A GA       CII
GAM126 TRPM1        GGCACTTCCTAGGCTATTTG     1775 TG  A __       AACA
                          GCAC TC GGGCTATTTG
                          |||| || ||||||||||
                          CGTG AG TCCGATAAAC
                           __  A GA       CIII
GAM127 GNAL         GAGATGGTCTGGTCTCTTCG    1782       CA____   IIIC
                          GAGATGGTC    CTTC
                          |||||||||    ||||
                          CTCTACCAG    GAAG
                            ACCAGA    CIII
GAM127 GNAL         GAGATGGTCTGGTCTCTTCG    1782 TG    CA____    ACCTGC
                          AGATGGTC    CTTCG
                          ||||||||    |||||
                          TCTACCAG    GAAGC
                          __     ACCAGA  CIIICC
GAM127 MYCL2        TGAGGTAATGGTCCACGTTGA   1784      ___      TTCGACCTGCC
                          TGAG ATGGTCCAC
                          |||| |||||||||
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                    ACTC  TACCAGGTG
                    CAT       CAACTIIICCG
GAM127 MYCL2        TGAGGTAATGGTCCACGTTGA   1784  ___        TTCGIII
                    TGAG  ATGGTCCAC
                    IIII  IIIIIIIII
                    ACTC  TACCAGGTG
                    CAT       CAACTII
GAM127 OAS3         GAAGGTACCCAACTGCGACCTGCC  1783 TGAGAT _ __  T     I
                      GGT CC  ACT CGACCTGCC
                      III II  III IIIIIIIII
                      CCA GG  TGA GCTGGACGG
                    _____   T GT  C     T
GAM127 OAS3         GAAGGTACCCAACTGCGACCTGCC  1783 ATGG  _ T    I
                      TCCA CT CGACCTGC
                      IIII II IIIIIIII
                      GGGT GA GCTGGACG
                    CAT_   T C     I
GAM127 SLC6A6       TGGTCCAC-TC-ACCTCCC     1785       CG  GCI
                    TGGTCCACTT ACCT
                    IIIIIIIIII IIII
                    ACCAGGTGAG TGGA
                     __   GGG
GAM127 SLC6A6       TGGTCCAC-TC-ACCTCCC     1785 TGAGATGGTC   GA TG
                       CACTTC  CC
                       IIIIII II
                       GTGGAG GG
                    GTGA_____   __ GT
GAM128 ARHC         GCTCACTCGGCGTA-G-CCTG   1798        C T  GA
                    GCTCACTCGGTGTA G CCTG
                    IIIIIIIIIIIIII I IIII
                    CGAGTGAGCCGCAT C GGAC
                             _ _   II
GAM128 CHRNB2       GCTCACTC---GTCCATCCT    1796      GTGTA   GG
                    GCTCACTCG  CGTCCT
                    IIIIIIIII   IIIIII
                    CGAGTGAGC   GTAGGA
                         AG___    II
GAM128 DBCCR1       GCTCCATTCTGTGGA-GTCCTGGAG 1793   AC_ G TAC      I
                    GCTC  TC GTG  GTCCTGGAG
                    IIII  II III  IIIIIIIII
                    CGAG  AG CAC  CAGGACCTC
                    GTA A  CT_       I
GAM128 EPHB4        CTCACTCGG-GTAGGATCC     1791 GC    T C_  TGG
                     TCACTCGG GTA  GTCC
                     IIIIIIII III  IIII
                     AGTGAGCC CAT  TAGG
                      __    _  CC  CII
GAM128 FUT8         CTCACTTCCCTGGA-GTCCTGGAG 1790 GC   _ GG TAC     I
                     TCACT C TG  GTCCTGGAG
                     IIIII I II  IIIIIIIII
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                        AGTGA G  AC   CAGGACCTC
              __      A GG  CT_        G
GAM128 GPD1            GCTCCCTGGG---A-GTCCTGGAG  1800    A TC  TGTAC
                      GCTC C  GG    GTCCTGGA
                      |||| | ||    ||||||||
                      CGAG G  CC    CAGGACCT
                       _ GA  CT___
GAM128 HS3ST4          GCTCCCTAGG---A-GTCCTGGAG  1799    A C  TGTAC
                      GCTC CT GG    GTCCTGGA
                      |||| || ||    ||||||||
                      CGAG GA CC    CAGGACCT
                       G T  T___
GAM128 IBSP           GCTTCCTCTG-GCA-GTCCTGGAG  1801   CA  GGT  C
                      GCT CTC  GTA GTCCTGGAG
                      ||| |||  ||| |||||||||
                      CGA GAG  CGT CAGGACCTC
                       AG  AC_   _
GAM128 LMCD1          GCTCACTCGGAATTGCATTCTGGA  1795      TGTA_  C   GI
                      GCTCACTCGG   CGT CTGGA
                      ||||||||||   ||| |||||
                      CGAGTGAGCC   GTA GACCT
                        TTAAC  A   ||
GAM128 LY64          TCATTCGGTGTACTTGCCTAGA   1802 GCTCAC       GT_
                      TCGGTGTAC  CCTGGAG
                      |||||||||  |||||||
                      AGCCACATG  GGATCTT
                    TA____        AAC
GAM128 MSI1          GCTCACTC-GTG---GTCCT    1797      G TAC   G
                      GCTCACTCG TG  GTCCT
                      ||||||||| ||  |||||
                      CGAGTGAGC AC  CAGGA
                        _ ___    |
GAM128 PAX5          CACTTGCTGGG-GTCCTGGAG    1789 GCTCACTCG GTAC
                      GT  GTCCTGGA
                      ||  ||||||||
                      CG  CAGGACCT
                    AA_____ ACCC
GAM128 SNTB1         CTCACTCGGT---CCTCCTG    1792 GC       GTACG
                      TCACTCGGT  TCCTGG
                      |||||||||  ||||||
                      AGTGAGCCA  AGGACT
                      __      GG___
GAM128 SURF6         ACTCAGAGGGTGTCCTGGAG    1749 GCTCACTC T AC
                      GG GT  GTCCTGGA
                      || || ||||||||
                      CC CA  CAGGACCT
                    TCT_____ _ __
GAM128 TYK2          GCTCAGCTGAGGGTGAGTCCTGGAG  1794    _ C__  TAC      ||
                      GCTCA CT GGTG  GTCCTGGAG
                      ||||| || ||||  |||||||||
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                          CGAGT GA  CCAC  CAGGACCTC
                            C  CTC   T__        II
GAM128  UBASH3A          CACTCGGTGTACATGCTGCAG   1788 GCTCAC       C  G
                            TCGGTGTACGT CTG AG
                            IIIIIIIIIII III II
                            AGCCACATGTA GAC TC
                            _____        C  G
GAM129  ASH1             AGGTATCTAGGAAGAAGCC   1806 TGAG    __     CGGA
                            GTATCTA AAGAGGCC
                            IIIIIII IIIIIIII
                            CATAGAT TTCTTCGG
                            ____      CC    AGII
GAM129  DRD5             AGCTATGGTAAAGAGGCCC   1805 TGA_  TCTA      GGA
                            GGTA   AAGAGGCCC
                            IIII   IIIIIIIII
                            CCAT   TTCTCCGGG
                            GATA   ____       GGI
GAM129  MNT             TGAGGTATCTGTGCAGGCCCGG   1811      AAAG    AA
                            TGAGGTATCT AGGCCCGG
                            IIIIIIIIII  IIIIIIII
                            ACTCCATAGA  TCCGGGCC
                            CACG        II
GAM129  RANBP3            TGAAGTCCC-AAAGAGGCCC   1809    A       GGA
                            TGAGGT TCTAAAGAGGCCC
                            IIIIII IIIIIIIIIIII
                            ACTTCA GGGTTTCTCCGGG
                            _                III
GAM129  RGS6            GAAGTATCTAAA-AGCGCC   1808 TG       AG  CGG
                            AGGTATCTAAAG GCC
                            IIIIIIIIIIII III
                            TTCATAGATTTT CGG
                            __           CG  TII
GAM129  SEC22L1          AGGGATCCAACACTGGCCCGGAA   1807 TGA T   AGA_      I
                            GG ATCTAA  GGCCCGGAA
                            II IIIIII  IIIIIIIII
                            CC TAGGTT  CCGGGCCTT
                            ___ _    GTGA       C
GAM129  WHSC1            TGAGTTAGCCAA-GAGGCCC   1810   G T  A    GGA
                            TGAG TA CTAA GAGGCCC
                            IIII II IIII IIIIIIII
                            ACTC AT GGTT CTCCGGG
                            A  C    _     III
GAM130  CNGB3            ATGTTCTGGGTGTTAGCAA   1815 GA  _     II
                            ATG CTGG TGTTAGCA
                            III IIII IIIIIIII
                            TAC GACC ACAATCGT
                            AA  C    TI
GAM130  DVL3            CATGGACTGG-GTTGGGAA   1818       T AGCAI
                            CATGGACTGG GTT
                            IIIIIIIIII III
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                         GTACCTGACC CAA
                          _   CCCTT
GAM130 EIF2C1        GGCAGATGGA---GTGTTAGCA   1822 _   C   CTG
                         GCA ATGGA  GTGTTAGC
                         ||| |||||  ||||||||
                         CGT TACCT  CACAATCG
                          C  C     ___
GAM130 EIF2C1        GGCAGATGGA---GTGTTAGCA   1822 TG  C   CTG
                         GCA ATGGA  GTGTTAGCA
                         ||| |||||  |||||||||
                         CGT TACCT  CACAATCGT
                          __  C    ___
GAM130 EIF4EBP2       GGAATATGAA-TGGTGTTAG    1821 GCAC_  C     I
                          ATGGA TGGTGTTA
                          ||||| ||||||||
                          TACTT ACCACAAT
                          CCTTA   _     I
GAM130 EIF4EBP2       GGAATATGAA-TGGTGTTAG    1821 TGGCAC  C     CA
                          ATGGA TGGTGTTAG
                          ||||| |||||||||
                          TACTT ACCACAATC
                          CTTA__   _     CI
GAM130 KCNK10        CACATGGACCCTTGCTAACAA   1816       GG    I
                         ACATGGACT TGTTAGCA
                         ||||||||| ||||||||
                         TGTACCTGG ACGATTGT
                          GA      I
GAM130 KCNK10        CACATGGACCCTTGCTAACAA   1816 TGGCAC    GG
                          ATGGACT TGTTAGCAA
                          ||||||| |||||||||
                          TACCTGG ACGATTGTT
                          _____    GA
GAM130 MAPK4         TGGCACATGAGGAGTGGTGT   1824     __  C   TAGCA
                        TGGCACAT GGA TGGTGT
                        |||||||| ||| ||||||
                        ACCGTGTA CCT ACCACA
                         CT  C   IIIAA
GAM130 MAPK4         TGGCACATGAGGAGTGGTGT   1824     __  C   III
                        TGGCACAT GGA TGGTG
                        |||||||| ||| |||||
                        ACCGTGTA CCT ACCAC
                         CT  C   AII
GAM130 MEN1          GCACATGGA--GAGGTTAGC   1819      CT GTTAI
                         GCACATGGA GGT
                         ||||||||| |||
                         CGTGTACCT CCA
                          CT ATCGI
GAM130 MEN1          GCACATGGA--GAGGTTAGC   1819 TGGC   CT T
                         ACATGGA GG GTTAGC
                         ||||||| || ||||||
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                              TGTACCT  TC CAATCG
                              ____         C_ _
GAM130  NT5E            GGCACATG----GGTGTT-GCAA   1823        ACTG    A
                           GGCACATGG   GTGTT GC
                           |||||||||   ||||| ||
                           CCGTGTACC   CACAA CG


                                       ____     _
GAM130  NT5E            GGCACATG----GGTGTT-GCAA   1823 TG      ACTG    A
                            GCACATGG   GTGTT GC
                            ||||||||   ||||| ||
                            CGTGTACC   CACAA CG


                                  __     ____   _
GAM130  RAD54L            CAGGAACTGGTGTTTGGAA        1817  T         AGCAII
                             CA GGACTGGTGTT
                             || |||||||||||
                             GT CTTGACCACAA
                              C        ACCTTI
GAM130  SFRP4            ACATGCTTACTG-TGTTAGCAA   1814 CATGG_    G       I
                            ACTG TGTTAGCA
                            |||| ||||||||
                            TGAC ACAATCGT
                            TACGAA   _     I
GAM130  SFRP4            ACATGCTTACTG-TGTTAGCAA   1814 TGGCACATGG   G
                               ACTG TGTTAGCAA
                               |||| |||||||||
                               TGAC ACAATCGTT
                            CGAA_____    _
GAM130  SUFU          GGCAGCAGAGAGCAGTGTTAGCAA   1820 __  CAT  CT         I
                             GCA  GGA  GGTGTTAGCA
                             |||  |||  ||||||||||
                             CGT  TCT  TCACAATCGT
                            GT  C__  CG       I
GAM130  SUFU          GGCAGCAGAGAGCAGTGTTAGCAA   1820 TG  _ T  CT         I
                           GCA CA GGA  GGTGTTAGCAA
                           ||| || |||  |||||||||||
                           CGT GT TCT  TCACAATCGTT
                           __   C  C  CG        T
GAM131  CDH13          GTACAGACTAAGTGAAATTG      1829     TC__       III
                            GTACAG   AGTGAAATT
                            ||||||   |||||||||
                            CATGTC   TCACTTTAA
                             TGAT       CII
GAM131  CDH13          GTACAGACTAAGTGAAATTG      1829 TGTGTA  TC__        AA
                            CAG   AGTGAAATTG
                            |||   ||||||||||
                            GTC   TCACTTTAAC
                            _____   TGAT        AT
GAM131  CORO1C           TGTACAGTCA-TCAAAATGA    1834 _        GT  TGI
                            GTACAGTCA  GAAAT
                            |||||||||  |||||
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                              CATGTCAGT TTTTA
                         A        AG    CII
GAM131  CORO1C          TGTACAGTCA-TCAAAATGA    1834 TGTG     GT    T A
                          TACAGTCA  GAAAT GA
                          |||||||| ||||| ||
                          ATGTCAGT TTTTA CT
                         ____      AG    _ G
GAM131  CRIM1            GTATACAGTCAGTTATATT    1832       GAAATII
                           GTGTACAGTCAGT
                           |||||||||||
                           CATATGTCAGTCA
                             ATATAAI
GAM131  CRIM1            GTATACAGTCAGTTATATT    1832 TG        GAAATTGAA
                            TGTACAGTCAGT
                            |||||||||||
                            ATATGTCAGTCA
                            __        ATATAAII
GAM131  EPB41L2          GTGCACAGTCAGTGAACTT    1833          ATII
                            GTGTACAGTCAGTGAA
                            ||||||||||||||
                            CACGTGTCAGTCACTT
                                GAAI
GAM131  EPB41L2          GTGCACAGTCAGTGAACTT    1833 TG        ATTGAA
                             TGTACAGTCAGTGAA
                             |||||||||||||
                             ACGTGTCAGTCACTT
                             __        GAAGII
GAM131  ESR1            AGACAGTGCAAAATTGAAG     1828  T  __      III
                           AG CAGTG AAATTGAA
                           || ||||| |||||||||
                           TC GTCAC TTTAACTT
                            T    GT     CII
GAM131  F2R            TGTGTACAGTGTGTAAAAT      1841       CA     TGAA
                          TGTGTACAGT GTGAAAT
                          |||||||||| |||||||
                          ACACATGTCA CATTTTA
                            CA       IIIG
GAM131  F2R            TGTGTACAGTGTGTAAAAT      1841       CA    II
                          TGTGTACAGT GTGAAA
                          |||||||||| ||||||
                          ACACATGTCA CATTTT
                            CA     AI
GAM131  KCNJ10         TGTGTT-AGTCACTCCAAATTGAAG 1839    AC    GTG_      I
                          TGTGT AGTCA   AAATTGAAG
                          ||||| ||||| |||||||||
                          ACACA TCAGT TTTAACTTC
                          A_   GAGG       I
GAM131  KCNJ10         TGTGTT-AGTCACTCCAAATTGAAG 1839    AC    GTG_      I
                          GTGT AGTCA   AAATTGAA
                          |||| ||||| |||||||||
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                              CACA  TCAGT   TTTAACTT
                                A_   GAGG      I
GAM131 KIAA0442       TGTGTACAGGTA-TGAAAT      1840       TCA     TGA
                         TGTGTACAG  GTGAAAT
                         |||||||||  |||||||
                         ACACATGTC  TACTTTA
                            CA_     III
GAM131 KIAA0442       TGTGTACAGGTA-TGAAAT      1840       TCA     I
                         TGTGTACAG  GTGAAA
                         |||||||||  ||||||
                         ACACATGTC  TACTTT
                            CA_     A
GAM131 LNK           TGTG-ACAGTGTCAGTGAAA      1836    T __        TTGAA
                        TGTG ACA  GTCAGTGAAA
                        |||| |||  ||||||||||
                        ACAC TGT  CAGTCACTTT
                          _  CA      IIIGA
GAM131 LNK           TGTG-ACAGTGTCAGTGAAA      1836    T __        II
                        TGTG ACA  GTCAGTGAA
                        |||| |||  |||||||||
                        ACAC TGT  CAGTCACTT
                          _  CA      TI
GAM131 MECP2          GTACAGACAAAATTGAAATTGA    1830     T ___      III
                         GTACAG CAG  TGAAATTG
                         |||||| |||  ||||||||
                         CATGTC GTT  ACTTTAAC
                           T    TTA      TII
GAM131 MECP2          GTACAGACAAAATTGAAATTGA    1830 TGTGTA  T ___        AG
                          CAG CAG  TGAAATTGA
                          ||| |||  |||||||||
                          GTC GTT  ACTTTAACT
                          _____  T  TTA       CC
GAM131 OTC           GTGCATCAG-CACTTAAATTGAAG   1831     A T GTG       I
                        TGTGT CAG CA  AAATTGAAG
                        ||||| ||| ||  |||||||||
                        ACGTA GTC GT  TTTAACTTC
                          _   _ GAA        C
GAM131 OTC           GTGCATCAG-CACTTAAATTGAAG   1831     _ T GTG       I
                        TGTA CAG CA  AAATTGAA
                        |||| ||| ||  ||||||||
                        ACGT GTC GT  TTTAACTT
                          A  _ GAA        I
GAM131 PPP2R4        TGTGGCTACAGTCAG-GAAA      1835      __     T TTGAA
                        TGTG TACAGTCAG GAAA
                        |||| |||||||||| ||||
                        ACAC ATGTCAGTC CTTT
                           CG      _  IIIGA
GAM131 PPP2R4        TGTGGCTACAGTCAG-GAAA      1835      __     T II
                        TGTG TACAGTCAG GAA
                        |||| |||||||||| |||
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                      ACAC ATGTCAGTC CTT
                        CG        _  TI
GAM131 SNCA        TGTATTCACTTCAGTGAAAGGGAAG 1837    A  G_       TT II
                      TGTGT CA TCAGTGAAA GAAG
                      ||||| || ||||||||| ||||
                      ACATA GT AGTCACTTT CTTC
                        A  GA        CC  II
GAM131 SNCA        TGTATTCACTTCAGTGAAAGGGAAG 1837 GTG_  AG      TT  I
                        TAC TCAGTGAAA GAA
                        ||| ||||||||| |||
                        GTG AGTCACTTT CTT
                      ATAA  A_        CC  I
GAM131 SP100       TGTGTACAGGCAGCTTAAAT     1838      T  GAAAII
                      TGTGTACAG CAGT
                      ||||||||| ||||
                      ACACATGTC GTCG
                         C  AATTTA
GAM131 SP100       TGTGTACAGGCAGCTTAAAT     1838      T  GAAATTGAA
                      TGTGTACAG CAGT
                      ||||||||| ||||
                      ACACATGTC GTCG
                         C  AATTTAIII
GAM131 WHSC1L1       ACAGTCCATGTTGAAATTGA    1827   AG___       III
                        ACAGTC   TGAAATTG
                        ||||||   |||||||||
                        TGTCAG   ACTTTAAC
                          GTACA       TII
GAM131 WHSC1L1       ACAGTCCATGTTGAAATTGA      1827 TGTGTA GTCAG       A
                          CA   TGAAATTGA
                          ||   |||||||||
                          GT   ACTTTAACT
                        G_____ ACA__      A
GAM132 EFG1        TAGCATTCATTAGGTTGAT      1849       ATGAIII
                      TAGCATTCATTG
                      ||||||||||||
                      ATCGTAAGTAAT
                          CCAACTA
GAM132 EFG1        TAGCATTCATTAGGTTGAT      1849 TT       A__  TCTTG
                        AGCATTCATTG TGAT
                        ||||||||||| ||||
                        TCGTAAGTAAT ACTA
                          __    CCA  CIIIT
GAM132 GSTM3       ATTCATATCTTGATGATTCT     1847    ____      IIIA
                      ATTCAT TGATGATTC
                      |||||| |||||||||
                      TAAGTA ACTACTAAG
                        TAGA     AIII
GAM132 GSTM3       ATTCATATCTTGATGATTCT     1847 TTAGCAT A       G
                        TC TTGATGATTCTT
                        || |||||||||||
```

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                              AG AACTACTAAGAG
                        AT_____  _          G
GAM132 ISL1         AGCATTCATTTCTTGATTC    1844       GA_    II
                        AGCATTCATT  TGATT
                        ||||||||||  |||||
                        TCGTAAGTAA  ACTAA
                           AGA    GI
GAM132 ISL1         AGCATTCATTTCTTGATTC    1844 TTAG      GA_    TTG
                        CATTCATT  TGATTC
                        ||||||||  ||||||
                        GTAAGTAA  ACTAAG
                     ____          AGA    TCI
GAM132 MAPK1        ATTCATAAA-GATTCTTGT    1848    TGAT     I
                        ATTCAT   GATTCTTG
                        ||||||   ||||||||
                        TAAGTA   CTAAGAAC
                          TTT_       A
GAM132 MS4A1       TTTGCATTCATTCACTATTGCTGT  1855 TA      G  G  _  TI
                        GCATTCATT AT ATT CT
                        ||||||||| || ||| ||
                        CGTAAGTAA TG TAA GA
                        A_       G A  C CI
GAM132 MS4A1       TTTGCATTCATTCACTATTGCTGT  1855 TTA     G  G  C  I
                        GCATTCATT AT ATT TTGT
                        ||||||||| || ||| ||||
                        CGTAAGTAA TG TAA GACA
                        AAA      G A  C  I
GAM132 MYCBP          TTTATTGATGATTCTATGT     1856 TTC        TGII
                        ATTGATGATTCT
                        ||||||||||||
                        TAACTACTAAGA
                        AAA       TACA
GAM132 NR2E1       TTAGCATTCATTCAT-CTCCTTG   1854       G  GA   T
                        TTAGCATTCATT AT  TTCTTG
                        |||||||||||| ||  ||||||
                        AATCGTAAGTAA TA  AGGAAC
                          G  G_    I
GAM132 NR2E1       TTAGCATTCATTCAT-CTCCTTG   1854 _      G  GA   I
                        TAGCATTCATT AT  TTCTT
                        |||||||||||| ||  |||||
                        ATCGTAAGTAA TA  AGGAA
                        A      G  G_    I
GAM132 PCDHB4      TTAGCATTCATGGAACATT     1853        T  TGATII
                        TTAGCATTCAT GA
                        ||||||||||| ||
                        AATCGTAAGTA CT
                          C  TGTAAI
GAM132 PCDHB4      TTAGCATTCATGGAACATT     1853        T  TGATTCTTG
                        TTAGCATTCAT GA
                        ||||||||||| ||
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                         AATCGTAAGTA CT
                         C  TGTAAIIIT
GAM132 PROS1       AGCATTCATCTAT-A-TCTT    1846        GATG  CI
                         AGCATTCATT   ATT
                         IIIIIIIII   III
                         TCGTAAGTAG   TAG
                           ATA_  AA
GAM132 PROS1       AGCATTCATCTAT-A-TCTT    1846 TTAG      GATGAT
                           CATTCATT   TCTT
                           IIIIIIII   IIII
                           GTAAGTAG   AGAA
                         ____        ATAT__
GAM132 SOX11       AGAATTCATTAAGATGATTCT     1845  C      __       III
                         AG ATTCATT  GATGATTC
                         II IIIIIII  IIIIIIII
                         TC TAAGTAA  CTACTAAG
                          T    TT     AII
GAM132 SOX11       AGAATTCATTAAGATGATTCT     1845 TTAGC     __        T
                          ATTCATT GATGATTCTTG
                          IIIIIII IIIIIIIIIII
                          TAAGTAA CTACTAAGAGT
                         T____     TT       I
GAM132 STATH       TTTGCATTGCTCTTTGATGATTCTT 1852 TA__ AT A        I
                          GC TC TTGATGATTCT
                          II II IIIIIIIIIII
                          CG AG AACTACTAAGA
                         GTAA __ A       I
GAM132 STATH       TTTGCATTGCTCTTTGATGATTCTT 1852 TTA   ___ A         GTII
                          GCAT TC TTGATGATTCTT
                          IIII II IIIIIIIIIIII
                          CGTA AG AACTACTAAGAA
                         AAA   ACG  A        IIIT
GAM132 TZFP        TAGCATTCAGTGGTATGGTTGTT   1850 TT     T ATG  TC  I
                         AGCATTCA TG  AT TTGT
                         IIIIIIII II  II IIII
                         TCGTAAGT AC  TA AACA
                         __      C CA_ CC  A
GAM132 VPS41       TTAGCAAATCCTATTGATGA-TCTT 1851      __ _       CTTGTI
                         TTAGCA TTC ATTGATGATT
                         IIIIII III IIIIIIIIII
                         AATCGT AGG TAACTACTAG
                          TT  A     AAIIIT
GAM132 VPS41       TTAGCAAATCCTATTGATGA-TCTT 1851 TA __ _       CTI
                         GCA TTC ATTGATGATT
                         III III IIIIIIIIII
                         CGT AGG TAACTACTAG
                         __  TT  A     AII
GAM133 AQP1        GGTCAG-GCAGTAAGTCCG       1869 TGGCCA        C  TT
                          GGGCAGTAAG CCG
                          IIIIIIIIII III
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                          TCCGTCATTC GGC
                     CAG___          A  TI
GAM133  BAIAP3       GGCCAGGGCGGTAGGCGCCG    1868 TG      A  A _    TG
                     GCCAGGGC GTA GC CCGT
                     |||||||| ||| || ||||
                     CGGTCCCG CAT CG GGCG
                          __      C   C   II
GAM133  CYLN2        GGCCAGGGCTGTA---CCGTT    1871 TG     A  AGC
                     GCCAGGGC GTA   CCGTT
                     |||||||| |||   |||||
                     CGGTCCCG CAT   GGCAA
                          __      A  ___
GAM133  GNA11        GCCAGGGCAGGGTGGCCGT      1864 TGGC     TAAGC   TG
                     CAGGGCAG    CCGT
                     ||||||||    ||||
                     GTCCCGTC    GGCA
                          ____     CCACC   CG
GAM133  HD           TGGCCAGGG-AACCAGCCCG     1874     C  TA    TTG
                     TGGCCAGGG AG  AGCCCG
                     ||||||||| ||  ||||||
                     ACCGGTCCC TT  TCGGGC
                          _  GG     III
GAM133  IL11         GCCAGGGCAG-AAGTCTGT      1863 TGGC     T  CCC T
                     CAGGGCAG AAG   G T
                     |||||||| |||   | |
                     GTCCCGTC TTC   C A
                          ____      _  AGA _
GAM133  KRT16        TGGCCAGG---GTCAGCTCGT    1875       _  AAGCCCGTT
                     TGGCCAGGG CAGT
                     ||||||||| ||||
                     ACCGGTCCC GTCG
                          A   AGCAIIIGG
GAM133  MGAM         GCCAGGGCAGGATGTAGCCC     1862 TGGC     TA___   GTTG
                     CAGGGCAG    AGCCC
                     ||||||||    |||||
                     GTCCCGTC    TCGGG
                          ____      CTACA    GGII
GAM133  MTMR3        TGCCCAGGGCAGT--GCTC-TTGG  1878 G       AA  CCG
                     TG CCAGGGCAGT GC  TTGG
                     || ||||||||| || ||||
                     AC GGTCCCGTCA CG  AACC
                          G       __  AG_
GAM133  P2RY6        TGCCCAGGGCAG--AGCCC      1873  G       TA   GTT
                     TG CCAGGGCAG AGCCC
                     || ||||||||| |||||
                     AC GGTCCCGTC TCGGG
                          G      __   III
GAM133  PAH          GGCCAGGGCAGCCTGCCGGATG    1872 TG      AA  CGT  G
                     GCCAGGGCAGT GCC  TG
                     ||||||||||| ||| ||
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                          CGGTCCCGTCG CGG  AC
                           __    CCT G
GAM133 PARN            GGCCAGGGCATACGGCAAGCCC  1866 TG       ____        GTTGG
                          GCCAGGGCA  GTAAGCCC
                          |||||||||  |||||||
                          CGGTCCCGT  CGTTCGGG
                           __    ATGC    AIIIG
GAM133 PMP22           CAGGGCAGTCAGAGACCCG      1859 TGGC  GG  TAA    TG
                          CAG CAG  GCCCGT
                          ||| |||  ||||||
                          GTC GTC  TGGGCG
                          C___  A_ TC_    TC
GAM133 PYCR1           TGGCCAGGGCA-AAAGCCAGCTGG  1879       T   C   I
                          TGGCCAGGGCAG AAGCC GTTGG
                          |||||||||||| ||||| |||||
                          ACCGGTCCCGTT TTCGG CGACC
                           _    T   I
GAM133 RAB26           GGCC-GGGCTGCAAGGCCCGTTGG  1867 TG  A  A   _     I
                          GCC GGGC GTAAG CCCGTTGG
                          ||| |||| ||||| ||||||||
                          CGG CCCG CGTTC GGGCAACC
                          __  _   A   C      C
GAM133 SLC22A12        GGCCAGGGCAACGGGCCTGTT    1870 TG      TAA  C  GG
                          GCCAGGGCAG  GCC GTT
                          ||||||||||  ||| |||
                          CGGTCCCGTT  CGG CAA
                           __     GCC  A  AI
GAM133 SYCP1           TGGCCTGAAAAGAAAGCCCGTT    1877    A  C  T      GG
                          TGGCC GGG AG AAGCCCGTT
                          ||||| ||| || |||||||||
                          ACCGG CTT TC TTCGGGCAA
                           A  T  T     II
GAM133 SYNGR1          TGGCCAGGGAAG--AGCACGT     1876      C  TA  C  TG
                          TGGCCAGGG AG AGC CGT
                          ||||||||| || ||| |||
                          ACCGGTCCC TC TCG GCA
                           T  __  T  II
GAM133 TMEM1           GGCCAGGGCTCTGAGTAAGCGGCGTCGG1865 TG       ____      C_   III
                          GCCAGGGC  AGTAAGC CGTTGG
                          ||||||||  ||||||| |||||
                          CGGTCCCG  TCATTCG GCAGCC
                           __     AGAC    CC   TII
GAM133 TNP1            CCAGGGCAG--AGCCGCTGG      1861 TGGCCA     TA
                          GGGCAG AGCCCGTTG
                          |||||| |||||||||
                          CCCGTC TCGGGCGAC
                          _____  __
GAM133 UBTF            CCAGGGCAGT--GCCTGTT       1860 TGGCCA      AA  C
                          GGGCAGT GCC GTT
                          ||||||| ||| |||
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                       CCCGTCA  CGG CAA
                       _____      __   A
GAM134  BRCA1     GTTTCACCATGTTGGCCAGG    1885 TG    A    I
                       TCACCAT TTGGCCAG
                       ||||||| |||||||||
                       AGTGGTA AACCGGTC
                        AA       C    I
GAM134  BRCA1     GTTTCACCATGTTGGCCAGG    1885 TGCAGTGT   A
                        CACCAT TTGGCCAG
                        |||||| |||||||||
                        GTGGTA AACCGGTC
                       _____      C
GAM134  CPT2      GTTTCACCATGTTGGCCAGG    1885 TG    A    I
                       TCACCAT TTGGCCAG
                       ||||||| |||||||||
                       AGTGGTA AACCGGTC
                        AA       C     I
GAM134  CPT2      GTTTCACCATGTTGGCCAGG    1885 TGCAGTGT    A
                        CACCAT TTGGCCAG
                        |||||| |||||||||
                        GTGGTA AACCGGTC
                       _____      C
GAM134  CYP1A2   CAGGGTCCCACTATGTTGGCCAGG  1883 A  G   C A     I
                        GT TCAC AT TTGGCCAG
                        || |||| || |||||||||
                        CA GGTG TA AACCGGTC
                        C  G    A  C      I
GAM134  CYP1A2   CAGGGTCCCACTATGTTGGCCAGG  1883 TGCA G   C A      I
                        GT TCAC AT TTGGCCAGG
                        || |||| || ||||||||||
                        CA GGTG TA AACCGGTCC
                        CC__ G   A  C       G
GAM134  CYP4F3   GTTTCACCATATTGGCCAGG    1884 TG            I
                        TCACCATATTGGCCAG
                        ||||||||||||||||
                        AGTGGTATAACCGGTC
                        AA           I
GAM134  CYP4F3   GTTTCACCATATTGGCCAGG    1884 TGCAGTGT
                        CACCATATTGGCCAG
                        |||||||||||||||
                        GTGGTATAACCGGTC
                       _____
GAM134  DNASE2    GTTTCACCATGTTGGCCAGG    1885 TG    A    I
                        TCACCAT TTGGCCAG
                        ||||||| |||||||||
                        AGTGGTA AACCGGTC
                         AA       C    I
GAM134  DNASE2    GTTTCACCATGTTGGCCAGG    1885 TGCAGTGT   A
                         CACCAT TTGGCCAG
                         |||||| |||||||||
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                             GTGGTA AACCGGTC
                             _____
                                         C
GAM134  EGFL4          GTTTCACCATATTGGCCAGG      1884 TG             I
                             TCACCATATTGGCCAG
                             |||||||||||||||
                             AGTGGTATAACCGGTC
                             AA              I
GAM134  EGFL4          GTTTCACCATATTGGCCAGG      1884 TGCAGTGT
                             CACCATATTGGCCAG
                             |||||||||||||||
                             GTGGTATAACCGGTC

                             _____
GAM134  FGFR2          GTTTCACCATGTTGGCCAGG      1885 TG      A      I
                             TCACCAT TTGGCCAG
                             ||||||| ||||||||
                             AGTGGTA AACCGGTC
                             AA      C       I
GAM134  FGFR2          GTTTCACCATGTTGGCCAGG      1885 TGCAGTGT     A
                             CACCAT TTGGCCAG
                             |||||| ||||||||
                             GTGGTA AACCGGTC
                             _____
                                         C
GAM134  FUT6           GTTTCACCATATTGGCCAGG      1884 TG              I
                             TCACCATATTGGCCAG
                             ||||||||||||||||
                             AGTGGTATAACCGGTC
                             AA               I
GAM134  FUT6           GTTTCACCATATTGGCCAGG      1884 TGCAGTGT
                             CACCATATTGGCCAG
                             |||||||||||||||
                             GTGGTATAACCGGTC

                             _____
GAM134  HIP1           GTTTCACCATGTTGGCCAGG      1885 TG      A      I
                             TCACCAT TTGGCCAG
                             ||||||| ||||||||
                             AGTGGTA AACCGGTC
                             AA      C       I
GAM134  HIP1           GTTTCACCATGTTGGCCAGG      1885 TGCAGTGT     A
                             CACCAT TTGGCCAG
                             |||||| ||||||||
                             GTGGTA AACCGGTC
                             _____
                                         C
GAM134  IL17R          GTTTCACCATGTTGGCCAGG      1885 TG      A      I
                             TCACCAT TTGGCCAG
                             ||||||| ||||||||
                             AGTGGTA AACCGGTC
                             AA      C       I
GAM134  IL17R          GTTTCACCATGTTGGCCAGG      1885 TGCAGTGT     A
                             CACCAT TTGGCCAG
                             |||||| ||||||||
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                              GTGGTA AACCGGTC
                              _____    C
GAM134 IRAK4        GTTTCACCATGTTGGCCAGG    1885 TG     A     I
                         TCACCAT TTGGCCAG
                         ||||||| ||||||||
                        AGTGGTA AACCGGTC
                         AA        C     I
GAM134 IRAK4        GTTTCACCATGTTGGCCAGG    1885 TGCAGTGT    A
                          CACCAT TTGGCCAG
                          |||||| ||||||||
                         GTGGTA AACCGGTC
                         _____    C
GAM134 LAMC2         GTTTCACCATGTTGGCCAGG    1885 TG     A     I
                         TCACCAT TTGGCCAG
                         ||||||| ||||||||
                        AGTGGTA AACCGGTC
                         AA        C     I
GAM134 LAMC2         GTTTCACCATGTTGGCCAGG    1885 TGCAGTGT    A
                          CACCAT TTGGCCAG
                          |||||| ||||||||
                         GTGGTA AACCGGTC
                         _____    C
GAM134 LEP        GTTTCACCATGTTGGCCAGG    1885 TG     A     I
                         TCACCAT TTGGCCAG
                         ||||||| ||||||||
                        AGTGGTA AACCGGTC
                         AA        C     I
GAM134 LEP        GTTTCACCATGTTGGCCAGG    1885 TGCAGTGT    A
                          CACCAT TTGGCCAG
                          |||||| ||||||||
                         GTGGTA AACCGGTC
                         _____    C
GAM134 OPA3        AGTTTCACCATGTTGGCCAGG    1882 G     A     I
                         GT TCACCAT TTGGCCAG
                         || ||||||| ||||||||
                         CA AGTGGTA AACCGGTC
                         A        C     I
GAM134 OPA3        AGTTTCACCATGTTGGCCAGG    1882 TGCAGTG     A
                          TCACCAT TTGGCCAGG
                          ||||||| |||||||||
                         AGTGGTA AACCGGTCC
                         A_____    C
GAM134 PAICS        GTTTCACCATGTTGGCCAGG    1885 TG     A     I
                         TCACCAT TTGGCCAG
                         ||||||| ||||||||
                        AGTGGTA AACCGGTC
                         AA        C     I
GAM134 PAICS        GTTTCACCATGTTGGCCAGG    1885 TGCAGTGT    A
                          CACCAT TTGGCCAG
                          |||||| ||||||||
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                              GTGGTA AACCGGTC
                              _____   C
GAM134 PDE4C        GTTTCACCATGTTGGCCAGG     1885 TG     A     I
                           TCACCAT TTGGCCAG
                           |||||||  ||||||||
                           AGTGGTA AACCGGTC
                             AA     C     I
GAM134 PDE4C        GTTTCACCATGTTGGCCAGG     1885 TGCAGTGT    A
                             CACCAT TTGGCCAG
                             ||||||  ||||||||
                             GTGGTA AACCGGTC
                           _____   C
GAM134 PSMB2        GTTTCACCATGTTGGCCAGG     1885 TG     A     I
                           TCACCAT TTGGCCAG
                           |||||||  ||||||||
                           AGTGGTA AACCGGTC
                             AA     C     I
GAM134 PSMB2        GTTTCACCATGTTGGCCAGG     1885 TGCAGTGT    A
                             CACCAT TTGGCCAG
                             ||||||  ||||||||
                             GTGGTA AACCGGTC
                           _____   C
GAM134 TCF7        GTTTCACCATGTTGGCCAGG     1885 TG     A     I
                           TCACCAT TTGGCCAG
                           |||||||  ||||||||
                           AGTGGTA AACCGGTC
                             AA     C     I
GAM134 TCF7        GTTTCACCATGTTGGCCAGG     1885 TGCAGTGT    A
                             CACCAT TTGGCCAG
                             ||||||  ||||||||
                             GTGGTA AACCGGTC
                           _____   C
GAM134 UPK1B        GTTTCACCATGTTGGCCAGG     1885 TG     A     I
                           TCACCAT TTGGCCAG
                           |||||||  ||||||||
                           AGTGGTA AACCGGTC
                             AA     C     I
GAM134 UPK1B        GTTTCACCATGTTGGCCAGG     1885 TGCAGTGT    A
                             CACCAT TTGGCCAG
                             ||||||  ||||||||
                             GTGGTA AACCGGTC
                           _____   C
GAM134 VHL        GTTTCACCATGTTGGCCAGG     1885 TG     A     I
                           TCACCAT TTGGCCAG
                           |||||||  ||||||||
                           AGTGGTA AACCGGTC
                             AA     C     I
GAM134 VHL        GTTTCACCATGTTGGCCAGG     1885 TGCAGTGT    A
                             CACCAT TTGGCCAG
                             ||||||  ||||||||
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                        GTGGTA AACCGGTC
                        _____      C
GAM134 VHL          GTTTTACCATGTTGGCCAGG    1886 TGCAGTGTC   A
                        ACCAT TTGGCCAG
                        ||||| ||||||||
                        TGGTA AACCGGTC

                    A_____      C
GAM134 VHL          GTTTTACCATGTTGGCCAGG    1886 TGTC   A     I
                          ACCAT TTGGCCAG
                          ||||| ||||||||
                          TGGTA AACCGGTC

                    AAAA      C       I
GAM135 B3GAT1         GGCCACGGGCGGCGGCAGCAC    1895 TGA CCAC        TG
                          GG  CGGCGGCAGTACG
                          ||  |||||||||||||
                          CC  GCCGCCGTCGTGT

                     GTG C___          CC
GAM135 DLG1          AGCCCACCGGCGTCCCGCAGT    1889 TGAGG      ____   ACGTG
                          CCACCGGCG  GCAGT
                          ||||||||| |||||
                          GGTGGCCGC  CGTCA

                     G____        AGGG   AGIII
GAM135 EIF1A         TGCGTCCACGCTCGGCGGCAG    1896 AGG  ___      TACGTG
                          TG CCAC  CGGCGGCAG
                          || ||||  |||||||||
                          AC GGTG  GCCGCCGTC

                     GCA  CGA        IIIGTG
GAM135 EVC          GCCACCGGCAGC-CTACATG    1894 TGAGGCCA      AG
                          CCGGCGGC TACGT
                          |||||||| |||||
                          GGCCGTCG ATGTA

                     _____        G_
GAM135 HR           GATGCCACCGGCTGC-GCACG    1893 TGAG     G  A   T
                          GCCACCGGC GC GTACG
                          ||||||||| || |||||
                          CGGTGGCCG CG CGTGC

                     TA__      A _   C
GAM135 MYO9A         GAGGCCACCGAGGGTCGGACG    1892 TG      C CAGT  TG
                          AGGCCACCGG GG  ACG
                          |||||||||| ||  |||
                          TCCGGTGGCT CC  TGC

                     __       C AGCC  CI
GAM135 PTEN         GAGGCCTGGCAGCGGCGGCAG    1890 TG   AC____      ACGTG
                          AGGCC    CGGCGGCAGT
                          |||||    ||||||||||
                          TCCGG    GCCGCCGTCG

                     __     ACCGTC        IIIGT
GAM135 SURF6        GAGGCCACCGTCTTCTGTCCCGTG    1891 TG      GCGGCA A_  I
                          AGGCCACCG   GT CGTG
                          |||||||||   || ||||
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                    TCCGGTGGC    CA GCAC
                    __      AGAAGA  GG   C
GAM135 TNFRSF14      TGAGGCCACAAGAGTCAG-ACG   1897      C C _  T TG
                    TGAGGCCAC GG GG CAG ACG
                    IIIIIIIII II II III III
                    ACTCCGGTG TC TC GTC TGC
                        T _ A _  II
GAM136 CHI3L1        TGAGCTCAAATCTGTGTGTT    1905         TTTTTCTA
                    TGAGCTCAAATCTGT
                    IIIIIIIIIIIIIII
                    ACTCGAGTTTAGACA
                        CACAAIII
GAM136 COL10A1       GAGCTCTATTTCTGTTTTTT    1902 TG   AAA_      CTA
                    AGCTC   TCTGTTTTTT
                    IIIII   IIIIIIIII
                    TCGAG   AGACAAAAAA
                        __ ATAA      AII
GAM136 DSC3         AGCTC---TCTCTTTTTTCTA    1900 TGAG  AAA  G
                    CTC   TCT TTTTTTCT
                    III   III IIIIIIII
                    GAG   AGA AAAAAAGA
                         ____  ___  G
GAM136 GALR1        AGCTCAAAT-T-TTTTTTCTA    1901 TGAG     CTG
                    CTCAAAT  TTTTTCTA
                    IIIIIII  IIIIIIIII
                    GAGTTTA  AAAAAAGAT
                         ____     A__
GAM136 NCOA3        GAGCTCAAAGCTGGTCCTTTCT    1903 TG    T _      AG
                    AGCTCAAA CTG TTTTTCT
                    IIIIIIII III IIIIIIII
                    TCGAGTTT GAC AGGAAAGA
                        __     C  C     AI
GAM136 NFIB         TGTGTTCAAA-CTGTTTTTT    1906 TGAGC   T     CTA
                    TCAAA CTGTTTTTT
                    IIIII IIIIIIIII
                    AGTTT GACAAAAAA
                    ACACA    _       III
GAM136 RGS1         GAGCTCCA--CTGTTTTTT    1904 TG   AAAT     CT
                    AGCTC  CTGTTTTTT
                    IIIII  IIIIIIIII
                    TCGAG  GACAAAAAA
                        __  GT__     TI
GAM137 ALDH3A2      ACA-AGAATGACAGGTGATGCT    1912 _ T    T A  I
                    CA AGAATGACA GT ATGC
                    II IIIIIIIII II IIII
                    GT TCTTACTGT CA TACG
                        T _    C C  I
GAM137 ALDH3A2      ACA-AGAATGACAGGTGATGCT    1912 TGACAT      T A
                    AGAATGACA GT ATGCT
                    IIIIIIIII II IIIII
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                              TCTTACTGT CA TACGA
                             T_____       C C
GAM137 APG5L          ACA-AGAAATGAAATGTAATGC   1910 TA    C     I
                             CA  GAATGA ATGTAATG
                             || |||||| |||||||||
                             GT  TTTACT TACATTAC
                              TC     T     I
GAM137 APG5L          ACA-AGAAATGAAATGTAATGC   1910 TGACATA   C      T
                                GAATGA ATGTAATGC
                                |||||| |||||||||
                                TTTACT TACATTACG
                             TTC____   T    T
GAM137 BACH1          CATA-AATG---TGTAATGCT    1914 ATA   ACA
                                GAATG  TGTAATGC
                                ||||| ||||||||
                                TTTAC  ACATTACG
                             GTA     ___
GAM137 CALCB          GACATAGAATTAAATATAA      1919      GAC   II
                             GACATAGAAT ATGTA
                             |||||||||| |||||
                             CTGTATCTTA TATAT
                              ATT    TI
GAM137 CALCB          GACATAGAATTAAATATAA      1919 TG     GAC   TGC
                             ACATAGAAT ATGTAA
                             ||||||||| ||||||
                             TGTATCTTA TATATT
                              __       ATT   TII
GAM137 DXF68S1E        ACATACATATG-CATGTAATGC    1909 TG   GAA A
                             ACATA TG CATGTAATGCT
                             ||||| || |||||||||||
                             TGTAT AC GTACATTACGG
                             TA    ___ _
GAM137 DXF68S1E        ACATACATATG-CATGTAATGC    1909 GA_ A      I
                             CATA  ATG CATGTAATG
                             ||||  ||| |||||||||
                             GTAT  TAC GTACATTAC
                              GTA    _      I
GAM137 EFG1           GACATAGAATTACCTTTGAAT     1917 TG     G ATGTAATGCT
                             ACATAGAAT AC
                             |||||||||| ||
                             TGTATCTTA TG
                              __        A GAAACTTATI
GAM137 ISL1          ACATAGAATTAGACATATAAT     1911      __       III
                             ACATAGAAT GACATGTAA
                             ||||||||| ||||||||||
                             TGTATCTTA CTGTATATT
                               AT       AII
GAM137 ISL1          ACATAGAATTAGACATATAAT    1911 TGAC    __        GCT
                             ATAGAAT GACATGTAAT
                             ||||||| |||||||||||
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                          TATCTTA  CTGTATATTA
                          ____     AT        AGI
GAM137 MKKS       CATAGAATG--ATTTAATG      1913        CATGTAATI
                          CATAGAATGA
                          |||||||||
                          GTATCTTACT
                                  AAATTACII
GAM137 NRG1       GACATAGAATCATCTGAAA      1918        GACATGTAII
                          GACATAGAAT
                          ||||||||||
                          CTGTATCTTA
                                  GTAGACTTTI
GAM137 NRG1       GACATAGAATCATCTGAAA      1918 TG     GACATGTAATGC
                          ACATAGAAT
                          |||||||||
                          TGTATCTTA
                          __      GTAGACTTTGII
GAM137 NT5C2      TGATATACAATACCATGTAATGC  1920  C  G  A        TI
                          TGA ATA AATG CATGTAATGC
                          ||| ||| |||| ||||||||||
                          ACT TAT TTAT GTACATTACG
                           A   G   G        II
GAM137 NT5C2      TGATATACAATACCATGTAATGC  1920  C  G  A        I
                          GA ATA AATG CATGTAATG
                          || ||| |||| |||||||||
                          CT TAT TTAT GTACATTAC
                           A   G   G        I
GAM137 RBBP5      GAGATAGGAAATGACATGTCAAAATG 1915 CATA        AATI
                          GAATGACATGT
                          |||||||||||
                          TTTACTGTACA
                          CC__      GTTT
GAM137 RBBP5      GAGATAGGAAATGACATGTCAAAATG 1915 T CATA        AATGCTII
                          GA   GAATGACATGT
                          ||   |||||||||||
                          CT   TTTACTGTACA
                          T ATCC        GTTTTACT
GAM137 WBSCR5      TGAAATAAACT-ACATGTAATGCT 1921   C   ATG        I
                          TGA ATAGA  ACATGTAATGCT
                          ||| |||||  ||||||||||||
                          ACT TATTT  TGTACATTACGA
                           T   GA_        I
GAM137 WBSCR5      TGAAATAAACT-ACATGTAATGCT 1921 _ C   ATG        I
                          GA ATAGA  ACATGTAATGC
                          || |||||  |||||||||||
                          CT TATTT  TGTACATTACG
                           A  T  GA_        I
GAM137 WDR1       GAAATAGAGAAATGACATGT     1916  C  ___        III
                          GA ATAGA  ATGACATG
                          || |||||  |||||||||
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                        CT TATCT  TACTGTAC
                         T   CTT       AII
GAM137 WDR1             GAAATAGAGAAATGACATGT   1916 TGAC    ___        AATGC
                        ATAGA  ATGACATGT
                        IIIII  IIIIIIIII
                        TATCT  TACTGTACA
                         TT__   CTT       AIIIT
GAM138 ADAMTS13        TCAGGAGAGCCAGCCCGAGGAGT 1941    GA ___       TCTAI
                      TCAGGAG CC  CCGAGGAGT
                      IIIIIII II  IIIIIIIII
                      AGTCCTC GG  GGCTCCTCA
                          TC TCG       IIIAT
GAM138 ADAMTS13        TCAGGAGAGCCAGCCCGAGGAGT 1941 CA  GAC_     I
                         GGAG   CCCGAGGAG
                         IIII   IIIIIIIII
                         TCTC   GGGCTCCTC
                         C_   GGTC       I
GAM138 ATP2B4          TCAGGAGGAGGAAGAGGAG    1945    CCCC   TTCT
                       TCAGGAGGA  GAGGAG
                       IIIIIIIII  IIIIII
                       AGTCCTCCT  CTCCTC
                          CCTT    IIIA
GAM138 ATP2B4          TCAGGAGGAGGAAGAGGAG    1945    CCCC   II
                       TCAGGAGGA  GAGGA
                       IIIIIIIII  IIIII
                       AGTCCTCCT  CTCCT
                          CCTT   CI
GAM138 BAZ2A           CAGTAGTTGTCCCTGAGGAGTTC  1931 AGGAGGA  C    I
                       CCC GAGGAGTT
                       III IIIIIIII
                       GGG CTCCTCAA
                        ATCAACA  A      I
GAM138 BAZ2A           CAGTAGTTGTCCCTGAGGAGTTC  1931 TCAGGAGGA  C     AI
                       CCC GAGGAGTTCT
                       III IIIIIIIIII
                       GGG CTCCTCAAGG
                       TCATCAACA  A       II
GAM138 CXCL16          AGGACGACGGCCCGAGGAG    1926  G __       III
                       AGGA GAC CCCGAGGA
                       IIII III IIIIIIII
                       TCCT CTG GGGCTCCT
                         G  CC       CII
GAM138 CXCL16          AGGACGACGGCCCGAGGAG    1926 TCAG G __       CT
                       GA GAC CCCGAGGAGTT
                       II III IIIIIIIIIII
                       CT CTG GGGCTCCTCGG
                       ____ G  CC        II
GAM138 CYP3A43         TCAGGAGGA-CTTGAGG-GTACTA 1946     CCC  A T
                       TCAGGAGGAC GAGG GT CTA
                       IIIIIIIII IIII II III
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                         AGTCCTCCTG  CTCC CA GAT
                            AA_   _ T
GAM138 CYP3A43        TCAGGAGGA-CTTGAGG-GTACTA  1946      CCC   A TCI
                         TCAGGAGGAC  GAGG GT
                         ||||||||||  |||| ||
                         AGTCCTCCTG  CTCC CA
                            AA_   _ TGA
GAM138 FMNL          TCAGGAGGACCTCCG-GGAG     1943      _  A   TTCT
                         TCAGGAGGACC CCG GGAG
                         |||||||||| ||| ||||
                         AGTCCTCCTGG GGC CCTC
                            A  _   IIIA
GAM138 FMNL          TCAGGAGGACCTCCG-GGAG     1943      _  A  II
                         TCAGGAGGACC CCG GGA
                         |||||||||| ||| |||
                         AGTCCTCCTGG GGC CCT
                            A  _  CI
GAM138 GCH1         TCGGGAAGGACCCCGGGGCGCTTC  1940 A  _     A A  CTAI
                         TC GGA GGACCCCG GG GTT
                         || ||| |||||||| || |||
                         AG CCT CCTGGGGC CC CGA
                            C  T     C G  AGII
GAM138 GCH1         TCGGGAAGGACCCCGGGGCGCTTC  1940 A      A A  I
                           GGAGGACCCCG GG GTT
                           |||||||||| || |||
                           CTTCCTGGGGC CC CGA
                           C       C G  I
GAM138 IGFBP4         GGAGGACCCGGACCCGGAG      1936     C ___  III
                         GGAGGACCC GA  GGA
                         ||||||||| ||  |||
                         CCTCCTGGG CT  CCT
                            C GGG  CII
GAM138 IGFBP4         GGAGGACCCGGACCCGGAG      1936 TCA ___    C  AGTTCT
                          GGA  GGACCC GAGG
                          ||| |||||| ||||
                          CCT  CCTGGG CTCC
                          ___  GGG   C  GGIIIA
GAM138 LTB4R          CAGGAGGACTCCTTAGAGG      1932     _ C__  III
                         CAGGAGGAC CC  GAG
                         |||||||| ||  |||
                         GTCCTCCTG GG  CTC
                            A AAT  CII
GAM138 LTB4R          CAGGAGGACTCCTTAGAGG      1932 TC    C GA   TTCT
                          AGGAGGAC CC  GGAG
                          |||||||| || ||||
                          TCCTCCTG GG  TCTC
                          __     A AA  CAII
GAM138 MCM7          CAAGAGGACCCC-AGG-GTT     1934       G  AGI
                         CAGGAGGACCCC AGG
                         |||||||||||| |||
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                        GTTCTCCTGGGG TCC
                        _    CAA
GAM138 MCM7             CAAGAGGACCCC-AGG-GTT   1934 TC      G  A  C
                        AGGAGGACCCC AGG GTT
                        ||||||||||| ||| |||
                        TTCTCCTGGGG TCC CAA
                        __      _  _  C
GAM138 MRPS12         GGAGGACCCC-AGGA-TTC    1937       G  GTTI
                        GGAGGACCCC AGGA
                        |||||||||| ||||
                        CCTCCTGGGG TCCT
                            _  AAGI
GAM138 MRPS12         GGAGGACCCC-AGGA-TTC    1937 TCAGGA    G   G
                          GGACCCC AGGA TTC
                          ||||||| |||| |||
                          CCTGGGG TCCT AAG

                          _____    _  _
GAM138 MUC4          TCAGGAGGACTCCGGTGGCGTT   1942       C  A_ A  CTA
                     TCAGGAGGAC CCG GG GTT
                     |||||||||| ||| || |||
                     AGTCCTCCTG GGC CC CAA
                        A  CA G  III
GAM138 MUC4          TCAGGAGGACTCCGGTGGCGTT   1942 C    C  A_ A  I
                       AGGAGGAC CCG GG GT
                       |||||||| ||| || ||
                       TCCTCCTG GGC CC CA
                       _     A  CA G  I
GAM138 MYCL1        AGGAGGGCCT---GGAGTTCTA   1929 _   A  CCGA
                      GGAGG CC   GGAGTTCT
                      ||||| ||   ||||||||
                      CCTCC GG   CCTCAAGA
                         T  C  A___
GAM138 MYCL1        AGGAGGGCCT---GGAGTTCTA   1929 TCAG   A  CCGA
                       GAGG CC   GGAGTTCT
                       |||| ||   ||||||||
                       CTCC GG   CCTCAAGA
                       ____    C  A___
GAM138 PKDREJ       CAGTGAGG---CCGAGGAGTT   1930  _   ACC     I
                       CAG GAGG  CCGAGGAG
                       ||| ||||  |||||||||
                       GTC CTCC  GGCTCCTC
                          A  ___     A
GAM138 PKDREJ       CAGTGAGG---CCGAGGAGTT   1930 TCAG  ACC      C
                        GAGG  CCGAGGAGTT
                        ||||  ||||||||||
                        CTCC  GGCTCCTCAA
                      TCA_  ___     A
GAM138 PTGS2        AGGAGGCGCTGCTGAGGAGTTC   1927 TCAG   ACCCC__      A
                        GAGG    GAGGAGTTCT
                        ||||    ||||||||||
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                        CTCC      CTCCTCAAGG
                    ____      GCGACGA        A
GAM138 PTK7         GGAGCCCGACCCCGAGGCGT   1935  ___       AGIII
                        GGAG  GACCCCGAGG
                        ||||  ||||||||||
                        CCTC  CTGGGGCTCC
                         GGG        GCAII
GAM138 PTK7         GGAGCCCGACCCCGAGGCGT   1935 TCAGGAG       A
                        GACCCCGAGG GTTCT
                        |||||||||| |||||
                        CTGGGGCTCC CAGGG
                    CGGG___        G
GAM138 RAD50        TCAGGAGGATCCGGGCGGGGAG   1944        _  C__  A  TTCTA
                        TCAGGAGGA CC  CG GGAG
                        ||||||||| ||   || ||||
                        AGTCCTCCT GG  GC CCTC
                         A CCC  C   IIIAT
GAM138 RAD50        TCAGGAGGATCCGGGCGGGGAG   1944       CC  A AIII
                        TCAGGAGGA  CCG GG
                        |||||||||  ||| ||
                        AGTCCTCCT  GGC CC
                          A_  _  GCCC
GAM138 RFC1         GGAGGA-CCCAAGCAGTCCTA   1938 _       C  G      I
                        GAGGACCC GAG AGTTCT
                        |||||||| ||| ||||||
                        CTCCTGGG TTC TCAGGA
                        C   _  G    I
GAM138 RFC1         GGAGGA-CCCAAGCAGTCCTA   1938 TCAGGA     C  G
                        GGACCC GAG AGTTCT
                        |||||| ||| ||||||
                        CCTGGG TTC TCAGGA
                        _____    _  G
GAM138 S100A6       TCAGAGAGGACCCCCAGAGGTGT  1939  _       G  GA  TCTAI
                        TCAG GAGGACCCC AG GT
                        |||| ||||||||| || ||
                        AGTC CTCCTGGGG TC  CA
                         T     G  TC  CAIII
GAM138 S100A6       TCAGAGAGGACCCCCAGAGGTGT  1939 CA        ___  AGI
                        GGAGGACCCC GAGG
                        |||||||||| ||||
                        TCTCCTGGGG CTCC
                          __      GT  ACI
GAM138 SAS         AGGACCCCGA-CAGCTTCT    1924       GG  CII
                        AGGACCCCGA AGTT
                        |||||||||| ||||
                        TCCTGGGGCT TCGA
                          G_  AGA
GAM138 TBL1X        CAGGAGGACCGCCAGGGGT    1933       _  G  AGII
                        CAGGAGGACC CC AGG
                        ||||||||||| || |||
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                      GTCCTCCTGG GG TCC
                        C _  CCAI
GAM138  TBL1X          CAGGAGGACCGCCAGGGGT    1933 TC      _ G  A  CT
                        AGGAGGACC CC AGG GTT
                        |||||||| || ||| |||
                        TCCTCCTGG GG TCC CAG
                          __       C _  C  II
GAM138  TCF21          AGAAGGAACCCCGAGGACTTCT  1925 G    _      G  I
                        GAGGA CCCCGAGGA TTC
                        ||||| ||||||||| |||
                        TTCCT GGGGCTCCT AAG
                          _     T    G  I
GAM138  TCF21          AGAAGGAACCCCGAGGACTTCT  1925 TCAG   _      G  A
                        GAGGA CCCCGAGGA TTCT
                        ||||| ||||||||| ||||
                        TTCCT GGGGCTCCT AAGA
                          ____    T    G  C
GAM138  VAMP8          AGGAGGA--CCGAGCAGCATTCT  1928    CC  G  TCI
                        GGAGGACC GAG AGT
                        |||||||| ||| |||
                        CCTCCTGG CTC TCG
                          __  G  TAA
GAM138  VAMP8          AGGAGGA--CCGAGCAGCATTCT  1928 TCAG   CC  G  __  A
                        GAGGACC GAG AGT TCT
                        ||||||| ||| ||| |||
                        CTCCTGG CTC TCG AGA
                          ____      __  G  TA  G
GAM139  BCAT1          ACTGCTC-ACTCCCGGGGTGC   1951 AACA   T CG     C
                        GCTT AC CCGGGGTGC
                        |||| || |||||||||
                        CGAG TG GGCCCCACG
                        GA__  _  AG     T
GAM139  BRCA1          CAGCTTTACCCAGAGCAGAGGGTG  1952 AACA      ____ C _   CCTI
                        GCTTTACC  GC G GGGTG
                        ||||||||  || | |||||
                        CGAAATGG  CG C CCCAC
                          ____     GTCT  T T  TTII
GAM139  KIAA0442       ACAGCTTTAGCCGACTGTGT    1950 AA      CC   G_  CC
                        CAGCTTTA GCCGG GTG
                        |||||||| ||||| |||
                        GTCGAAAT CGGCT CAC
                          __      __   GA  AA
GAM139  LCP1           AACAGCTTTGTCAAGCCTGGGTG  1949      ACC__  G   CCTI
                        AACAGCTTT  GCC GGGTG
                        |||||||||  ||| |||||
                        TTGTCGAAA  CGG CCCAC
                          CAGTT  A   IIIT
GAM139  P2RY2          GCTTCTCCTCTCGGGGTGCCT    1953 AACAGCTTTA GC_
                        CC  CGGGGTGCCT
                        ||  ||||||||||
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                        GG  GCCCCACGGA
                    GA_____ AGA
GAM140 ADAR         TGGCA--CTGGGAACTGCAGTTTT 1965   AT  TGTAG
                    TGGC ACTG  TGCAGTTTT
                    IIII IIII   IIIIIIIII
                    ACCG TGAC   ACGTCAAAA
                      __  CCTTG
GAM140 APPBP2       TGGCATG-TGTTCACTGCAGTTTT 1966    AC  G G       I
                    TGGCAT TGT TA TGCAGTTTT
                    IIIIII III II IIIIIIIII
                    ACCGTA ACA GT ACGTCAAAA
                       C_  A  G     I
GAM140 CAPN2        TGGCATACTG----GTTCAGTT  1964       T AGTG
                    TGGCATACTG GT  CAGTT
                    IIIIIIIIII II  IIIII
                    ACCGTATGAC CA  GTCAA
                      _   A___
GAM140 CENTD1       CATAAACTGTCCTGCAGTTTT  1957 TGGCAT   GTAG
                       ACTGT  TGCAGTTTT
                       IIIII  IIIIIIIII
                       TGACA  ACGTCAAAA
                    TT____  GG__
GAM140 CYP3A4       GCCTCCTGTGTAGTG-AGATT   1960 TGGCATA     C TTT
                       CTGTGTAGTG AG
                       IIIIIIIIII II
                       GACACATCAC TC
                    GAG____      _ TAA
GAM140 DAAM2        GCATACACCTG-GTAGTGCAG   1958 TG  A T      TT
                       GCAT CTG GTAGTGCAGT
                       IIII III IIIIIIIIII
                       TGTG GAC CATCACGTCG
                    TA  _ _      TI
GAM140 FBXL7        GCCTACAGTAGGAGTGCAGTT   1959 TGGCA T T_     TT
                      TAC GTG AGTGCAGTT
                      III III IIIIIIIII
                      ATG CAT TCACGTCAA
                    G____ T CC     CA
GAM140 IL7R         GCAGACTGTGTAGTGGGGTTTT  1961 TGGCAT      CA
                       ACTGTGTAGTG GTTTT
                       IIIIIIIIIII IIIII
                       TGACACATCAC CAAAA
                    TC____      CC
GAM140 PEA15        GGCAGACATG-GCAGTGCAGTTTT 1962 TG  T _ T       I
                       GCA AC TG GTAGTGCAGTTTT
                       III II II IIIIIIIIIIII
                       CGT TG AC CGTCACGTCAAAA
                    __  C T _      T
GAM140 RANBP9       TGCCATGACCTTTGTAGTGCA   1963 G _ G_      GTTTT
                       TG CAT ACT TGTAGTGCA
                       II III III IIIIIIIII
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                    AC GTA TGG  ACATCACGT
                     G  C  AA        IIITT
GAM140  SLC4A5       CATACTGTGATGGTGTCAG    1956 TGGCAT     TA_  _   TT
                    ACTGTG  GTG CAGT
                    |||||| ||| ||||
                    TGACAC  CAC GTCG
                    _____    TAC  A   TG
GAM141  CD34         ACACTACTCGGCTTGGCCAGG    1973 TGACACAG  T T
                    TTC G CTTGGCCAGG
                    ||| | |||||||||
                    GAG C GAACCGGTCC
                    AT_____    C _
GAM141  CIAS1        ACAGAGCTGTGGTCTTGGCCTGG  1971 TGACAC   CT_      A I
                    AGTT  GTCTTGGCC GG
                    ||||  |||||||||| ||
                    TCGA  CAGAACCGG CC
                    TC____    CAC      A T
GAM141  DCLRE1C      GACACATTTCACTGTGTTGGCCAGG 1978 TG    GTT__  C       II
                    ACACA   CTGT TTGGCCAGG
                    |||||   |||| |||||||||
                    TGTGT   GACA AACCGGTCC
                    __   AAAGT  C    GI
GAM141  DGCR2        ACACAGTTCTGAGGCCTGG-CAGG  1970 TGAC       T__    C I
                    ACAGTTCTG  CTTGGC AGG
                    |||||||||  |||||| |||
                    TGTCAAGAC  GGACCG TCC
                    ____        TCC    _  T
GAM141  DPYSL2       TGGCCCATTCCTGCACTTGGCCAGG 1981 TGACA G    _         II
                    CA TTCTGT CTTGGCCAGG
                    || |||||| |||||||||||
                    GT AGGACG GAACCGGTCC
                    ACCGG  A    T      II
GAM141  EIF4EBP2     ACAGGTTTCTTTCTTGGCCA     1972 TGACACAG   G
                    TTCT TCTTGGCCAG
                    |||| ||||||||||
                    AAGA AGAACCGGTT
                    CA_____    A
GAM141  GPR48        CACAGTTCTAGCTGGGACAG     1975 TGACAC      T T C
                    AGTTCTG CT GG CAG
                    ||||||| || || |||
                    TCAAGAT GA CC GTC
                    _____      C C T
GAM141  IL2RB        ACACAGTTCCTGGCTCGGGCAG    1969 TGAC     GT_   C G
                    ACAGTTCT  CTTGG CAG
                    ||||||||  ||||| |||
                    TGTCAAGG  GAGCC GTC
                    ____        ACC    C G
GAM141  IL8RA        GACAAAGGGATCTTCCTTGGCCAGG 1977 TG  C T__  GT       II
                    ACA AG  TCT  CTTGGCCAGG
                    ||| ||  |||  |||||||||||
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                      TGT TC  AGA  GAACCGGTCC
                      __  T CCT  AG        CI
GAM141  MAP3K14        GACAAAGG-CTGTCTTGGCAAG   1979 TG  C  TT       C
                      ACA AG  CTGTCTTGGC AGG
                      ||| ||  |||||||||| |||
                      TGT TC  GACAGAACCG TCT
                      __  T C_        T
GAM141  MEN1          TGAAACAGG-CTGTCTTGGCCA   1982  C  TT       GG
                      TGA ACAG  CTGTCTTGGCCA
                      ||| ||||  ||||||||||||
                      ACT TGTC  GACAGAACCGGT
                        T  C_       ||
GAM141  RIG           ACAGTTCTGTCCTTCTCAGG    1974 TGACACAG     GGC
                         TTCTGTCTT  CAG
                         ||||||||| |||
                         AAGACAGGA  GTC
                         _____      AGA
GAM141  STIM1         CAGTAATGCCTTCTTGGCCAGG   1976 TGACACA T G
                         GT CT TCTTGGCCAGG
                         || || |||||||||||
                         CG GA AGAACCGGTCC
                       TA_____  _  _
GAM141  VNN3          GATAGAGTTGTC-CTTGGCCAGG  1980 TGACAC  CTG
                         AGTT  TCTTGGCCAGG
                         ||||  |||||||||||
                         TCAA  GGAACCGGTCC
                       TATC__   CA_
GAM142  CYP17         TGGAGTAGA--AGAGCTGTG    1990        TTAC _ TTG
                      TGGAGTAGA   AGC GTG
                      |||||||||   ||| |||
                      ACCTCATCT   TCG CAC
                         TC__ A |||
GAM142  CYP17         TGGAGTAGA--AGAGCTGTG    1990        TTAC GTI
                      TGGAGTAGA   AGC
                      |||||||||   |||
                      ACCTCATCT   TCG
                         TC__  ACA
GAM142  CYP3A4        TGTAGTGAGATTACAGGCGAGT   1989 G  _      _ T TGGA
                      TG AGT AGATTACAG CG GT
                      || ||| |||||||||| || ||
                      AC TCA TCTAATGTC GC CA
                       A  C       C T IIIA
GAM142  CYP3A4        TGTAGTGAGATTACAGGCGAGT   1989 GG  _      C I
                       AGT AGATTACAG GTG
                       ||| |||||||||| |||
                       TCA TCTAATGTC CGC
                       __  C      _ T
GAM142  KRTHA4        TGGAGCTCAGATTACAGGGAGCTG 1988     __      CGT  GAI
                      TGGAGT AGATTACAG GTTG
                      |||||| |||||||||| ||||
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                        ACCTCG TCTAATGTC CGAC
                          AG       CCT   III
GAM142 KRTHA4        TGGAGCTCAGATTACAGGGAGCTG 1988 AG        CGT  I
                       GG TAGATTACAG  GTT
                       II IIIIIIIIII III
                       TC GTCTAATGTC CGA
                        GA       CCT  I
GAM142 MPP5         AGTAGATTAGAGTGTGTTG      1985      C C   II
                     AGTAGATTA AG GTGTT
                     IIIIIIIII II IIIII
                     TCATCTAAT TC CACAA
                         C A   CI
GAM142 MPP5         AGTAGATTAGAGTGTGTTG      1985 TGGAGT   C C
                       AGATTA AG GTGTTGG
                       IIIIII II IIIIIII
                       TCTAAT TC CACAACT
                     _____      C A
GAM142 SNX6        GGAGTAGATTTATTACAGC      1986         ____  IIIG
                     GGAGTAGAT  TACAG
                     IIIIIIIII  IIIII
                     CCTCATCTA  ATGTC
                         AATA   GIII
GAM142 SNX6        GGAGTAGATTTATTACAGC      1986 TG     ____     GTGTTGG
                      GAGTAGAT  TACAGC
                      IIIIIIII  IIIIII
                      CTCATCTA  ATGTCG
                      __       AATA   AIIIAGG
GAM142 USP18      TGGA--AAATGACAGCGTGT      1991    TA  T    TG
                    TGGAG GAT ACAGCGTGT
                    IIIII III IIIIIIIII
                    ACCTT TTA TGTCGCACA
                      __  C   II
GAM142 USP18      TGGA--AAATGACAGCGTGT      1991 _  TA  T    I
                     GGAG GAT ACAGCGTG
                     IIII III IIIIIIII
                     CCTT TTA TGTCGCAC
                     A  __  C   I
GAM142 VCL       GGAGTAGA-TGCAGAGAGCTTGG    1987 TG    _ C C G  A
                    GAGTAGAT TA AG GT TTGG
                    IIIIIIII II II II IIII
                    CTCATCTA GT TC CG AACC
                    __      C C T _  A
GAM142 VCL       GGAGTAGA-TGCAGAGAGCTTGG    1987       TA CGT  GI
                    GAGTAGAT CAG  GTT
                    IIIIIIII III  III
                    CTCATCTA GTC  CGA
                       C_   TCT  AC
GAM143 ACATN      TCTCAGCA---AATT-CCACAT    2006      ACA  A
                    TCTCAGCAA ATT CCACAT
                    IIIIIIIII III IIIIII
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                        AGAGTCGTT  TAA GGTGTA
                        ___  _
GAM143 ADCY1       TCAGCAAACAGGATGCTCACATT  2003 TCTC      ATTAC__     TI
                        AGCAAACA     CACATT
                        ||||||||     ||||||
                        TCGTTTGT     GTGTAA
                            ____    CCTACGA    CA
GAM143 BAZ2B       TCTGCAAACAATATATACACAT   2004 TCTCA     TAC__   TT
                        GCAAACAAT    CACAT
                        |||||||||    |||||
                        CGTTTGTTA    GTGTA
                        A____        TATAT   TT
GAM143 COX6B     CTCAGCAAAGA--CACCACA    2002 TC     CAAT     T
                        TCAGCAAA   TACCACA
                        ||||||||   |||||||
                        AGTCGTTT   GTGGTGT
                        __      CT__    C
GAM143 CUL4B       CTCAAGCAAACAATCAACA     1997 TC  _       C CATT
                        TCA GCAAACAATTA CA
                        ||| |||||||||| ||
                        AGT CGTTTGTTAGT GT
                        __  T       T CIII
GAM143 CX3CR1      CAGCAATTTAACAGTTACCACAT  1995 TCTCAGCA   A       I
                         AACA TTACCACATTT
                         |||| |||||||||||
                         TTGT AATGGTGTAGA
                        GTTAAA__   C        C
GAM143 HUNK      CTCAGCA---AATCACCACA    2001 TC     ACA      T
                        TCAGCAA  ATTACCACA
                        |||||||  |||||||||
                        AGTCGTT  TAGTGGTGT
                        __   ___       C
GAM143 ITGA1     CTCAGCAAAGATAATTTCAGCATTT 1999 TC     C__  AC _  II
                        TCAGCAAA  AATT CA CATTT
                        ||||||||  |||| || |||||
                        AGTCGTTT  TTAA GT GTAAA
                        __     CTA  A_ C   GI
GAM143 MEN1    TCAG-AAATGCTTACCACATT    2005 TCTCAGCAAACAA
                            TTACCACATT
                            ||||||||||
                            AATGGTGTAA
                        TCTTTACG_____
GAM143 NOTCH2      TCTCAGCAAATTATGACATCAT   2007        ACA  CC  T
                        TCTCAGCAA  ATTA  ACATT
                        |||||||||  ||||  |||||
                        AGAGTCGTT  TAAT  TGTAG
                        ___    AC   T
GAM143 PLS1    CACCAAAAAAATCAAACCACATTT  1996 TCTCAGCAAA  TT     I
                        CAA  ACCACATTT
                        |||  |||||||||
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                          GTT  TGGTGTAAA
                    GTTTTTTA_  __      G
GAM143  RNTRE         CTGAGTAATAAATTACCAC      2000 TCTCAGCAAAC      ATT
                           AATTACCAC
                           ||||||||
                           TTAATGGTG
                    ACTCATTAT__        AII
GAM143  SLC25A14       CTAACCAATTACATTTAACCACATTT 1998 TC_   CAA  A  _      II
                         TCAG  ACA TTA CCACATTT
                         ||||  ||| ||| ||||||||
                         GGTT  TGT AAT GGTGTAAA
                    ATT  AA_  A  T     CI
GAM143  THBD        AGCAA-CAATTACCATTTTT      1994 TCTCAGCAA       CATT
                           ACAATTACCA
                           ||||||||||
                           TGTTAATGGT
                    _____       AAAA
GAM144  CNN1        TGAGTTCTA---CAGGGGCTGG    2018      ACC  C    G
                         TGAGTTCT  GCAG GGCTGG
                         ||||||||  |||| ||||||
                         ACTCAAGA  TGTC CCGACC
                          ___     C    I
GAM144  CYFIP2      TGAGG-CTACCGCAG-GGC      2015    TT     C  TGG
                         TGAG  CTACCGCAG GGC
                         ||||  ||||||||| |||
                         ACTC  GATGGCGTC CCG
                         C_       _   III
GAM144  FGF1        TTCTGCCTTCCTGCGGCTGGGC    2019 TGAGT  A  GCA
                         TCT CC  GCGGCTGGGC
                         ||| ||  ||||||||||
                         GGA GG  CGCCGACCCG
                    C____  A A__
GAM144  GRAF        TGTGGTCGGCCGCAGCGGCT      2016 __ A  CTA        GGG
                         TG GTT  CCGCAGCGGCT
                         || |||  ||||||||||
                         AC CAG  GGCGTCGCCGA
                    AC _  CC_        III
GAM144  INHBB       GTTCGGCCG--GCGGCTGGG      2011 TGAGTTCTA  CA
                          CCG  GCGGCTGG
                          |||  ||||||||
                          GGC  CGCCGACC
                    GCC_____  __
GAM144  INSRR       TGGGTTCGGCTGCCAGCAGCGGCT 2012 A  TA___  _      GGGCI
                         TG GTTC    CC GCAGCGGCT
                         || ||||    || |||||||||
                         AC CAAG    GG CGTCGCCGA
                          C  CCGAC  T      IIICG
GAM144  LETM1       TGAGTGTGACA-CAGCCGGCTGGGC 2013     TCTAC    _     I
                         TGAGT    CGCAGC GGCTGGGC
                         |||||    |||||| ||||||||
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                              ACTCA    GTGTCG CCGACCCG
                               CACT_    G     I
GAM144  PKM2          TGAGTTCTAC--AAGCGTTGCTGG  2014        CGC   __   GC
                      TGAGTTCTAC AGCG GCTGG
                      |||||||||| |||| |||||
                      ACTCAAGATG TCGC CGACC
                                T__   AA   II
GAM144  RAI14         TGAGAACAATGGCAGCGGCTG  2017 TTCTACC      GGC
                      TGAG    GCAGCGGCTG
                      ||||    ||||||||||
                      ACTC    CGTCGCCGAC
                       TTGTTAC       III
GAM144  WRN           AGTCTCTTC-GCAGGTGCGGCTGGGC 2010 TGAG   AC   ___       II
                      TTCT CGCA  GCGGCTGGGC
                      |||| ||||  ||||||||||
                      GAGA GCGT  CGCCGACCCG
                      A___   A_   CCA       TC
GAM145  AQP8          AAGTGGCCAGGCCCCCAACA    2029 AC  AGAA     I
                          TGG  GCCCCCAAC
                          |||  |||||||||
                          ACC  CGGGGGTTG
                       TC  GGTC       I
GAM145  AQP8          AAGTGGCCAGGCCCCCAACA    2029 TCTAAACT AGAA
                          GG  GCCCCCAAC
                          ||  |||||||||
                          CC  CGGGGGTTG
                      _____     GGTC
GAM145  ARCN1         TCTAAACTGGAAGGACAGGCCC   2038        AA C__  AACA
                      TCTAAACTGGAG GC  CCC
                      |||||||||||| || |||
                      AGATTTGACCTT TG  GGG
                         CC TCC   IIIA
GAM145  ARCN1         TCTAAACTGGAAGGACAGGCCC   2038        __ A__   III
                      TCTAAACTGGA GA  GCCC
                      ||||||||||| || ||||
                      AGATTTGACCT CT  CGGG
                       TC GTC   III
GAM145  ATP10C        ACTGGCTGAAGCCCCCACCA    2031    A_      ACII
                      ACTGG GAAGCCCCCA
                      ||||| ||||||||||
                      TGACC CTTCGGGGGT
                       GA       GGTI
GAM145  ATP10C        ACTGGCTGAAGCCCCCACCA    2031 TCTAAACTGGA     AC
                          GAAGCCCCCA
                          ||||||||||
                          CTTCGGGGGT
                      GA_____      GG
GAM145  BAZ2A         AAAAAGCAGA-GCCCCCAAC   2023 AACTGG_ A    I
                      AGA GCCCCCAA
                      ||| ||||||||
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                        TCT CGGGGGTT
                      TTTTTCG  _       I
GAM145  BAZ2A          AAAAAGCAGA-GCCCCCAAC     2023 TCTAAACTGG  A
                          AGA GCCCCCAAC
                          ||| |||||||||
                          TCT CGGGGGTTG
                       TTCG_____  _
GAM145  CRY2          AACAGG-GAAGCCCCCAAC     2027   T  A       I
                          AAC GG GAAGCCCCCAA
                          ||| || ||||||||||
                          TTG CC CTTCGGGGGTT
                            T _       G
GAM145  CRY2          AACAGG-GAAGCCCCCAAC     2027 TCTAAACT  A
                            GG GAAGCCCCCAA
                            || ||||||||||
                            CC CTTCGGGGGTT
                          _____  _
GAM145  EFNB1            ACTGGGCAGCCGCCCCCAAC     2030    __ AA       |||
                            ACTGG AG GCCCCCAA
                            ||||| || ||||||||
                            TGACC TC CGGGGGTT
                            CG GG     G||
GAM145  EFNB1            ACTGGGCAGCCGCCCCCAAC     2030 TCTAAACT G  AA
                              G AG  GCCCCCAAC
                              | ||  |||||||||
                              C TC  CGGGGGTTG
                            _____ G  GG
GAM145  FGF1           AACTGCAGAAACTCTGCCCCCAAC  2026    G  _____     |||G
                          AACTG AGAA    GCCCCCAA
                          ||||| ||||    ||||||||
                          TTGAC TCTT    CGGGGGTT
                            G   TGAGA      G|||
GAM145  FGF1           AACTGCAGAAACTCTGCCCCCAAC  2026 TCTAAACT    A___      A|
                             GGAGA   GCCCCCAAC
                             |||||   |||||||||
                             TCTTT   CGGGGGTTG
                          CG_____    GAGA     GG
GAM145  GAB2           AAACTGGAGACAGCAGCCA     2022        ____    CCC||
                          AAACTGGAGA   AGCC
                          |||||||||    ||||
                          TTTGACCTCT   TCGG
                            GTCG   T|||C
GAM145  GAB2           AAACTGGAGACAGCAGCCA     2022 TCTAAA     _ CC  AC
                            CTGGAGA AGC  CCA
                            ||||||| ||| |||
                            GACCTCT TCG GGT
                          _____     G  TC  AA
GAM145  HD            AAACAGGAG---CCCCCAAC     2024    T  GAA      I
                          AAAC GGA  GCCCCCA
                          |||| |||  |||||||
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                      TTTG CCT   CGGGGGT
                       T   ___      T
GAM145 HD             AAACAGGAG---CCCCCAAC    2024 TCTAAACTGG  A
                       AG AGCCCCCAA
                       || |||||||||
                       TC TCGGGGGTT
                       G_____   C
GAM145 IHPK1          TAAGACTGGA-AAGCCCCCAA    2034 AA_      A    I
                       ACTGGAGA GCCCCCA
                       |||||||| |||||||
                       TGACCTTT CGGGGGT
                       TTC      _      I
GAM145 IHPK1          TAAGACTGGA-AAGCCCCCAA    2034 TCTAA    A     C
                       ACTGGAGA GCCCCCAA
                       |||||||| ||||||||
                       TGACCTTT CGGGGGTT
                       TC___     _       C
GAM145 M17S2          CTAAACTGGAGA--CCTCCA    2032        AG_ CCI
                       CTAAACTGGAGA  CC
                       ||||||||||||  ||
                       GATTTGACCTCT  GG
                         GGA  TII
GAM145 M17S2          CTAAACTGGAGA--CCTCCA    2032 TC      AA  C  A
                       TAAACTGGAG  GCC CCA
                       ||||||||||  ||| |||
                       ATTTGACCTC  TGG GGT
                       __        __  A  A
GAM145 MMP14          AAGTGCAGA-GCCCCCAACA    2028 AC_  G  A     I
                       TG AGA GCCCCCAAC
                       || ||| |||||||||
                       AC TCT CGGGGGTTG
                       TTC G  _      I
GAM145 MMP14          AAGTGCAGA-GCCCCCAACA    2028 TCTAAACT G  A
                       G AGA GCCCCCAAC
                       | ||| |||||||||
                       C TCT CGGGGGTTG
                       _____ G  _
GAM145 NKTR           TCTGTACTTGAGAGAAGCCCCC    2037 AA  __      AACA
                       TCT ACT GGAGAAGCCCCC
                       ||| ||| ||||||||||||
                       AGA TGA TCTCTTCGGGGG
                         CA  AC        IIIA
GAM145 NKTR           TCTGTACTTGAGAGAAGCCCCC    2037 CTAA  __      I
                       ACT GGAGAAGCCCC
                       ||| ||||||||||
                       TGA TCTCTTCGGGG
                       CA__  AC      I
GAM145 OAS3           CTAGACCGG-GAAGCCCCCAA    2033 _ A  A       I
                       TA ACTGG GAAGCCCCCA
                       || ||||| ||||||||||
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                              AT TGGCC CTTCGGGGGT
                               G C    _       I
GAM145  OAS3        CTAGACCGG-GAAGCCCCCAA   2033 TCTAA    A       C
                          ACTGG GAAGCCCCCAA
                          ||||| |||||||||||
                          TGGCC CTTCGGGGGTT
                         ATC__    _       T
GAM145  PDGFB       TAAAA-GGA-AAGCCCCCAA    2036 AAACT    A    I
                          GGAGA GCCCCCA
                          ||||| |||||||
                          CCTTT CGGGGGT
                         ATTTT    _    I
GAM145  PDGFB       TAAAA-GGA-AAGCCCCCAA     2036 TCTAAACT    A
                          GGAGA GCCCCCAA
                          ||||| ||||||||
                          CCTTT CGGGGGTT
                        TTT_____    _
GAM145  RAB3A       TCCACACAGG-GAAACCCCCAACA 2039   A T A       I
                       TCTA AC GG GAAGCCCCCAACA
                       |||| || || |||||||||||||
                       AGGT TG CC CTTTGGGGGTTGT
                        G   T  _        I
GAM145  RAB3A       TCCACACAGG-GAAACCCCCAACA 2039 _  A T A       I
                       CTA AC GG GAAGCCCCCAAC
                       ||| || || ||||||||||||
                       GGT TG CC CTTTGGGGGTTG
                       A   G  T  _        I
GAM145  TRPM8       AACTGGAGATAGCCTTCAA      2025      _ CCCAII
                       AACTGGAGA AGCC
                       ||||||||| ||||
                       TTGACCTCT TCGG
                         A   AAGTTI
GAM145  TRPM8       AACTGGAGATAGCCTTCAA      2025 TCTAAACT  _ CC C
                       GGAGA AGCC  CAA
                       ||||| |||| |||
                       CCTCT TCGG  GTT
                       _____   A  AA  A
GAM145  WARS        TAAACTGGA-AAGTTTCACCCCCAA 2035 AAAC    A____    I
                       TGGAGA   GCCCCCA
                       ||||||   |||||||
                       ACCTTT   TGGGGGT
                       ____    CAAAG    I
GAM145  WARS        TAAACTGGA-AAGTTTCACCCCCAA 2035 TCTA     A____    CAI
                       AACTGGAGA   GCCCCCAA
                       |||||||||   ||||||||
                       TTGACCTTT   TGGGGGTT
                       ____       CAAAG    CAI
GAM146  ABCF1       GGGGCAGCTGGGCCTGAAG      2089 _ A    GA  II
                       GG GCAGCTGGG TGAA
                       || ||||||||| ||||
```

```
                              CC CGTCGACCC ACTT
                              C _        GG  CI
GAM146  ABCF1        GGGGCAGCTGGGCCTGAAG     2089 TAGGA      GA   GG
                          GCAGCTGGG TGAAG
                          |||||||||| |||||
                          CGTCGACCC ACTTC
                          C____       GG  GA
GAM146  ACAD8        TAGAACCAGAGGTGGATGAAGG    2095   G  CT _     GG
                        TAGGA CAG GG GGATGAAGG
                        ||||| ||| || |||||||||
                        ATCTT GTC CC CCTACTTCC
                         G  T_ A     II
GAM146  ACAD8        TAGAACCAGAGGTGGATGAAGG    2095   G  CT _     I
                         AGGA CAG GG GGATGAAG
                         |||| ||| || ||||||||
                         TCTT GTC CC CCTACTTC
                          G  T_ A    I
GAM146  ADAT1        AGGAAGGCAGTTCAGGATGAAGGG  2047 _ A   CTG      I
                          GG GCAG  GGGATGAAGG
                          || ||||  ||||||||||
                          TC CGTC  TCCTACTTCC
                          T _ AAG       I
GAM146  ADAT1        AGGAAGGCAGTTCAGGATGAAGGG  2047 TA  __   CTG     GI
                          GGA GCAG  GGGATGAAGGG
                          ||| ||||  |||||||||||
                          CCT CGTC  TCCTACTTCCC
                          __ TC  AAG        AI
GAM146  ADCY6        AGGACCAGTGCTGGGGATGCAGG   2051 AGGAGCA       AI
                              GCTGGGGATG
                              ||||||||||
                              CGACCCCTAC
                          GTCA___       GT
GAM146  ADCY6        AGGACCAGTGCTGGGGATGCAGG   2051 TA  G  __     A GGI
                          GGA CA  GCTGGGGATG AGG
                          ||| ||  |||||||||| |||
                          CCT GT  CGACCCCTAC TCC
                          __  G  CA       G AII
GAM146  ANXA6        CCCCTCCCCCCACC--CCTGCCC   2072 T  A       GC
                          CCC TCCCCCCACCC CTGCCC
                          ||| |||||||||| ||||||
                          GGG AGGGGGGTGGG GACGGG
                          _  _       __
GAM146  APOC3        GGAGCAGCTGCCTCTAGGGATGAA  2085            _____       IIIT
                          GGAGCAGCTG    GGGATGA  T
                          ||||||||||    |||||||  |
                          CCTCGTCGAC    CCCTACT  A
                              GGAGAT    TIII
GAM146  ASIC4        TCCCCTCCCCCCACCCGGCT      2103   A        C GCC
                          TCCC TCCCCCCACCCG CT
                          |||| ||||||||||| ||
```

```
                        AGGG AGGGGGGTGGGC GA
                         G        C  III
GAM146 ATF5           TAGAGGCAG--GGGGATGAAGG   2096   GA  CT        G
                         TAG GCAG  GGGGATGAAGG
                         III IIII  IIIIIIIIIII
                         ATC CGTC  CCCCTACTTCC
                          TC   __          I
GAM146 ATF5           TAGAGGCAG--GGGGATGAAGG   2096 _ GA   CT        I
                          AG GCAG  GGGGATGAAG
                          II IIII  IIIIIIIIII
                          TC CGTC  CCCCTACTTC
                          A TC   __         I
GAM146 ATP8B2          TCCCATTCCCTGCCCACCCGCC   2098    _  __        TGCCC
                         TCCCAT CCC CCCACCCGCC
                         IIIIII III IIIIIIIIIII
                         AGGGTA GGG GGGTGGGCGG
                              A  AC      IIICC
GAM146 BGLAP            GCAGCT-GGGATGATGGGG   2081       G  A  I
                         GCAGCTGGG ATGA GGG
                         IIIIIIIII IIII III
                         CGTCGACCC TACT CCC
                           _        A  C
GAM146 BHMT2           AGG-GCATGGTGAGGATGAAGG   2050  A  GC_        I
                         GG GCA  TGGGGATGAAG
                         II III  IIIIIIIIIII
                         CC CGT  ACTCCTACTTC
                          _ ACC          I
GAM146 BHMT2           AGG-GCATGGTGAGGATGAAGG   2050 TA A  GC_       GG
                         GG GCA  TGGGGATGAAGG
                         II III  IIIIIIIIIII
                         CC CGT  ACTCCTACTTCC
                         __ _ ACC          AI
GAM146 BHMT2           AGCAGCTGGAGATAGCAGGG    2043         A_ II
                         AGCAGCTGGGGATG AGG
                         IIIIIIIIIIIII III
                         TCGTCGACCTCTAT TCC
                           CG  CI
GAM146 BHMT2           AGCAGCTGGAGATAGCAGGG    2043 TAGGAGCA      A_
                          GCTGGGGATG AGGG
                          IIIIIIIIII IIII
                          CGACCTCTAT TCCC
                         _____      CG
GAM146 CDKN2D          TCCCCCCACCCCCCATGCC    2110 TC  T    CCC   CC
                         CCA CCCCCCA  GCCTG
                         III IIIIIII  IIIII
                         GGT GGGGGGT  CGGAC
                         __ _    A__   TT
GAM146 CHGA            GAGCAGCTGGCGGTGTGGGG    2077      _ A AA  I
                         AGCAGCTGG GG TG  GG
                         IIIIIIIII II II  II
```

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                    TCGTCGACC CC AC  CC
                       G _ AC  I
GAM146 CHGA         GAGCAGCTGGCGGTGTGGGG   2077 TAGGAG     _ A AA
                       CAGCTGG GG TG  GGG
                       IIIIIII II II  III
                       GTCGACC CC AC  CCC
                    _____      G _ A_
GAM146 CHI3L1       GAGCAGCTGTGGAATTAGGAAGGGG 2073 AGCA   _   ___    I
                       GCTG GGGAT  GAAGGG
                       IIII IIIII  IIIIII
                       CGAC CCTTA  CTTCCC
                    ____     A  ATC    I
GAM146 CSNK2A1      AGAAGCAGCTGGGGGT-AAG      2057 _         ATGAAI
                       GGAGCAGCTGGGG
                       IIIIIIIIIIIII
                       CTTCGTCGACCCC
                       T       CATTII
GAM146 CSNK2A1      AGAAGCAGCTGGGGGT-AAG      2057 TA        ATG  G
                       GGAGCAGCTGGGG  AAGG
                       IIIIIIIIIIIII  IIII
                       CTTCGTCGACCCC  TTCT
                       __        CA_  I
GAM146 CYP2B6       TAGGAAGAGGCAGCTGGGAATGA  2093  ____         AGGGGI
                       TAGGA  GCAGCTGGGGATGA
                       IIIII  IIIIIIIIIIIIII
                       ATCCT  CGTCGACCCTTACT
                       TCTC          IIIGGG
GAM146 CYP2B6       TAGGAAGAGGCAGCTGGGAATGA  2093  ____         IIIT
                       TAGGA  GCAGCTGGGGATG
                       IIIII  IIIIIIIIIIIII
                       ATCCT  CGTCGACCCTTAC
                       TCTC          TIII
GAM146 DNMT3B       GGAGCAGCTGCTGCGAGGAAGCGG 2086 A     GG__ T GGI
                       GCAGCTG  GA GAAG
                       IIIIIII  II IIII
                       CGTCGAC  CT CTTC
                       _     GACG  C   GII
GAM146 DNMT3B       GGAGCAGCTGCTGCGAGGAAGCGG 2086 TAGG    GG__ T G I
                       AGCAGCTG  GA GAAG GG
                       IIIIIIII  II IIII II
                       TCGTCGAC  CT CTTC CC
                       ____      GACG  C  G  G
GAM146 DUSP4        TCCCA---CCCAACCCGCCTGC   2104     CCCC      C
                       TCCCATCC  ACCCGCCTGC
                       IIIIIIII  IIIIIIIIII
                       AGGGTGGG  TGGGCGGACG
                          T___        I
GAM146 EEF2         TCCCATCCCGCCTCCC-CCTCCCC 2109     C A  G  G I
                       TCCCATCCC CC CCC CCT CCC
                       IIIIIIIII II III III III
```

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                           AGGGTAGGG GG GGG GGA GGG
                              C A  _   G  I
GAM146 EGR3         AGGA-CAGCTGGGGAAGAGGGG   2060 _  G      T A  I
                        GGA CAGCTGGGGA GA GG
                        ||| ||||||||| || ||
                        CCT GTCGACCCCT CT CC
                         T  _     T C  I
GAM146 EGR3         AGGA-CAGCTGGGGAAGAGGGG   2060 TA  G      T A
                        GGA CAGCTGGGGA GA GGGG
                        ||| ||||||||| || ||||
                        CCT GTCGACCCCT CT CCCC
                        __ _        T _
GAM146 EPB49        GAGCAGCTGGGAGTGTGGGGG   2079       GA AA  I
                       AGCAGCTGGG TG GGG
                       |||||||||| || |||
                       TCGTCGACCC AC CCC
                          TC AC  I
GAM146 EPB49        GAGCAGCTGGGAGTGTGGGGG   2079 TAGGAG   GA AA
                         CAGCTGGG TG GGGG
                         |||||||| || ||||
                         GTCGACCC AC CCCC
                         _____      TC AC
GAM146 EPHB4        AGGCAGCAGCTGGGG--GAGGGG  2046 _  _      AT A  I
                        GG AGCAGCTGGGG GA GG
                        || ||||||||||| || ||
                        CC TCGTCGACCCC CT CC
                         T  G      __ C  I
GAM146 EPHB4        AGGCAGCAGCTGGGG--GAGGGG  2046 TA  _      ATGA
                        GG AGCAGCTGGGG  AGGGG
                        || |||||||||||  |||||
                        CC TCGTCGACCCC  TCCCC
                        __ G       C___
GAM146 ETF1       TCCCATCCCTTCCCACCCGCC    2100      __      TGCCC
                       TCCCATCCC CCCACCCGCC
                       ||||||||| |||||||||||
                       AGGGTAGGG GGGTGGGCGG
                          AA      IIICC
GAM146 ETS2        GGAGCAGCTGGTCAGGATGGG   2090       ___     AAGGI
                       GAGCAGCTGG GGATG
                       |||||||||| |||||
                       CTCGTCGACC CCTAC
                        AGT    CIIIG
GAM146 ETS2        GGAGCAGCTGGTCAGGATGGG   2090 TAGG    GGAT A  G
                        AGCAGCTGG  GA GGG
                        |||||||||  || |||
                        TCGTCGACC  CT CCC
                        ____     AGTC A  G
GAM146 FLRT1       AGG-GCAGCTGGGGCTGAGGCGG   2062 _  A      A  A  GI
                        GG GCAGCTGGGG TGA GG
                        || |||||||||| ||| ||
```

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                        CC CGTCGACCCC ACT CC
                        T _       G _ GC
GAM146  FLRT1           AGG-GCAGCTGGGGCTGAGGCGG   2062 TA A      A  A _
                        GG GCAGCTGGGG TGA GG GG
                        || |||||||||| ||| || ||
                        CC CGTCGACCCC ACT CC CC
                        __ _      G _ G
GAM146  FRDA            AGCAGCTGGNTATGTGGGG   2044  C      T A I
                        AG AGCTGGGGA GA GG
                        || |||||||| || ||
                        TC TCGACCCCT CT CC
                         C     _ C C
GAM146  FXYD6           TAGGAGCAGAAGGTGATGGAGGG  2097      CT _ A  GI
                        TAGGAGCAG  GGG GATG AGGG
                        |||||||||  ||| |||| ||||
                        ATCCTCGTC  TCC CTAC TCCC
                             T_  A  C  II
GAM146  FXYD6           TAGGAGCAGAAGGTGATGGAGGG  2097      CT _ A  I
                        AGGAGCAG  GGG GATG AGG
                        ||||||||  ||| |||| |||
                        TCCTCGTC  TCC CTAC TCC
                            T_  A  C  I
GAM146  FY              AGG-GCAGCTGGGGCTGGAGG   2058 _ A      A AAGI
                          GG GCAGCTGGGG TG
                          || |||||||||| ||
                          CC CGTCGACCCC AC
                          T _       G CTCI
GAM146  FY              AGG-GCAGCTGGGGCTGGAGG   2058 TA A      A A
                          GG GCAGCTGGGG TG AGGG
                          || |||||||||| || ||||
                          CC CGTCGACCCC AC TCCT
                          __ _      G C
GAM146  GA              AGGAGC-GTTGGGGATGAAGG   2059 _   AGC       I
                         GGAGC  TGGGGATGAAG
                         |||||  ||||||||||||
                         CCTCG  ACCCCTACTTC
                         T   CA_       I
GAM146  GA              AGGAGC-GTTGGGGATGAAGG   2059 TA   AGC
                         GGAGC  TGGGGATGAAGGG
                         |||||  |||||||||||||
                         CCTCG  ACCCCTACTTCCT
                         __   CA_
GAM146  GAS7            AGGAAGCAGCTGGGG--GAAGG   2048 __        AT  I
                         GGAGCAGCTGGGG GAAG
                         ||||||||||||| ||||
                         CTTCGTCGACCCC CTTC
                         TC        __  I
GAM146  GAS7            AGGAAGCAGCTGGGG--GAAGG   2048 TA        AT
                         GGAGCAGCTGGGG GAAGGG
                         ||||||||||||| ||||||
```

```
                              CTTCGTCGACCCC CTTCCT
                              C_           __
GAM146  GFAP          GGAGCAGCTGGGG-TGGTGGGG  2092 _         A AA  I
                        GAGCAGCTGGGG TG GGG
                        ||||||||||| || |||
                        CTCGTCGACCCC AC CCC
                        C         _ CA  I
GAM146  GFAP          GGAGCAGCTGGGG-TGGTGGGG  2092 TAGG       A AA
                         AGCAGCTGGGG TG GGGG
                         |||||||||| || ||||
                         TCGTCGACCCC AC CCCC
                         ____          _ CA
GAM146  GGA3          CCCA-CCCCCCACCCCCCACCCC  2069 TC  T      G TG
                        CCA CCCCCCACCC CC CCC
                        ||| |||||||||| || |||
                        GGT GGGGGGTGGG GG GGG
                        __  _        _ GT
GAM146  GNA15          TCCCA-CCTCCCACCCGCCCGCC  2106    T C        C
                        TCCCA CC CCCACCCGCCTGCC
                        ||||| || |||||||||||||
                        AGGGT GG GGGTGGGCGGGCGG
                         _ A            I
GAM146  GNAZ          GAGCAGCTGTG--TGCAGG  2076          _____  ATGAAGI
                        GAGCAGCTG    GGG
                        |||||||||    |||
                        CTCGTCGAC    TCC
                         ACACG  IIIGAAG
GAM146  GNAZ          GAGCAGCTGTG--TGCAGG  2076 TAGGAG    GGGA A
                          CAGCTG   TG AGG
                          ||||||   || |||
                          GTCGAC   AC TCC
                          _____    AC__ G
GAM146  HMGCS1         TCCCATACCCCCACCC-CATGCCC  2108    C      GCC   I
                        TCCCAT CCCCCACCC  TGCCC
                        |||||| ||||||||  |||||
                        AGGGTA GGGGGTGGG  ACGGG
                         T      GT_  I
GAM146  HRMT1L2        CCCATCCCCCCAGCC-CAGGCCC  2071 TC        _  CCT
                         CCATCCCCCCA CCCG  GCCC
                         ||||||||||| |||| ||||
                         GGTAGGGGGGT GGGT  CGGG
                         __     C  C__
GAM146  HUS1           AGGAGCAGC-GGGG-TGAA  2056     T  A  I
                        AGGAGCAGC GGGG TGA
                        ||||||||| |||| |||
                        TCCTCGTCG CCCC ACT
                         _  _   T
GAM146  HUS1           AGGAGCAGC-GGGG-TGAA  2056 TA     T  A  GG
                        GGAGCAGC GGGG TGAA
                        ||||||||| |||| ||||
```

```
                          CCTCGTCG CCCC ACTT
                          __     _  _   GI
GAM146  ICMT         AGGAGCAGCTCG---TGAAGGGG  2063 _        GGGGA
                          GGAGCAGCT   TGAAGGG
                          ||||||||    |||||||
                          CCTCGTCGA   ACTTCCC
                          T      GC___
GAM146  ICMT         AGGAGCAGCTCG---TGAAGGGG  2063 TA       GGGGA
                          GGAGCAGCT   TGAAGGG
                          ||||||||    |||||||
                          CCTCGTCGA   ACTTCCC
                          __         GC___
GAM146  ICOS         TAGGAGCAGATGTGGA-GACAGGG  2094       C__    GA  GI
                          TAGGAGCAG  TGGGGAT AGGG
                          |||||||||  ||||||| ||||
                          ATCCTCGTC  ACCTCTG TCCC
                             TAC       ___  II
GAM146  ICOS         TAGGAGCAGATGTGGA-GACAGGG  2094       C__    GA  I
                          AGGAGCAG  TGGGGAT AGG
                          ||||||||  ||||||| |||
                          TCCTCGTC  ACCTCTG TCC
                             TAC       ___ I
GAM146  IVD          GAGCAGCTGGGCAGGAGGG       2075       GATGAAGII
                          GAGCAGCTGGG
                          |||||||||||
                          CTCGTCGACCC
                             GTCCTCCCI
GAM146  IVD          GAGCAGCTGGGCAGGAGGG       2075 TAGGAG     GAT A
                          CAGCTGGG  GA GGG
                          ||||||||  || |||
                          GTCGACCC  CT CCC
                          _____       GTC _
GAM146  KCNK3        GGAGACACAGCTGGGGATGAGGAAGGGG2082 GAG           ___  I
                          CAGCTGGGGATGA  AGGG
                          |||||||||||||  ||||
                          GTCGACCCCTACT  TCCC
                          ___           CCT  I
GAM146  KCNK3        GGAGACACAGCTGGGGATGAGGAAGGGG2082 T GA           ___    III
                          AG GCAGCTGGGGATGA  AGGGG
                          || |||||||||||||  |||||
                          TC TGTCGACCCCTACT  TCCCC
                          _ TG           CCT  TCI
GAM146  KCNK4        TCCCTGCACCCCACCCGCC      2102  ATCC       TGCC
                          TCCC  CCCCACCCGCC
                          ||||  |||||||||||
                          AGGG  GGGGTGGGCGG
                             ACGT       IIIC
GAM146  KCNK7        AGCAGCT-GGGATGGTGGGG     2045 _      G  AA  I
                          GCAGCTGGG ATG  GGG
                          ||||||||| ||| |||
```

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                         CGTCGACCC TAC  CCC
                         T      _   CA  I
GAM146  MAG              AGGGGCAGCTGGGAAGGAGGGGG  2064 _  A        T A  I
                         GG GCAGCTGGGGA GA GGG
                         || ||||||||||| || |||
                         CC CGTCGACCCTT CT CCC
                         C  _          C  C  I
GAM146  MAG              AGGGGCAGCTGGGAAGGAGGGGG  2064 TA A        T A  I
                         GG GCAGCTGGGGA GA GGGG
                         || ||||||||||| || ||||
                         CC CGTCGACCCTT CT CCCC
                         C_ _          C  C  T
GAM146  MAP3K12          CCCCTCCCCCCACCC-CCT      2067 T  A        G   C
                         CCC TCCCCCCACCC CCTG
                         ||| |||||||||| ||||
                         GGG AGGGGGGTGGG GGAT
                         _   _         _  I
GAM146  MT3              AGCAGCAGCTGGAGGCGGTGAACGGG 2052 GGA        A___  G  I
                         GCAGCTGGGG   TGAA GG
                         ||||||||||   |||| ||
                         CGTCGACCTC   ACTT CC
                         ___          CGCC  G  I
GAM146  MT3              AGCAGCAGCTGGAGGCGGTGAACGGG 2052 TA G        A___  G  II
                         G AGCAGCTGGGG   TGAA GGG
                         | |||||||||||   |||| |||
                         C TCGTCGACCTC   ACTT CCC
                         __ G          CGCC  G  GI
GAM146  MTMR2            GGTGAAGCGGGAGGGATGAAGG   2087 _  AGCT       I
                         GAGC   GGGGATGAAG
                         ||||   ||||||||||
                         TTCG   TCCCTACTTC
                         C  CCC_        I
GAM146  MTMR2            GGTGAAGCGGGAGGGATGAAGG   2087 TA  AGCT       G
                         GGAGC   GGGGATGAAGGG
                         |||||   |||||||||||
                         CTTCG   TCCCTACTTCCT
                         A_  CCC_        G
GAM146  MUC3B            AGCAGCTGGGGTATTTAGGG    2042          _ GA  II
                         AGCAGCTGGGG AT AGG
                         ||||||||||| || |||
                         TCGTCGACCCC TA TCC
                         A AA  CI
GAM146  MUC3B            AGCAGCTGGGGTATTTAGGG    2042 TAGGAGCA    _ GA
                         GCTGGGG AT AGGG
                         ||||||| || ||||
                         CGACCCC TA TCCC
                         _____       A AA
GAM146  NAP1L3           GGAGCTGGAGCTGGGGATGCAGAGG 2083 GAGC        A  I
                         AGCTGGGGATG AGGG
                         |||||||||| ||||
```

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                    TCGACCCCTAC TCTC
                    GACC        G    I
GAM146 NAP1L3       GGAGCTGGAGCTGGGGATGCAGAGG 2083 TA__    AGC      A    II
                        GGAGC  TGGGGATG AGGGG
                        ||||| ||||||||| |||||
                        CCTCG  ACCCCTAC TCTCC
                    TCGA         G   GG
GAM146 NDST1        AGGAGCAGCTGGGAACGGAATGG  2053              AAGGI
                        GAGCAGCTGGGGATG
                        |||||||||||||||
                        CTCGTCGACCCTTGC
                            CTTAI
GAM146 NDST1        AGGAGCAGCTGGGAACGGAATGG  2053 TA             _ G  I
                        GGAGCAGCTGGGGATG AA GGG
                        ||||||||||||||| || |||
                        CCTCGTCGACCCTTGC TT CCT
                        __             C A  I
GAM146 NGB          GGAGCGGGTTGGTGATGAAGGG  2088 G AGC_  G        I
                        AGC   TGG GATGAAGG
                        |||   ||| |||||||||
                        TCG   ACC CTACTTCC
                        _  CCCA  A       I
GAM146 NGB          GGAGCGGGTTGGTGATGAAGGG  2088 TAGG  AGC_  G      G
                        AGC   TGG GATGAAGGG
                        |||   ||| |||||||||
                        TCG   ACC CTACTTCCC
                        ____  CCCA  A       G
GAM146 NRXN2        GGAGCGGGGTAGGGATGAAGCGG  2084   AGC_       GGI
                        AGC   TGGGGATGAAG
                        |||   ||||||||||
                        TCG   ATCCCTACTTC
                        CCCC         GII
GAM146 NRXN2        GGAGCGGGGTAGGGATGAAGCGG  2084 TAGG  AGC_      G  I
                        AGC   TGGGGATGAAG GG
                        |||   |||||||||| ||
                        TCG   ATCCCTACTTC CC
                        ____  CCCC         G T
GAM146 NRXN2        TCCCA-CCCCCCACC--CCTGC  2105    T      GC  C
                        TCCCA CCCCCCACCC CTGC
                        ||||| |||||||||| ||||
                        AGGGT GGGGGGTGGG GACG
                            _     __   I
GAM146 OTP          GGCGCAGCTGGGTGGGAAGGG  2091 GA      GAT  I
                        GCAGCTGGG GAAGG
                        ||||||||| |||||
                        CGTCGACCC CTTCC
                        CG       ACC  I
GAM146 OTP          GGCGCAGCTGGGTGGGAAGGG  2091 TAGGA     GAT
                        GCAGCTGGG GAAGGGG
                        ||||||||| |||||||
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```
                          CGTCGACCC  CTTCCCT
                        G____         ACC
GAM146 PAFAH1B1         CCCTCCCCCCACCCCACTG    2065 TCCCA       GC  CC
                        TCCCCCCACCC CTG
                        |||||||||| |||
                        AGGGGGGTGGG GAC
                        G____        GT  CT
GAM146 PCSK2            AGGCGGAGCTGGGGAGGGAGGG  2061 AGC       TGA  I
                        GG AGCTGGGGA AGG
                        || ||||||||| |||
                        CC TCGACCCCT TCC
                         GCC        CCC  I
GAM146 PCSK2            AGGCGGAGCTGGGGAGGGAGGG  2061 TA AGC      TGA  G
                        GG AGCTGGGGA AGGG
                        || ||||||||| ||||
                        CC TCGACCCCT TCCC
                        __ GCC        CCC  G
GAM146 PKD2            TCCCCCCACCCCACTCCCC      2111 TC     CCCA   C CC
                        CCATCCC  CCCGC TG
                        ||||||| ||||| ||
                        GGTGGGG  GGGTG AC
                        __      TGAG   C II
GAM146 PRKACG          TCCCATCCCCCAAACCACC      2101       CAC   TGCC
                        TCCCATCCCCC  CCGCC
                        |||||||||||  |||||
                        AGGGTAGGGGG  GGTGG
                           TTT    IIIC
GAM146 PRX            TCCCATCCCAGCCCCAGCC-CTTGCCC2099       ___  _  GCC   II
                        TCCCATCCC  CCCA CCC  TGCCC
                        ||||||||| |||| ||| |||||
                        AGGGTAGGG  GGGT GGG  ACGGG
                           TCG  C  A__    II
GAM146 RASGRP2         CCCAT--CCCCAGCCTCCTGCCC  2070 TC      CCAC G
                        CCATCCCC   CC CCTGCCC
                        ||||||||   || |||||||
                        GGTAGGGG   GG GGACGGG
                        __      TC__  A
GAM146 SLC16A2         GAGCAGGGTGGGATGAAGGGG    2080      CTG        I
                        AGCAG  GGGATGAAGGG
                        ||||| |||||||||||
                        TCGTC  CCCTACTTCCC
                          CCA          I
GAM146 SLC16A2         GAGCAGGGTGGGATGAAGGGG    2080 TAGGAG  CTG
                        CAG  GGGATGAAGGGG
                        |||  |||||||||||
                        GTC  CCCTACTTCCCC
                        _____   CCA
GAM146 SLC23A1         GAGCAGCTGGAAGTGAAGG      2074          GA  II
                        GAGCAGCTGGG TGAAG
                        |||||||||| |||||
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                            CTCGTCGACCT ACTTC
                               TC    CI
GAM146 SLC23A1         GAGCAGCTGGAAGTGAAGG      2074 TAGGAG      GA    G
                          CAGCTGGG TGAAGG
                          |||||||| ||||||
                          GTCGACCT ACTTCC
                          _____            TC    G
GAM146 SORCS3          CCCCTCCCCCCACCCCCCT      2068 T  A      G  GCC
                         CCC TCCCCCCACCC CCT
                         ||| ||||||||||| |||
                         GGG AGGGGGGTGGG GGA
                         _  _          G  AII
GAM146 SPTBN2          GAGCAGCTGGAGATGGAGTGG      2078          A GGI
                         AGCAGCTGGGGATG AG
                         ||||||||||||| ||
                         TCGTCGACCTCTAC TC
                               C  ACI
GAM146 SPTBN2          GAGCAGCTGGAGATGGAGTGG      2078 TAGGAG        A _ G
                          CAGCTGGGGATG AG GG
                          ||||||||||| || ||
                          GTCGACCTCTAC TC CC
                          _____          C  A  G
GAM146 SYNGR1          AGG-GCAGCT-GGGAGGAA      2054 A        ATGAI
                         AGG GCAGCTGGGG
                         ||| ||||||||||
                         TCC CGTCGACCCT
                          _           CCTTI
GAM146 SYNGR1          AGG-GCAGCT-GGGAGGAA      2054 TA A      AT   G
                         GG GCAGCTGGGG GAAG
                         || |||||||||| ||||
                         CC CGTCGACCCT CTTT
                          __ _         C_    I
GAM146 SYNGR1          AGGAACAGCTGGGGCAGAA      2055          ATGAII
                         AGGAGCAGCTGGGG
                         ||||||||||||||
                         TCCTTGTCGACCCC
                               GTCTTI
GAM146 SYNGR1          AGGAACAGCTGGGGCAGAA      2055 TA        AT  GGG
                          GGAGCAGCTGGGG GAA
                          ||||||||||||| |||
                          CCTTGTCGACCCC CTT
                          __          GT  GII
GAM146 TBXAS1          CCCTCCCCCCACCCGGCAGCC      2066 TCCCA        CCT  C
                          TCCCCCCACCCG GCC
                          |||||||||||| |||
                          AGGGGGGTGGGC CGG
                          G____          CGT  A
GAM146 TGFB1           AGGAGACAGGCCGGGGATGAAGG      2049 G  _        I
                          GGA CAG CTGGGGATGAAG
                          ||| ||| ||||||||||||
```

```
                    TCT GTC GGCCCCTACTTC
                     _   C          I
GAM146 TGFB1        AGGAGACAGGCCGGGGATGAAGG  2049 TA  _ _        GGI
                     GGAG CAG CTGGGGATGAAGG
                     |||| ||| |||||||||||||
                     CCTC GTC GGCCCCTACTTCC
                     __   T  C        GII
GAM146 TMEM1        TCCC-TCCCCC-ACCCGCCTCCCC  2107   ATC       G
                     TCCC  CCCCCACCCGCCT CCC
                     ||||  ||||||||||| |||
                     AGGG  GGGGGTGGGCGGA GGG
                      A__       G
GAM147 ADRA1A       CAGGTGGGTTTGGCTGGGGGTGA  2115  CT_  ___      AGGGI
                     CAG  GGTTT  TGGGGGTGA
                     |||  |||||  |||||||||
                     GTC  CCAAA  ACCCCCACT
                      CAC   CCG       IIIGG
GAM147 ATP11B       CTGGTTTTGGCAGATAAGGG    2122 CAGCTG   G  TG
                      GTTTTGG GG  AAGGG
                      ||||||| ||  |||||
                      CAAAACC TC  TTCCC
                      _____     G  TA
GAM147 ATP8A2       CAGCAGGTGT-GGGGGTGAGGGG  2121  T  TT    A I
                     CAGC GGT  TGGGGGTGA GGG
                     |||| ||| |||||||| |||
                     GTCG CCA  ACCCCCACT CCC
                      T  C_     C  I
GAM147 G6PC         CAGCTTTTTTTGGGGG-GTAGG   2120    GG    TGA  G
                     CAGCT TTTTGGGGG  AGG
                     ||||| ||||||||| |||
                     GTCGA AAAACCCCC  TCC
                      AA      CA_  I
GAM147 NCYM         CAGCTGGTTCTCAGAGTGCAG    2119       G   A GG
                     CAGCTGGTTTT GGGGTG AG
                     |||||||||| ||||| ||
                     GTCGACCAAGA TCTCAC TC
                      G   G  II
GAM147 OTC          AGCTA-TTTTGGGGGTGCAAG   2114 CA  G     _  G
                      GCTG TTTTGGGGGTG AAGG
                      |||| |||||||||| ||||
                      CGAT AAAACCCCCAC TTCT
                      __  _      G  I
GAM147 PIN1         GGTTTAATTGGGGGTGAAAGG   2124 CAGCTGGTT
                          TTGGGGGTGAAGGG
                          ||||||||||||||
                          AACCCCCACTTTCC
                      TT_____
GAM147 RNASE2       CAGCTGGTTGTTCTGGGGTTCAGGG  2116     TTG__  GA II
                     CAGCTGGTT  GGGGT AGGG
                     |||||||||  |||| ||||
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                      GTCGACCAA   CCCCA TCCC
                        CAAGA   AG   II
GAM147 SLC22A12       GCTGGGTTTGGGGGTTAAG     2123 CAGC   T      G  G
                        TGG TTTGGGGGT AAG
                        ||| ||||||||| |||
                        ACC AAACCCCCA TTC
                        ____   C      A  A
GAM147 SOX12          CAGCTGGTTTGGGGGCGTG     2117      T    AAGG
                        CAGCTGGTTT GGGGGTG
                        |||||||||| |||||||
                        GTCGACCAAA CCCCCGC
                          _     ACII
GAM147 TIMP3          CAGCAGGACTTGGG-GTGAAG    2118   T TTTTG      GG
                        CAGC GG   GGGGTGAAG
                        |||| ||   |||||||||
                        GTCG CC   CCCCACTTC
                        T TGAA_      II
GAM148 ADAMTS13       TGGAATGGGA--CAGGC--CTGC  2131       TCAC GA
                        TGGAATGGGAT  GC CTGC
                        ||||||||||   || ||||
                        ACCTTACCCTG  CG GACG
                          TC__  __
GAM148 GRIN2A         GAATGGGATAATGCAGGCGACT   2128 TGGA   T___ C    GCA
                        ATGGGAT   CA GCGACT
                        |||||||   || ||||||
                        TACCCTA   GT CGCTGA
                        ____       TTAC C    GTI
GAM148 KCNJ15         ATGGGATTC-TGCTACTGC       2127 TGGAATGG   AC G
                          GATTC GC ACTG
                          ||||| || ||||
                          CTAAG CG TGAC
                        _____   A_ A
GAM148 MFGE8          TGGAATGGG---CACGCTGGGCTGC 2130     ATT  GA__  A
                        TGGAATGGG CACGC  CTGC
                        ||||||||| |||||  ||||
                        ACCTTACCC GTGCG  GACG
                          ___    ACCC  I
GAM148 VBP1           GGGATGCGAG-CGCGCGACTGC    2129 T A G TTCA     A
                        GGA TG GA   CGCGACTGC
                        ||| || ||   |||||||||
                        CCT AC CT   GCGCTGACG
                        _ _ G CGC_      G
GAM149 CASP8          TCATCGTGGGGCTTGATCTCAA    2139 TATC      AG___   G
                        ATCGTGGGGC   CTCAAGA
                        ||||||||||   |||||||
                        TAGCACCCCG   GAGTTTT
                        ____        AACTA  I
GAM149 GRAP2          TCTTGTGGGCAGCTCCAGA       2140 TATCATCGTG      A
                        GGGCAGCTC AGA
                        ||||||||| |||
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                        CCCGTCGAG TCT
                        A_____          G
GAM149 MAP3K14      CAT-GTGGA-CAGCTCAAGA     2135 TATCATCGTG
                        GGGCAGCTCAAG
                        ||||||||||||
                        CCTGTCGAGTTC
                        CA_____
GAM149 NESH         TATC-TCTGTGGGGCAG-TCA    2136   A _      C AGA
                        TATC TC GTGGGGCAG TCA
                        |||| || |||||||| |||
                        ATAG AG CACCCGTC AGT
                            _ A     _ |||
GAM149 PACSIN1      CATCGTGGGTGCAG-GCAGGAG   2134 TATCAT    _  CT A
                        CGTGGG GCAG  CA GAG
                        |||||| |||| || |||
                        GCACCC CGTC  GT CTC
                        _____      A  C_ C
GAM149 PROX1        TCAGC-TGGGCACAGCTCAAGA   2138 TATCATCG   _
                        TGGG GCAGCTCAAGAG
                        |||| |||||||||||
                        ACCC TGTCGAGTTCTT
                        TCG_____     G
GAM149 ZNF148       TATCATCGTATATCAGCTTAA    2137       GGG    CAAGAG
                        TATCATCGTG  CAGCT
                        ||||||||||  |||||
                        ATAGTAGCAT  GTCGA
                          ATA    ATT|||
GAM150 ACRV1        TGAGAG--AA--AGAGTTGGAG   2154      TTAA
                        TGAGAG   GGAGAGTTGGAG
                        ||||||   ||||||||||||
                        ACTCTC   TTTCTCAACCTC
                            ____
GAM150 ACRV1        TGAGAG--AA--AGAGTTGGAG   2154 _   TTAA
                        GAGAG   GGAGAGTTGGA
                        |||||   |||||||||||
                        CTCTC   TTTCTCAACCT
                        A    ____
GAM150 BTG2         GAGGGTTAGAGGAGAGTTG      2146  A _        ||
                        GAG GTTA AGGAGAGTT
                        ||| |||| |||||||||
                        CTC CAAT TCCTCTCAA
                          C  C    C|
GAM150 BTG2         GAGGGTTAGAGGAGAGTTG      2146 TG A _       GAGG
                        AG GTTA AGGAGAGTTG
                        || |||| |||||||||||
                        TC CAAT TCCTCTCAAC
                        __ C  C    A|||
GAM150 F8           AGAGTTAAGTTAAATTGGATGC   2144      GA    GG|
                        GAGTTAAG GAGTTGGA
                        |||||||| ||||||||
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                            CTCAATTC TTTAACCT
                               AA      ACI
GAM150 F8              AGAGTTAAGTTAAATTGGATGC   2144 TGAG    GA    G
                            AGTTAAG GAGTTGGA GC
                            ||||||| |||||||| ||
                            TCAATTC TTTAACCT CG
                            ____    AA      A
GAM150 FGR            TGAGATAAAAGGAGAGTAGGA    2153    GTT    T GGC
                           TGAGA  AAGGAGAGT GGA
                           |||||  ||||||||| |||
                           ACTCT  TTCCTCTCA CCT
                            ATT      T  III
GAM150 FGR            TGAGATAAAAGGAGAGTAGGA    2153    GTT    T I
                            GAGA  AAGGAGAGT GG
                            ||||  ||||||||| ||
                            CTCT  TTCCTCTCA CC
                            ATT       T I
GAM150 GPR4          TGAGAGGGAA--A-AGTTGGAGG   2156    TTAA
                           TGAGAG  GGAGAGTTGGAGG
                           ||||||  ||||||||||||
                           ACTCTC  CTTTTCAACCTCC
                               C___
GAM150 GPR4          TGAGAGGGAA--A-AGTTGGAGG  2156 _   TTAA
                            GAGAG  GGAGAGTTGGAG
                            |||||  |||||||||||
                            CTCTC  CTTTTCAACCTC
                            A   C___
GAM150 HOXC6        TGTGA-TTAGGGGAGAGTTGGTGG  2151 A GTTAA      AI
                            GA   GGAGAGTTGG
                            ||   ||||||||||
                            CT   CCTCTCAACC
                            A AATCC       AI
GAM150 HOXC6        TGTGA-TTAGGGGAGAGTTGGTGG  2151 TGA GTTAA      A CI
                            GA   GGAGAGTTGG GG
                            ||   |||||||||| ||
                            CT   CCTCTCAACC CC
                            ACA AATCC      A II
GAM150 KPNA3         TGAGATTGTTAAGGAGAGTT     2150    __       GGAGG
                           TGAGA GTTAAGGAGAGTT
                           ||||| |||||||||||||
                           ACTCT CAATTCCTCTCAA
                             AA       IIICG
GAM150 KPNA3         TGAGATTGTTAAGGAGAGTT     2150    __       III
                           TGAGA GTTAAGGAGAGT
                           ||||| ||||||||||||
                           ACTCT CAATTCCTCTCA
                             AA      AII
GAM150 MAML1         AGAGTTAAGGGCAGTAGAAG     2143       AG  T I
                           GAGTTAAGG AGT GGA
                           ||||||||| ||| |||
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                        CTCAATTCC TCA CTT
                          CG   T   I
GAM150 MAML1          AGAGTTAAGGGCAGTAGAAG   2143 TGAG      AG  T
                        AGTTAAGG AGT GGAGG
                        |||||||| ||| |||||
                        TCAATTCC TCA CTTCT
                        ____      CG   T
GAM150 MAPK10        GAGGATGAAGAAGAGTTGGAGG   2148 AG T         I
                       AG T AAGGAGAGTTGGAG
                       || | |||||||||||||
                       TC  A TTCTTCTCAACCTC
                         CT C           I
GAM150 MAPK10        GAGGATGAAGAAGAGTTGGAGG   2148 TG AG T        C
                       AG  T AAGGAGAGTTGGAGG
                       || | |||||||||||||||
                       TC  A TTCTTCTCAACCTCC
                       __ CT C        T
GAM150 MME          TGGGA-TTCGGGAGAAGTTGGAGGC 2152 A GTTAA   _     I
                       TG GA   GGAGA GTTGGAGGC
                       || ||    ||||| |||||||||
                       AC CT   CCTCT CAACCTCCG
                        C AAGC_   T      I
GAM150 MME          TGGGA-TTCGGGAGAAGTTGGAGGC 2152 GAGA  AA   _     I
                       GTT GGAGA GTTGGAGG
                       ||| ||||| |||||||||
                       TAA CCTCT CAACCTCC
                       CCC_ GC  T     I
GAM150 MYEOV        GAGAGGGTAGGAGAGTTGG    2147    TTA     II
                      GAGAG AGGAGAGTTG
                      ||||| |||||||||||
                      CTCTC TCCTCTCAAC
                        CCA      CI
GAM150 MYEOV        GAGAGGGTAGGAGAGTTGG    2147 T A TA      AGG
                      GAG GT AGGAGAGTTGG
                      ||| || ||||||||||
                      CTC CA TCCTCTCAACC
                       T  C __     CII
GAM150 PDE4B        AGTTAAAAGTACTGTTGGAGGC   2145 GTTAAGGAGA    I
                            GTTGGAGG
                            ||||||||
                            CAACCTCC
                       ATTTTCATGA      I
GAM150 PDE4B        AGTTAAAAGTACTGTTGGAGGC   2145 T   TAAGGAGA
                       GAGAGT    GTTGGAGGC
                       ||||||    |||||||||
                       TTTTCA    CAACCTCCG
                       _    TGA____
GAM150 STK38       GTTATGGGAAGTTGGAGGC     2149 A AG     II
                      GTTA GG AGTTGGAGG
                      |||| || |||||||||
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                        CAAT CC  TCAACCTCC
                          A CT       GI
GAM150  TEM7            TGAGAGACAAGG--AGTTGGAG   2155      TTA  A       G
                          TGAGAG  AGG GAGTTGGAG
                          |||||  |||  |||||||||
                          ACTCTC  TTC CTCAACCTC
                            TG_  _        I
GAM150  TEM7            TGAGAGACAAGG--AGTTGGAG   2155 _    TTA  A      I
                           GAGAG  AGG GAGTTGGA
                           |||||  |||  |||||||
                           CTCTC  TTC CTCAACCT
                           A   TG_  _       I
GAM151  ATP5G2            CCAACTGTGGAAAAGAAATAT   2168 TACC     CTT    C
                           AACTGTGGA  GGAATAT
                           |||||||||  |||||||
                           TTGACACCT  CTTTATA
                           ____        TTT      T
GAM151  CNGB3           ACCATCTTTGGGGGACTTGGAA   2161 TA  A GT___      TATC
                          CCA CT   GGACTTGGAA
                          ||| ||   ||||||||||
                          GGT GA   CCTGAACCTT
                          __  A  AACCC      TIII
GAM151  ENO2            CAACTGTGGAACGTGGCAT     2165 TACCAA    _T AATAT
                           CTGTGGA C TGG
                           ||||||| | |||
                           GACACCT G ACC
                           _____     T C  GTACC
GAM151  FZD4           ACCACCTGTAACTGACTTGGAA   2160 TA  A  ___      TATC
                          CCA CTGTG GACTTGGAA
                          ||| |||||  |||||||||
                          GGT GACAT  CTGAACCTT
                          __  G  TGA      CIII
GAM151  GAS1           ACCAA--GTTGACTTGGAA      2162 TA  CT G     TA
                          CCAA GT GACTTGGAA
                          |||| || |||||||||
                          GGTT CA CTGAACCTT
                          __   __  A    TI
GAM151  PIM1           CAGCTATGGAAGCTTGGAATA    2166 TACCAA    __      TC
                          CTGTGGA CTTGGAATA
                          ||||||| |||||||||
                          GATACCT GAACCTTAT
                          _____   TC     CC
GAM151  PLGL           ACCAACTGTGGA--TGGAA      2163 TA       CT  TA
                          CCAACTGTGGA TGGAA
                          ||||||||||| |||||
                          GGTTGACACCT ACCTT
                          __        __  TI
GAM151  PTPN2          ACCAACTGTTTACCT-GACTATC  2164 TA      GG   AA
                          CCAACTGT ACTTGG TATC
                          |||||||| |||||| ||||
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                              GGTTGACA TGGACT ATAG
                              __       AA    G_
GAM151  RNH         TACCAACTG-GGA---GGAA      2169       T  CTT   T
                              TACCAACTG GGA  GGAA
                              ||||||||| |||  ||||
                              ATGGTTGAC CCT  CCTT
                                        _  ___    I
GAM151  TIMP3       AAATGTCAACTTGGAATGTC      2159 TACCAACT G      AT
                              GT GACTTGGAAT
                              || |||||||||
                              CA TTGAACCTTA
                              _____ G     CA
GAM151  ZNF80       CCAACTGTGTCC--GGAAT       2167 TACC     GACT   A
                              AACTGTG  TGGAAT
                              |||||||  ||||||
                              TTGACAC  GCCTTA
                              ____      AG__   A
GAM152  ABCB8       TGGCAGCGACCACACCTCA       2180       ACT      TTGC
                              TGGCAG  TCACACCTCA
                              ||||||  ||||||||||
                              ACCGTC  GGTGTGGAGT
                                  GCT      IIIT
GAM152  CDC23       TGGCAGACTT---TCCTCCTTTCT  2181       CACA   ATTG
                              TGGCAGACTT CCTC  CT
                              |||||||||| ||||  ||
                              ACCGTCTGAA GGAG  GA
                                    A___   GAAA
GAM152  CDKN1A      GGCAG-CTGCTCACACCTCA      2175 TG  AC_      TTGC
                              GCAG  TTCACACCTCA
                              ||||  ||||||||||
                              CGTC  GAGTGTGGAGT
                                __  GAC      CIII
GAM152  CYP27B1     GCATACTTCACA---CATTG      2174 TGGCAG      CTC
                              ACTTCACAC  ATTG
                              |||||||||  ||||
                              TGAAGTGTG  TAAC
                              TA____      ___
GAM152  DCTN1       GGCA-ACTTCACA-CACATAGC    2177 TG  A     CT  T
                              GCAG CTTCACAC  CAT GC
                              |||| |||||||| ||| ||
                              CGTT GAAGTGTG  GTA CG
                                __   _   T_  T
GAM152  FLNB        GGCAAAATTCCCTACACCTCATTTCT 2176 TG   ___ TC      GCTII
                              GCAGA  CT ACACCTCATT
                              ||||   || ||||||||||
                              CGTTT  GG TGTGGAGTAA
                                __    TAA GA      AGACI
GAM152  MMP15       TGGCAGACTCCACTCGCTCA      2179          AC_ TTGC
                              TGGCAGACTTCAC  CTCA
                              |||||||||||||  ||||
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                                  ACCGTCTGAGGTG  GAGT
                                      AGC    IIIT
GAM152  PDGFRA          CAAACTTCACACACCACTG     2172 TGGCAG      C     C
                             ACTTCACAC TCATTG
                             IIIIIIIII IIIIII
                             TGAAGTGTG GGTGAC
                          _____         T    T
GAM152  TARBP2         CAGGCT-C-CACCTCATTGC     2173 TGGCAGAC  A
                             TTC CACCTCATTG
                             III IIIIIIIIII
                             GAG GTGGAGTAAC
                          C_____   _
GAM152  XK            TGGCT-ACTCCCACACCTCA     2178  AG   _      TTGC
                          TGGC ACTTC ACACCTCA
                          IIII IIIII IIIIIIII
                          ACCG TGAGG TGTGGAGT
                            A_   G      IIIT
GAM153  GAS1          GCCAACGGCGGGGGGCGCG     2190  CT        II
                          GCC CGGCGGGGGGTGC
                          III IIIIIIIIIIIII
                          CGG GCCGCCCCCGCG
                            TT        CI
GAM153  GAS1          GCCAACGGCGGGGGGCGCG     2190  TGTCGCCCT
                             CGGCGGGGGGTGCG
                             IIIIIIIIIIIIII
                             GCCGCCCCCGCGC
                          T_____
GAM153  GRLF1         GCTCTCGCCTGGGGGGTGC     2189  C  GC_     II
                          GC CTCG GGGGGGTG
                          II IIII IIIIIIII
                          CG GAGC CCCCCCAC
                           A  GGA     GI
GAM153  GRLF1         GCTCTCGCCTGGGGGGTGC     2189 TG   CTCGGC      G
                          TCGCC   GGGGGGTGC
                          IIIII   IIIIIIIII
                          AGCGG   CCCCCCACG
                          __  A_____     G
GAM153  HPCA         TGTTGCCTCTGGGATTGGGGGGTGC 2193  C  _ C C__    GGII
                          TGT GCC CT GG  GGGGGGTGC
                          III III II II  IIIIIIIII
                          ACA CGG GA CC  CCCCCCACG
                           A  A  C TAA       IIIG
GAM153  HPCA         TGTTGCCTCTGGGATTGGGGGGTGC 2193 GTC  _ C C__    I
                             GCC CT GG  GGGGGGTG
                             III II II  IIIIIIII
                             CGG GA CC  CCCCCCAC
                           ___  A C TAA      I
GAM153  IFI35        CCTTGGCGGGGGGGTGGGG     2186  C       _ CGII
                          CCT GGCGGGGGG TG
                          III IIIIIIIII II
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                              GGA CCGCCCCC AC
                               A      C CCCI
GAM153 LBX1            CCCTCGGCGGTCCGGTCCGG   2184       GG_  G II
                          CCCTCGGCGG  GGT CG
                          IIIIIIIII  III II
                          GGGAGCCGCC  CCA GC
                               AGG  G CI
GAM153 LBX1            CCCTCGGCGGTCCGGTCCGG   2184 TGTC CC_  __     GCG
                           GC  TCGG CGGGGGGT
                           II  IIII IIIIIIII
                           CG  GGCC GCCCTCCG
                            C___ CCA  AG      III
GAM153 PTPRF          CCCACGGCGGGGGTGGCGG     2185  T     GT II
                          CCC CGGCGGGGG GCG
                          III IIIIIIIII III
                          GGG GCCGCCCCC CGC
                           T      AC  CI
GAM153 SLC6A8        GCCCCCTG-GAGGGGTGCGG     2192 _  GGC       I
                          CCCTC GGGGGGTGCG
                          IIIII IIIIIIIIII
                          GGGGG CTCCCCACGC
                            C  AC_      I
GAM153 SUFU         GCCAGCGGCG--GGGTGCGG     2191 CCC      _    I
                            TCGGCGG GGGGTGCG
                            IIIIIII IIIIIIII
                            GGTCGCC CCCCACGC
                            C__    G    I
GAM153 TEF          CGCCCG-GGCGGGGGGCACGG    2188 _  TC     TG I
                          GCCC GGCGGGGGG CG
                          IIII IIIIIIIII II
                          CGGG CCGCCCCC GC
                          G  C_     GT I
GAM153 TEF          CGCCCG-GGCGGGGGGCACGG    2188 ____ T     GGC
                           TG CGCCCTC
                           II IIIIIII
                           GC GTGGGGG
                        IIIG _     GCG
GAM153 VGF          CGCGCGCGGCGGGGGCGCGCGG   2187 _ CCT      _  I
                          GC  CGGCGGGGG GTGCG
                          II  IIIIIIIIII IIIII
                          CG  GCCGCCCCC CGCGC
                          G C__     G  I
GAM153 VGF          CGCGCGCGGCGGGGGCGCGCGG   2187 TGTC CCT       _
                           GC  CGGCGGGGG GTGCGG
                           II  IIIIIIIII IIIII
                           CG  GCCGCCCCC CGCGCC
                          ____  C__    G
GAM154 CRIM1        GGCTTCCTCACTGCCTACT      2202 TGCGGC    GC    A
                          TTCCTCG GTCTACT
                          IIIIIII IIIIIII
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                          AAGGAGT CGGATGA
                          _____    GA    C
GAM154 FZD4        GCCGCGTCCGTTCGGCGTCT    2197 TGCG  T  __      ACTA
                          GC TCC  TCGGCGTCT
                          II III  IIIIIIIII
                          CG AGG  AGCCGCAGA
                          GG__  C  CA     GIII
GAM154 HPS1        TGGGGCTTCCTCCCCATCT    2203 C      GG   ACTA
                          TG GGCTTCCTC CGTCT
                          II IIIIIIIII IIIII
                          AC CCGAAGGAG GTAGA
                          C     GG   IIIC
GAM154 MNT         CGGCTTCCTC-CCG-CTAC    2196 TGCG    GG  T  T
                          GCTTCCTC  CG CTAC
                          IIIIIIII  II IIII
                          CGAAGGAG  GC GATG
                          ____      G_ _  T
GAM154 MYO1D       GCTGCT-CCTCGGCGCCTTCT    2198 TGCG  T     A A
                          GCT CCTCGGCGTCT CT
                          III IIIIIIIIIII II
                          CGA GGAGCCGCGGA GA
                          GA__  _       A G
GAM154 NRXN3       GCGGCTTCCTCCGGATCT-CTA    2199 TG      _  C  A  C
                          CGGCTTCCTC GG GTCT CTA
                          IIIIIIIIII II IIII III
                          GCCGAAGGAG CC TAGA GAT
                          __      G _  _  C
GAM154 TGFB1       GGCTGCTCCTCGGCGACTCCT    2200 TGCG  T    T A AC
                          GCT CCTCGGCG CT CT
                          III IIIIIIII II II
                          CGA GGAGCCGC GA GA
                          A___  _     T G AG
GAM154 TNFSF7      GGCT-CCTGGGCGTCTACT    2201 TGCGGCT  C
                          TCCT GGCGTCTACT
                          IIII IIIIIIIIII
                          AGGA CCGCAGATGA
                          _____    C
GAM155 ADCY7       CAGCATT-TGTGAGGGGGCGG    2209 TGGCAGCATCA GA
                          TG AGGGGGCG
                          II IIIIIIII
                          AC TCCCCCGC
                          GTAA_____  AC
GAM155 C18orf1     TGGGAGCATCAAGTGCAGGAGGGGGCGG2219  C     T_____ A     III
                          TGG AGCATCA   GGA GGGGGCGG
                          III IIIIIII   III IIIIIII
                          ACC TCGTAGT   CCT CCCCCGCC
                          C    TCACGT _    III
GAM155 CAV3        TGGGGGCATCATGGTGGGG    2224 CA    AA   GCG
                          TGG GCATCATGG GGGG
                          III IIIIIIIII IIII
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                          ACC  CGTAGTACC CCCC
                          CC      A_    III
GAM155 CFL1        TGGCAGCATG--GGAAGGGGGAGG 2226      CAT      C
                   TGGCAGCAT  GGAAGGGGG GG
                   |||||||||  ||||||||| ||
                   ACCGTCGTA  CCTTCCCCC CC
                          C__      T
GAM155 DAPP1       TGGCAACATCATGGAAGGG    2223           GGCG
                   TGGCAGCATCATGGAAGGG
                   |||||||||||||||||||
                   ACCGTTGTAGTACCTTCCC
                           IIIG
GAM155 DRIL1       GGCAGTGCAGGGTGGCAGGGGGCGG 2211 TG___   CATCA  A      II
                    GCAG    TGG AGGGGGCGG
                    ||||    ||| |||||||||
                    CGTC    ACC TCCCCCGCC
                   CGTCA   CC___  G      CI
GAM155 FOXF1       AGGAACATGGAAGGGGACGG    2207 TGGCAGCAT
                        CATGGAAGGGGGCG
                        ||||||||||||||
                        GTACCTTCCCCTGC
                   T_____
GAM155 HTR6        AGCCCCCTGGA-GGGGGCGG    2206 TGGCAGCATCA   A
                        TGGA GGGGGCG
                        |||| |||||||
                        ACCT CCCCCGC
                   GGG_____   _
GAM155 IL1F5       TGGCAGGATTAAAGGGAAGGGGGTGG 2221     CATCAT__      C II
                   TGGCAG     GGAAGGGGG GG
                   ||||||     ||||||||| ||
                   ACCGTC     CCTTCCCCC CC
                    CTAATTTC     A II
GAM155 MECP2       GGCAGAA--ATGGAAGGGG     2214 TG  CATC      C
                    GCAG  ATGGAAGGGGG
                    ||||  |||||||||||
                    CGTC  TACCTTCCCCT
                   __   TT__      I
GAM155 MSF         TGGCAGCAT-GTCGAAGGG    2225      CATG    GCG
                   TGGCAGCAT  GAAGGGG
                   |||||||||  |||||||
                   ACCGTCGTA  CTTCCCC
                        CAG_     III
GAM155 NPEPPS      GGCGGCGAGCGAGGGAGGGGGCGG 2212 T_ _ ATCAT  A      I
                    GGC AGC   GG AGGGGGCGG
                    ||| |||   || |||||||||
                    CCG TCG   CC TCCCCCGCC
                   CG  C  CT___  C     G
GAM155 NRXN2       GGCAGGA----GGAAGGGGGCG 2216 TG  CATCAT
                    GCAG    GGAAGGGGGC
                    ||||    ||||||||||
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                              CGTC    CCTTCCCCG
                           __    CT____
GAM155 PLIN              TGGCAGCATCATCAGGATGAGG   2220        __  A   GCGG
                           TGGCAGCATCAT GGA GGGG
                           |||||||||| ||| ||||
                           ACCGTCGTAGTA CCT CTCC
                                GT  A   |||G
GAM155 PLOD3              GGGAGC-TCCGGAAAGGGGGCG   2217 T  C  A  A   _    G
                             GG AGC TC TGGAA GGGGGCG
                             || ||| || ||||| |||||||
                             CC TCG AG GCCTT CCCCCGC
                             _ _ _ _    T    G
GAM155 POLH              TGGAAGGAAAATGGAAGGG     2222  C CATC       GGCG
                           TGG AG  ATGGAAGGG
                           ||| ||   |||||||||
                           ACC TC   TACCTTCCC
                            T  CTTT      |||G
GAM155 RAB2L             GCTGCACTCATGGAAGGTGG    2210 TGGCA _      _ CG
                            GCA TCATGGAAGG GGG
                            ||| |||||||||| |||
                            CGT AGTACCTTCC CCC
                           A____  G     A  T|
GAM155 SERPINH2          CAGCATCATGGTATCTGGGGC   2208 TGGCAG     AAG__   GG
                             CATCATGG   GGGGC
                             ||||||||   |||||
                             GTAGTACC   CCCCG
                           _____         ATAGA   GG
GAM155 SOX4              GGAAGC-TCGTTGGAAGGGGGAGG 2213 TGGC  A A_     C |
                            AGC TC  TGGAAGGGGG GG
                            ||| ||  ||||||||| ||
                            TCG AG  ACCTTCCCCC CC
                           CT__ _ CA      T C
GAM155 WNT3A             GGCAGCTGCAAAGAAGGGGGCG   2215 TG   AT T      G
                            GCAGC CA GGAAGGGGGCG
                            ||||| || |||||||||||
                            CGTCG GT TCTTCCCCCGC
                           __   AC T       G
GAM155 ZNF22             TGGCACCATTCTCATGGAAG     2218    G ___       GGGGCG
                           TGGCA CA  TCATGGAAG
                           ||||| ||  |||||||||
                           ACCGT GT  AGTACCTTC
                            G  AAG     |||GGC
GAM156 CASP8             TGGCACCATCGCAGTCTCCG     2238        GGA ___   TGA
                           TGGCACCAT TGC  CTTCG
                           ||||||||| |||  |||||
                           ACCGTGGTA GCG  GAGGC
                            ___  TCA    |||
GAM156 CASP8             TGGCACCATCGCAGTCTCCG     2238        GGA ___  |
                           GGCACCAT TGC  CTTC
                           |||||||| |||  ||||
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                          CCGTGGTA  GCG  GAGG
                          ___    TCA    I
GAM156 CD83       CCATGCAACACTTCGTGAA     2234    GAT _      II
                      CCATG  GC CTTCGTGA
                      ||||| || ||||||||
                      GGTAC  TG GAAGCACT
                          GT_  T    TI
GAM156 DISC1      GCACCA--GATGCCTTCTGGAA    2235    TG      GTGI
                      GCACCA GATGCCTTC
                      |||||| |||||||||
                      CGTGGT CTACGGAAG
                          __       ACCT
GAM156 DISC1      GCACCA--GATGCCTTCTGGAA    2235 TGGC   TG      G  A
                       ACCA GATGCCTTC TG
                       |||| |||||||||| ||
                       TGGT CTACGGAAG AC
                          ____   __      _ C
GAM156 GCSH       ACCATGGATAATTTCATGAA     2231       CC    I
                      CCATGGATG TTCGTGA
                      ||||||||| |||||||
                      GGTACCTAT AAGTACT
                          TA    I
GAM156 HNRPF      ACCACGGATGCCTTCAGTG     2230         TII
                      ACCATGGATGCCTTCG
                      ||||||||||||||||
                      TGGTGCCTACGGAAGT
                          CAC
GAM156 IFNGR2     CACCATGGATG--TACATGAA    2233 _      CCTT   I
                      ACCATGGATG  CGTGA
                      |||||||||| |||||
                      TGGTACCTAC  GTACT
                      G    AT__   I
GAM156 IFNGR2     CACCATGGATG--TACATGAA    2233 TGGCAC     CCTT
                      CATGGATG  CGTGA
                      |||||||| |||||
                      GTACCTAC  GTACT
                      _____     AT__
GAM156 MTMR3      GGCACAAAACATGGATGCC    2236    ____     IIIG
                      GGCAC  CATGGATGC
                      ||||| |||||||||
                      CCGTG  GTACCTACG
                      TTTT     GIII
GAM156 MTMR3      GGCACAAAACATGGATGCC    2236 TG  ____       TTCGTGA
                      GCAC  CATGGATGCC
                      |||| ||||||||||
                      CGTG  GTACCTACGG
                      __   TTTT      TIIIAAG
GAM156 PAICS      ACCATGGATAGGCTTCGGGA    2229       C_  TGII
                      ACCATGGATG CTTCG
                      |||||||||| |||||
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                         TGGTACCTAT GAAGC
                           CC    CCTI
GAM156 SOX12          GGCACCATGGTGAATG-CTTC    2237        ___   CTTIII
                         GGCACCATGG ATGC
                         |||||||||| ||||
                         CCGTGGTACC TACG
                          ACT    AAGIII
GAM156 SOX12          GGCACCATGGTGAATG-CTTC    2237 TG       ___   C GTGA
                         GCACCATGG ATGC TTC
                         ||||||||| |||| |||
                         CGTGGTACC TACG AAG
                          __       ACT  _ AIII
GAM156 SQSTM1          CAACATTGCGGATGCCCTTCGTGA 2232 ACCA        _    I
                         TGGATGCC TTCGTG
                         |||||||| ||||||
                         GCCTACGG AAGCAC
                         AAC_      G    I
GAM156 WNT6         TGGCGCCCTGG--GCCTTCGTG     2239   A A AT       A
                         TGGC CC TGG GCCTTCGTG
                         |||| || ||| |||||||||
                         ACCG GG ACC CGGAAGCAC
                           C G  __      I
GAM156 WNT6         TGGCGCCCTGG--GCCTTCGTG    2239 _  A A AT      I
                         GGC CC TGG GCCTTCGT
                         ||| || ||| ||||||||
                         CCG GG ACC CGGAAGCA
                         A  C G  __      I
GAM157 CA14         GAGAGAGAGCGAG-CGAGCTC     2257 TGAA       AA
                         AGAGAGCGAG GAGTTCT
                         |||||||||| |||||||
                         TCTCTCGCTC CTCGAGG
                         TC__      G_
GAM157 CCKAR          AAAGAGACCTTGAAGAGTTC      2245 TGAA    GCGA
                         AGAGA   GAAGAGTTCT
                         |||||   |||||||||||
                         TCTCT   CTTCTCAAGG
                         ____       GGAA
GAM157 COL2A1          GAAAGAGAGGGGAGAAAAGT      2250 TG     C_       CT
                         AAAGAGAG GAGAAGAGTT
                         |||||||| ||||||||||
                         TTTCTCTC CTCTTTTCAG
                          __       CC      II
GAM157 EGR3          TGAAAGAGATGGGAGAAG-GTT     2260       GC_   A CTA
                         TGAAAGAGA GAGAAG GTT
                         ||||||||| |||||| |||
                         ACTTTCTCT CTCTTC CAA
                          ACC    _ III
GAM157 ELK4         GAGAGAGAGCGAG-AGAGT       2256 TGAA       A TC
                         AGAGAGCGAGA GAGT
                         |||||||||||| ||||
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                    TCTCTCGCTCT CTCA
                    TC__      _   CI
GAM157 EPHX1        GAAAGAGAGC-TGTGGAGCTCT    2258 TG      GAGAA      A
                    AAAGAGAGC   GAGTTCT
                    ||||||||   |||||||
                    TTTCTCTCG   CTCGAGA
                    __     ACAC_      C
GAM157 EYA3         GAAAGAGAGAGAGATAGAG       2254 TG    C  _   TTCT
                    AAAGAGAG GAGA AGAG
                    |||||||| |||| ||||
                    TTTCTCTC CTCT TCTC
                    __      T  A  TIII
GAM157 EYA3         GAAAGAGAGAAAGAGAGAG       2252 TG    C  _   TTCT
                    AAAGAGAG GAGA AGAG
                    |||||||| |||| ||||
                    TTTCTCTC TTCT TCTC
                    __      T  C  TIII
GAM157 FVT1         GAAAGAGAGAGAGAGAG         2253 TG    C  _   TTCT
                    AAAGAGAG GAGA AGAG
                    |||||||| |||| ||||
                    TTTCTCTC CTCT TCTC
                    __      T  C  TIII
GAM157 GM2A         TGAAAGAGAGAGAGTCATAAAGA-TTCT2262      C  A___  _  AIII
                    TGAAAGAGAG GAG   AGAG TTCT
                    |||||||||| |||   |||| ||||
                    ACTTTCTCTC CTC   TTTC AAGA
                    T  AGTA   T  IIIA
GAM157 GRM7         TGAAAGAGAATGGAAAGAG       2263       CGA    TTCT
                    TGAAAGAGAG  GAAGAG
                    ||||||||||  ||||||
                    ACTTTCTCTT  TTTCTC
                    ACC    IIIA
GAM157 KLF8         AAACATATGGATAAGAGTTCTA    2247 TGAAAGAGAGC G
                    GA AAGAGTTCTA
                    || |||||||||
                    CT TTCTCAAGAT
                    TGTATAC____  A
GAM157 MFRP         GAGAGATGAGGGTGGAGAGTTCTA  2248 TGAA    GC A____      I
                    AGAGA GAG   AGAGTTCTA
                    ||||| |||   |||||||||
                    TCTCT CTC   TCTCAAGAT
                    ____   A_ CCACC     C
GAM157 MYO1E        GAAAGAGTT-GAGAAGAGT       2255 TG   AGC      C
                    AAAGAG  GAGAAGAGTT
                    ||||||  ||||||||||
                    TTTCTC  CTCTTCTCAG
                    __    AA_      I
GAM157 NCOA6        AAAGTGATGGCGTGAGAAGAGTTCTA 2242 TGAAA  GA __         II
                    GA GC GAGAAGAGTTCTA
                    || || |||||||||||||
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                            CT  CG  CTCTTCTCAAGAT
                        TCA__  AC  CA          AG
GAM157 OLR1             AAACAGAGTTGAGAAGAGTTC    2243 TGAAAG   C_        TA
                           AGAG  GAGAAGAGTTC
                           ||||  |||||||||||
                           TCTC  CTCTTCTCAAG

                        TG____     AA        TA
GAM157 RAD52            GAAAGAGAGCAAGTTGAAGAG    2251 TG       ___     TTCTA
                        AAAGAGAGCGA  GAAGAG
                        ||||||||||  ||||||
                        TTTCTCTCGTT  CTTCTC

                          __        CAA    CIIIA
GAM157 RBL1            AAAGAGAGCTA-AAAAGTT      2244 TGAA    GA      C
                          AGAGAGC  GAAGAGTT
                          ||||||||  |||||||||
                          TCTCTCG  TTTTTCAA

                          ____      A_     T
GAM157 SLC13A3         TGAAAGAGAGAGA-AAGTATCCTA 2265      C  A A   I
                          TGAAAGAGAG GAGA G GTTCTA
                          |||||||||| |||| | ||||||
                          ACTTTCTCTC CTTT C TAGGAT

                              T  _A    I
GAM157 SLC29A2         GAAGGAGACGTCGAGAAGAG     2249 TGAAA   G__       TTCT
                            GAGA  CGAGAAGAG
                            ||||  |||||||||
                            CTCT  GCTCTTCTC

                        TTC__  GCA      CIII
GAM157 SLC38A3         TGAAGGGAGATGGGAGAAGAGT   2259   A_  GC_       TCTA
                          TGAA GAGA  GAGAAGAGT
                          |||| ||||  |||||||||
                          ACTT CTCT  CTCTTCTCA

                          CC  ACC      IIIA
GAM157 TNFSF15         TGAAAGAGAGAGACAGGAG      2264      C GAA  TTCT
                          TGAAAGAGAG GA  GAG
                          |||||||||| ||  |||
                          ACTTTCTCTC CT  CTC

                            T GTC  IIIA
GAM157 TNFSF5          TGAAAGAGAGAGATGGAGAG     2261      C GA_  TTCT
                          TGAAAGAGAG GA  AGAG
                          |||||||||| ||  ||||
                          ACTTTCTCTC CT  TCTC

                            T ACC  IIIA
GAM157 TR2            AAAGA-AG--AAAAGAGTTCT     2246 TGAAAG   C
                          AGAG GAGAAGAGTTC
                          |||| |||||||||||
                          TCTT CTTTTCTCAAG

                        _____  _
GAM158 CDKN2C            TGCCACCTCTCGCGGTCCCCGG  2275        _ __       III
                          TGCCACCTCTC CG CCCCGG
                          ||||||||||| || ||||||
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                              ACGGTGGAGAG GC GGGGCC
                                   C  CA     III
GAM158 CDKN2C              TGCCACCTCTCGCGGTCCCCGG   2275       _ __      III
                              TGCCACCTCTC CG CCCCG
                              ||||||||||| || |||||
                              ACGGTGGAGAG GC GGGGC
                                   C  CA    CII
GAM158 CPT2               GCCATCGGCTCCGCCCCGG   2270    CCT_       II
                             GCCA   CTCCGCCCCG
                             ||||   ||||||||||
                             CGGT   GAGGCGGGGC
                               AGCC         CI
GAM158 CPT2               GCCATCGGCTCCGCCCCGG    2270 TG  CCT_        I
                             CCA   CTCCGCCCCGG
                             |||   |||||||||||
                             GGT   GAGGCGGGGCC
                              __  AGCC          T
GAM158 FMOD            TGCCACGGGGGCTCTCCGCCC   2272    _____      CGGII
                         TGCCAC   CTCTCCGCCC
                         ||||||   ||||||||||
                         ACGGTG   GAGAGGCGGG
                            CCCCC        IIIGG
GAM158 FMOD            TGCCACGGGGGCTCTCCGCCC   2272    _____      IIIG
                         TGCCAC   CTCTCCGCC
                         ||||||   |||||||||
                         ACGGTG   GAGAGGCGG
                            CCCCC       GIII
GAM158 GATA6            GCCCGCTCTCCGCCCCGG     2268  AC_       II
                          GCC  CTCTCCGCCCCG
                          |||  |||||||||||||
                          CGG  GAGAGGCGGGGC
                            GGC        CI
GAM158 GATA6            GCCCGCTCTCCGCCCCGG      2268 TG  AC       I
                          CC  CTCTCCGCCCCGG
                          ||  |||||||||||||
                          GG  GAGAGGCGGGGCC
                           G_  GC        C
GAM158 KCNF1           TGGCACCGTCCTCCGCCCCGG   2273  C  __      II
                         TG CACC TCTCCGCCCCGG
                         || |||| |||||||||||||
                         AC GTGG GGAGGCGGGGCC
                           C  CA        II
GAM158 KCNF1           TGGCACCGTCCTCCGCCCCGG   2273  C  __      III
                         TG CACC TCTCCGCCCCG
                         || |||| |||||||||||
                         AC GTGG GGAGGCGGGGC
                           C  CA     CII
GAM158 MIC2          TGCGCCCGCCCCGCCCCGG    2276  CA T        I
                       TGC CC CTCCGCCCCGG
                       ||| || |||||||||||
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                        ACG  GG GGGGCGGGGCC
                         CG  C          I
GAM158 MIC2            TGCGCCCGCCCCGCCCCGG    2276  CA T       II
                        TGC  CC CTCCGCCCCG
                        III II IIIIIIIIII
                        ACG  GG GGGGCGGGGC
                         CG  C        CI
GAM158 MLF2           TGCCACCTCCGTACGCCCC     2274       C__      GGI
                       TGCCACCTCT CGCCCC
                       IIIIIIIIII IIIIII
                       ACGGTGGAGG GCGGGG
                          CAT     III
GAM158 MLF2           TGCCACCTCCGTACGCCCC     2274       C__     III
                        TGCCACCTCT CGCCC
                        IIIIIIIIII IIIII
                        ACGGTGGAGG GCGGG
                          CAT   GII
GAM158 MTCP1          GCCACCGCCCTCCGCCCCG     2271       __      III
                       GCCACC TCTCCGCCCC
                       IIIIII IIIIIIIIII
                       CGGTGG GGAGGCGGGG
                          CG       CII
GAM158 MTCP1          GCCACCGCCCTCCGCCCCG     2271 T_ A T      I
                        GCC CC CTCCGCCCCGG
                        III II IIIIIIIIIII
                        TGG GG GAGGCGGGGCT
                        GG  C _      I
GAM158 PRDM2         GCCCCCTTCCTGCCGCCCCGG    2269 A _ __       III
                      GCC CCT CT CCGCCCCG
                      III III II IIIIIIII
                      CGG GGA GG GGCGGGGC
                       G  A AC     CII
GAM158 PRDM2         GCCCCCTTCCTGCCGCCCCGG    2269 TG A _ __      II
                       CC CCT CT CCGCCCCGG
                       II III II IIIIIIIII
                       GG GGA GG GGCGGGGCC
                       G_ _ A AC     CI
GAM159 CCKBR         GCCTCGGTCCTTAACTGGA      2287 TAACGCCT   AGC _
                       CGGTC  AAC GGAG
                       IIIII  III IIII
                       GCCAG  TTG CCTT
                       _____   GAA  A
GAM159 CLU         ACGCCTCGGTCAGCGGCGGA      2282 TAAC        AA
                     GCCTCGGTCAGC CGGAG
                     IIIIIIIIIIII IIIII
                     CGGAGCCAGTCG GCCTT
                     ____           CC
GAM159 DPYSL3       AACGGC---GACAGCAACGG      2280 TAACGCCT   __
                      CGGT CAGCAACGG
                      IIII IIIIIIIII
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                        GCCG  GTCGTTGCC
                  T_____      CT
GAM159 GLS          CGCC---GACAGCAACGGA      2286 TAACGCCT  T
                      CGG CAGCAACGG
                      ||| |||||||||
                      GCT GTCGTTGCC
                   _____ _
GAM159 HAS3          CGCCTCGGTGCAGTGCCGGAG    2285 TAACGC    _ CAA   C
                      CTCGGT CAG  CGGAG
                      |||||| |||  |||||
                      GAGCCA GTC  GCCTC
                   _____      C  ACG   C
GAM159 NXF1          CCTCGGTCACAGTCACGGGGC    2283 TAACGCCT   AGCA   A
                      CGGTC   ACGG GC
                      |||||   |||| ||
                      GTCAG   TGCC CG
                    CAGT____   ____   C
GAM159 SLC4A10        TAACGCCTCTGGAATAAGCA    2288       _ TC__   ACGGAG
                      TAACGCCTC GG   AGCA
                      ||||||||| ||   ||||
                      ATTGCGGAG CC   TCGT
                      A TTAT   |||CGA
GAM159 SNRPN          AACGCCTCGGGTA-CAACTGA   2281 TA       TCA   G G
                      ACGCCTCGG  GCAAC GA
                      |||||||||  ||||| ||
                      TGCGGAGCC  TGTTG CT
                     __       CA_   A G
GAM159 SNX6          AACGCACTCAGCCAGCAACGGA   2279 TA   _          C
                      ACGC CTCGGTCAGCAACGGAG
                      |||| |||||||||||||||
                      TGCG GAGTCGGTCGTTGCCTT
                     __  T             |
GAM159 STK6         CGCCTCGGTGCCCAGGAGCGGA    2284 TAACGC    CA AAC
                      CTCGGT GC  GGAGC
                      |||||| ||  |||||
                      GAGCCA CG  CCTCG
                   _____      __  GGT
GAM159 TSSC3         TAAGGCGCCCGT--GCAACGGAGC  2289 TAA__   T GTCA
                      CGCC CG   GCAACGGAGC
                      |||| ||   |||||||||||
                      GCGG GC   CGTTGCCTCG
                    ATTCC   _ A___
GAM160 AANAT         CCCGGG--CAGCC-TGTGGTGCT   2293 TC  AGAA   C
                      CCG   CAGCC TGTGGTGC
                      |||   ||||| ||||||||
                      GGC   GTCGG ACACCACG
                    __  CC__   _
GAM160 GPR30         TCCCCAGGAGGAGCACCTGTGGTG  2294   G AAC_ _      CTI
                      TCCC AG   AGC CCTGTGGTG
                      |||| ||   ||| |||||||||
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                          AGGG TC   TCG GGACACCAC
                           G CTCC  T       III
GAM160 MATN1              CCCG-GCCCAGCCCTGTCCTGC   2292 TC  AGAA      GG  T
                           CCG   CAGCCCTGT TGC
                           III   IIIIIIIIII III
                           GGC   GTCGGGACA ACG
                           __   CGG_       GG  T
GAM161 ATSV              GACACCC--C-CCCACTCTCC   2306 TG    TCT
                          ACACCCT  CCCACTCTCC
                          IIIIIII  IIIIIIIIII
                          TGTGGGG  GGGTGAGAGG

                           __       __
GAM161 CELSR3           CCCTGCACAGCCACTCTCC      2303 TGACACCCTTCTC
                                 CCACTCTCCT
                                 IIIIIIIIII
                                 GGTGAGAGGG
                          GTGTC_____
GAM161 ECM2            ACACCCTTCTGCCAGCTTTCCT   2300 TGAC     C _ C   A
                          ACCCTTCT CCA CT TCCT
                          IIIIIIII III II IIII
                          TGGGAAGA GGT GA AGGA
                           ____      C  C A  A
GAM161 GADD45B          ACTCCCTTCTCCTCTCTCTC     2299 TGACA     CA   _
                          CCCTTCTCC CTCTC CT
                          IIIIIIIIII IIIII II
                          GGGAAGAGG GAGAG GA
                          A____      A_  A
GAM161 HNRPD            CCCTTCGCCTCCCACTCTC      2302 TGACACCCT       CT
                            TCTCCCACTCTC
                            IIIIIIIIIIII
                            GGAGGGTGAGAG
                          GC_____      CG
GAM161 HOXC4          TGCCTCTCTCTCTCCCACTCTC    2308 TGACA _ ___      CTA
                          CC CT  TCTCCCACTCTC
                          II II  IIIIIIIIIIII
                          GG GA  AGAGGGTGAGAG
                          AC___ A GAG      III
GAM161 IGFBP5         ACACCTCTTTTCTCCCACT      2297 TGAC _ __     CTCCT
                          ACC CT TCTCCCACT
                          III II IIIIIIIII
                          TGG GA AGAGGGTGA
                           ____  A AA     AAIII
GAM161 IL4R           CCCTTCTGTTCCACTCTCCT      2304 TGACACCCTTCTC
                            CCACTCTCCT
                            IIIIIIIIII
                            GGTGAGAGGA
                          GACAA_____
GAM161 PAX4           ACACCACCTCTCCCACTGCCCT    2298 TGAC _       C  A
                          ACC CTTCTCCCACT TCCT
                          III IIIIIIIIII IIII
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                              TGG GGAGAGGGTGA GGGA
                              ___    T      C   C
GAM161  PIP5K1A        CCCTTCTCCGTCCTTCCTA    2305 TGACAC    C__    TCTCCT
                              CCTTCT  CCAC
                              ||||||  ||||
                              GGAAGG  GGTG
                              GAGGCA     ATT  IIIATC
GAM161  RNF4          TGACTCCCTTTCTCCCACTCT    2309  A   _       CCTA
                              TGAC CCCTT CTCCCACTCT
                              |||| ||||| ||||||||||
                              ACTG GGGAA GAGGGTGAGA
                               A    A      IIIA
GAM161  SLC6A8         TGCCTCCCTTCTCCTCTCTCCT 2310  ACA       CA_      AI
                              TG  CCCTTCTCC  CTCTCCT
                              ||  |||||||||  |||||||
                              AC  GGGAAGAGG  GAGAGGA
                               GGA      AGA     II
GAM161  STK38            CACCCATTGTGC-ACTCTCCTA   2301 TGACAC TTCTCC
                              CC   CACTCTCCTA
                              ||   ||||||||||
                              GG   GTGAGAGGAT
                              _____  TAACAC
GAM161  TFF3          TGACACCC-TCCCGCCCTCTCC    2311      C A   TA
                              TGACACCCTTCT CC CTCTCC
                              |||||||||||| || ||||||
                              ACTGTGGGAGGG GG GAGAGG
                                    C  _   II
GAM161  UBTF           GACCCCCCACCCCCACTCTCC    2307 TG A  T      TA
                              AC CCCT CTCCCACTCTCC
                              || |||| |||||||||||||
                              TG GGGG GGGGGTGAGAGG
                              __  G   T     CI
GAM162  ABR          GAGTGTGTCTGCTTGT-CCAACAT 2322  C        A G     I
                              GA TGTGTCTGCT GT CCGGCAT
                              || |||||||||| || |||||||
                              CT ACACAGACGA CA GGTTGTA
                               C      A  _   I
GAM162  ABR          GAGTGTGTCTGCTTGT-CCAACAT 2322 AC_      A G    I
                              TGTGTCTGCT GT CCGGCA
                              |||||||||| || ||||||
                              ACACAGACGA CA GGTTGT
                              CTC      A _   I
GAM162  ADRA2A         CTGTGTCTGCCTG-GAAGGCAT    2320 _       AGTGCC   I
                              TGTGTCTGCT    GGCA
                              ||||||||||    ||||
                              ACACAGACGG    CCGT
                              G   ACCTT_  I
GAM162  ADRA2A         CTGTGTCTGCCTG-GAAGGCAT    2320 GACT      AGTGCC
                              GTGTCTGCT    GGCAT
                              |||||||||    |||||
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                     CACAGACGG    CCGTA
            ____           ACCTT_
GAM162 CYP17        GTGGCTGG--GTGCCGGCA      2324   T  CTA      I
                     GTG CTG  GTGCCGGC
                     ||| |||  ||||||||
                     CAC GAC  CACGGCCG
                      C  C__       T
GAM162 DGAT1        GACTGTGTCTGGCCTGCTGTCGCCAT 2321        _  A  GC_  G  II
                     GACTGTGTCTG CT GT  CG CAT
                     |||||||||| || ||  || |||
                     CTGACACAGAC GG CG  GC GTA
                            C  A  ACA  G   II
GAM162 DGAT1        GACTGTGTCTGGCCTGCTGTCGCCAT 2321 GA_  T     AG    GI
                       CTG GTCTGCT  TGCCG
                       ||| ||||||||  |||||
                       GAC CGGACGA  GCGGT
                       ACA  _    CA   AI
GAM162 F2R         CTGTGTCTGACATGGCCCTGGCAT  2316 GACT     C  GT  __   I
                      GTGTCTG TA GCC  GGCAT
                      |||||||| || ||| |||||
                      CACAGAC GT CGG  CCGTA
                      ____       T  AC  GA    C
GAM162 F2R         CTGTGTCTGACATGGCCCTGGCAT  2316 TG     C  GT  __   I
                       TGTCTG TA GCC  GGCA
                       |||||| || ||| ||||
                       ACAGAC GT CGG  CCGT
                       __     T  AC  GA    I
GAM162 FCER2       CTGTGTCTGTCCTCCTAGTG     2314          _____     IIIC
                     CTGTGTCTG   CTAGT
                     |||||||||   |||||
                     GACACAGAC   GATCA
                        AGGAG    CIII
GAM162 FCER2       CTGTGTCTGTCCTCCTAGTG      2314 GA__  G  G    CCGGCA
                     CTGT TCT CTAGTG
                     |||| ||| ||||||
                     GACA GGA GATCAC
                     CACA   _  G   ACIIIT
GAM162 HDAC4       TGTGTCTGCGCGTCGCCGGC     2327        TA _    II
                     TGTGTCTGC GT GCCGG
                     ||||||||| || |||||
                     ACACAGACG CA CGGCC
                        CG  G   GI
GAM162 HDAC4       TGTGTCTGCGCGTCGCCGGC     2327 GACTGT    TA _    A
                      GTCTGC GT GCCGGC
                      |||||| || ||||||
                      CAGACG CA CGGCCG
                       _____    CG  G    C
GAM162 HDAC7A      TGTGTCTGCACAGGGCCTGGGGCA 2326 GTGT   _  T  ___   I
                       CTGC TAG GCC  GGC
                       |||| ||| |||  |||
```

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                         GACG GTC CGG  CCG
                         ____    T  C  ACC   I
GAM162 IL10RA          CTGTGTCTGATACTGTCTTGGCAT  2317 GACT     C  G  CC__    I
                         GTGTCTG TA TG   GGCAT
                         ||||||| || ||    |||||
                         CACAGAC AT AC   CCGTA
                         ____      T  G  AGAA    C
GAM162 IL10RA          CTGTGTCTGATACTGTCTTGGCAT  2317 TG      C  G  CC__    I
                         TGTCTG TA TG   GGCA
                         |||||| || ||    ||||
                         ACAGAC AT AC   CCGT
                         __      T  G  AGAA    I
GAM162 MAPK8IP1         CTGTGTCTGGCAGGGCGCGGCA   2315 GACT     C  T  _
                         GTGTCTG TAG GC CGGCAT
                         ||||||| ||| || ||||||
                         CACAGAC GTC CG GCCGTG
                         ____       C  C
GAM162 MAPK8IP1         CTGTGTCTGGCAGGGCGCGGCA   2315 T      C  T  _   I
                         GTGTCTG TAG GC CGGC
                         ||||||| ||| || ||||
                         CACAGAC GTC CG GCCG
                         _      C  C  C   I
GAM162 OGT             TGTGTCTGCCCTAGATCCAGGC   2325          AGTG__   III
                         TGTGTCTGCT    CCGG
                         |||||||||     ||||
                         ACACAGACGG    GGTC
                         GATCTA    CGI
GAM162 OGT             TGTGTCTGCCCTAGATCCAGGC   2325 GACTGT      AGTG__ _ AT
                         GTCTGCT    CC GGC
                         ||||||     || |||
                         CAGACGG    GG CCG
                         _____          GATCTA T  GA
GAM162 SHANK2           CTGAGTTTGCTGGTGCAGG     2318   T  C  A  CGII
                         CTG GT TGCT GTGC
                         ||| || |||| ||||
                         GAC CA ACGA CACG
                         T  A  C  TCCI
GAM162 SHANK2           CTGAGTTTGCTGGTGCAGG     2318 GACTGT C  A  C CA
                         GT TGCT GTGC GG
                         || |||| |||| ||
                         CA ACGA CACG CC
                         CT____  A  C  T CC
GAM162 UCP2            CTGTGTCTG-TCG-GCTGGC     2319       CTA __ CGI
                         CTGTGTCTG  GT GC
                         |||||||||  || ||
                         GACACAGAC  CG CG
                         AGC AC III
GAM162 UCP2            CTGTGTCTG-TCG-GCTGGC     2319 GACT     CTAGT  C
                         GTGTCTG   GC GGC
                         |||||||    || |||
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                            CACAGAC    CG CCG
                            ____       AGC__  A
GAM162 ZAP70        GTGTCTGCTGAGCTCCGGCA     2323       _  G    II
                        GTGTCTGCT AGT CCGGC
                        IIIIIIIII III IIIII
                        CACAGACGA TCG GGCCG
                              C  A   TI
GAM162 ZAP70        GTGTCTGCTGAGCTCCGGCA     2323 GACTGTGT   _  G
                            CTGCT AGT CCGGCA
                            IIIII III IIIIII
                            GACGA TCG GGCCGT
                        _____          C  A
GAM163 ADAR         GCAGCCATCACCACGGCAC       2340       T  _  II
                        GCAGCCATC CCGCG CA
                        IIIIIIIII IIIII II
                        CGTCGGTAG GGTGC GT
                            T   C GI
GAM163 ADAR         GCAGCCATCACCACGGCAC       2340 TCGC    T  _  AGT
                            AGCCATC CCGCG CAC
                            IIIIIII IIIII III
                            TCGGTAG GGTGC GTG
                          ____       T   C  GTI
GAM163 ARHGDIA      CGGAGCCATCTCCACAGCCCTGT   2335 C          _  ACAGI
                            AGCCATCTCCGC GC
                            IIIIIIIIIIII II
                            TCGGTAGAGGTG CG
                        C       T  GGAII
GAM163 ARHGDIA      CGGAGCCATCTCCACAGCCCTGT   2335 TCGC         _  ACA  GI
                            AGCCATCTCCGC GC  GT
                            IIIIIIIIIIII II  II
                            TCGGTAGAGGTG CG  CA
                        CC__         T GGA GI
GAM163 BAZ1B        CGCAGAGTTC-CCGCGCACA      2336 _  CCA  T      I
                            GCAG  TC CCGCGCAC
                            IIII  II IIIIIIII
                            CGTC  AG GGCGCGTG
                          G   TCA  _      I
GAM163 BAZ1B        CGCAGAGTTC-CCGCGCACA      2336 TC   CCA  T      GT
                            GCAG  TC CCGCGCACA
                            IIII  II IIIIIIIII
                            CGTC  AG GGCGCGTGT
                          __  TCA  _      GI
GAM163 BCL7A        CGCCGCTCACTCACTCGCGCACAG  2333 _  A_  _ T  C      TGI
                            TCGC  GC CA CTC GCGCACAG
                            IIII  II II III IIIIIIII
                            GGCG  TG GT GAG CGCGTGTC
                          C  AG A _  _      TII
GAM163 BCL7A        CGCCGCTCACTCACTCGCGCACAG  2333 GCA  _  T  ___      I
                            GC CA CTC  CGCGCACA
                            II II III  IIIIIIII
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                            CG GT GAG   GCGCGTGT
                            ___  A  _  TGA      I
GAM163 CDX1          GCAGCCA--TCAGAGCCCAGTG   2341       TCC G CAGI
                         GCAGCCATC  GC CA
                         |||||||| || ||
                         CGTCGGTAG  CG GT
                           TCT G CACI
GAM163 CDX1          GCAGCCA--TCAGAGCCCAGTG   2341 TCGC     TCCGC A
                          AGCCATC   GC CAGT
                          ||||||| || ||||
                          TCGGTAG   CG GTCA
                          ____        TCT__ G
GAM163 DIO3          CCCTCTCCGCGCGCGACAG       2332 _ A     ACAIII
                         CC TCTCCGCGC
                         || |||||||||
                         GG AGAGGCGCG
                         G _       CGCTGT
GAM163 FKBP1B        GCAGCCATCTCCAGC-CAC       2339         C AII
                        GCAGCCATCTCCG GC
                        ||||||||||| ||
                        CGTCGGTAGAGGT CG
                          _ GTG
GAM163 FKBP1B        GCAGCCATCTCCAGC-CAC       2339 TCGC       _ G  AG
                          AGCCATCTCC GC CAC
                          |||||||||| || |||
                          TCGGTAGAGG CG GTG
                          ____          T _ GA
GAM163 KCNK3        TCGCCGC--TCTCCGCGCA      2343   A CA      CAG
                        TCGC GC  TCTCCGCGCA
                        |||| ||  |||||||||
                        AGCG CG  AGAGGCGCGT
                          G __        III
GAM163 KCNK3        TCGCCGC--TCTCCGCGCA      2343   A CA      I
                        TCGC GC  TCTCCGCGC
                        |||| ||  ||||||||
                        AGCG CG  AGAGGCGCG
                          G __      T
GAM163 MN1         TCGCCGGAGTCTCCGCGCACCGT   2344   AGCCA       A GI
                        TCGC   TCTCCGCGCAC GT
                        ||||   ||||||||||| ||
                        AGCG   AGAGGCGCGTG CA
                        GCCTC        G II
GAM163 MN1         TCGCCGGAGTCTCCGCGCACCGT   2344 CA A___       AGI
                          GCC  TCTCCGCGCAC
                          |||  ||||||||||
                          CGG  AGAGGCGCGTG
                          G_ CCTC        III
GAM163 POLR2E       TCGCACCCCTTCTCCGCGC       2342   G A_     ACAGT
                        TCGCA CC  TCTCCGCGC
                        ||||| ||  |||||||||
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                              AGCGT GG  AGAGGCGCG
                                G  GA       IIIGT
GAM163 POLR2E         TCGCACCCCTTCTCCGCGC      2342    G  A_       II
                     TCGCA CC  TCTCCGCG
                     IIIII II  IIIIIIIII
                     AGCGT GG  AGAGGCGC
                       G  GA       GI
GAM163 PRKAR2A        GCGGCCACTGTCTCCGCGCTCA    2338  A    ___       ACIII
                     GC GCCA  TCTCCGCGC
                     II IIII  IIIIIIIII
                     CG CGGT  AGAGGCGCG
                       C  GAC       AGTII
GAM163 PRKAR2A        GCGGCCACTGTCTCCGCGCTCA    2338 TCGCA   ___      A GTG
                       GCCA  TCTCCGCGC CA
                       IIII  IIIIIIIII II
                       CGGT  AGAGGCGCG GT
                       C____   GAC       A GAI
GAM163 PTPN11         AGCCAGCCGGCCGCGCACAG      2330    T __       III
                     AGCCA CT  CCGCGCACA
                     IIIII II  IIIIIIIII
                     TCGGT GG  GGCGCGTGT
                       C CC       CII
GAM163 PTPN11         AGCCAGCCGGCCGCGCACAG      2330 TCGC   ATCT      T
                       AGCC   CCGCGCACAG
                       IIII   IIIIIIIIII
                       TCGG   GGCGCGTGTC
                       ____    CC__       T
GAM163 PTPN7          AGCCATCTCTGAGCTAACCAGTG   2331 GCC    C__  GCA_   I
                     ATCTC  GC  CAGT
                     IIIII  II  IIII
                     TAGAG  CG  GTCA
                     ___   ACT  ATTG  I
GAM163 RGL           CGCAGCC-TCTAGCAGCGCACAGT   2334 G    A  CC__     I
                       CAGCC TCT   GCGCACAG
                       IIIII III   IIIIIIIII
                       GTCGG AGA   CGCGTGTC
                       _    _ TCGT       I
GAM163 RGL           CGCAGCC-TCTAGCAGCGCACAGT   2334 TC    A  CC__     GI
                       GCAGCC TCT   GCGCACAGT
                       IIIIII III   IIIIIIIIII
                       CGTCGG AGA   CGCGTGTCA
                       __    _ TCGT      GI
GAM163 TCEA1          GCAGGTCTTCTCCGCGCCCA      2337   CCA_       ACII
                       GCAG  TCTCCGCGC
                       IIII  IIIIIIIII
                       CGTC  AGAGGCGCG
                       CAGA       GGTI
GAM163 TCEA1          GCAGGTCTTCTCCGCGCCCA      2337 TCGCAGCCA       A GT
                       TCTCCGCGC CA
                       IIIIIIIII II
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                          AGAGGCGCG GT
                        TCCAGA___      G GG
GAM164 ADRBK1           TGGCACAAGTG---CAGCCCACA  2361    CT  TTC
                        TGGCAC GTG  CAGCCCACA
                        ||||| |||  |||||||||
                        ACCGTG CAC  GTCGGGTGT
                              TT  ___
GAM164 ADRBK1           TGGCACAAGTG---CAGCCCACA  2361 _  CT  TTC
                         GGCAC GTG  CAGCCCAC
                         ||||| |||  ||||||||
                         CCGTG CAC  GTCGGGTG
                          A    TT  ___
GAM164 BRCA1            CACTCTGTGCTTCCAGCCC      2347  _   _    |||
                        CAC CTGTGTT CCAGCC
                        ||| ||||||| ||||||
                        GTG GACACGA GGTCGG
                          A      A    G||
GAM164 BRCA1            CACTCTGTGCTTCCAGCCC      2347 TGGCAC    _    ACA
                            CTGTGTT CCAGCCC
                            ||||||| |||||||
                            GACACGA GGTCGGG
                          A_____      A    ATT
GAM164 CA6              GCAGC-GTGTTCCAGACACACAT  2354 CACCT      _ C   |
                            GTGTTCCAG C CACA
                            ||||||||| | ||||
                            CACAAGGTC G GTGT
                          GTCG_        T T   |
GAM164 CA6              GCAGC-GTGTTCCAGACACACAT  2354 TGGCACCT       _ C
                            GTGTTCCAG C CACAT
                            ||||||||| | |||||
                            CACAAGGTC G GTGTA
                          TCG_____       T T
GAM164 CDH10           TGGAAGTTG-GTTCCAGCCAAAAT  2362   CACC  T     CACAT|
                        TGG   TG GTTCCAGCC
                        |||   || |||||||||
                        ACC   AC CAAGGTCGG
                          TTCA _       TTTTA|
GAM164 CDH10           TGGAAGTTG-GTTCCAGCCAAAAT  2362 _ CACC  T     CACA|
                         GG   TG GTTCCAGCC
                         ||   || |||||||||
                         CC   AC CAAGGTCGG
                          A TTCA _       TTTT|
GAM164 EPAC           CACCTG-G--CCAGCCCAC        2350     T TT
                       CACCTG G  CCAGCCCA
                       |||||| |  ||||||||
                       GTGGAC C  GGTCGGGT
                              _ __
GAM164 ERH           CACCTGTGTTCCAAGCCCAC        2349            _  ||
                      CACCTGTGTTCCA GCCCA
                      ||||||||||||| |||||
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                    GTGGACACAAGGT CGGGT
                         T   GI
GAM164 ERH          CACCTGTGTTCCAAGCCCAC    2349 TGGCAC       _     A
                    CTGTGTTCCA GCCCAC
                    |||||||||| ||||||
                    GACACAAGGT CGGGTG
                    _____        T    G
GAM164 GNG5         CCTCTGTTCCAGCTCCACA     2352  G      _    II
                    CCT TGTTCCAGC CCAC
                    ||| |||||||| ||||
                    GGA ACAAGGTCG GGTG
                     G    A  TI
GAM164 GYPC         TGGCACCTGCTGTTCC-CCCCAAAT 2359      _    AG   CATI
                    TGGCACCTG TGTTCC CCCA
                    ||||||||| |||||| ||||
                    ACCGTGGAC ACAAGG GGGT
                       G    G_  TTAI
GAM164 GYPC         TGGCACCTGCTGTTCC-CCCCAAAT 2359      _    AG   CAI
                    GGCACCTG TGTTCC CCCA
                    |||||||| |||||| ||||
                    CCGTGGAC ACAAGG GGGT
                       G    G_  TTI
GAM164 LDLR         GGCACCTGTGT--CTGGCCAAAT   2357      CCA  CACI
                    GGCACCTGTGTT GCC
                    |||||||||||| |||
                    CCGTGGACACAG CGG
                        AC_  TTTA
GAM164 LDLR         GGCACCTGTGT--CTGGCCAAAT   2357 TG      CCA  CACAT
                    GCACCTGTGTT GCC
                    ||||||||||| |||
                    CGTGGACACAG CGG
                    __        AC_  TTTAA
GAM164 MYO1C        GGCACCAGAGC-CCAGCCCACA    2356 _  TGT T      I
                    GCACC  GT CCAGCCCAC
                    |||||  || |||||||||
                    CGTGG  CG GGTCGGGTG
                     C   TCT _      I
GAM164 MYO1C        GGCACCAGAGC-CCAGCCCACA    2356 TG   TGT T
                    GCACC  GT CCAGCCCACAT
                    |||||  || |||||||||||
                    CGTGG  CG GGTCGGGTGTG
                    __     TCT _
GAM164 NEO1         GGCGCCGCTGCTCCAGCCCA      2355  A TG      I
                    GC CC TGTTCCAGCCC
                    || || |||||||||||
                    CG GG ACGAGGTCGGG
                     C  CG        I
GAM164 NEO1         GGCGCCGCTGCTCCAGCCCA      2355 TG A TG       CA
                    GC CC TGTTCCAGCCCA
                    || || |||||||||||
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                        CG GG  ACGAGGTCGGGT
                        __  C  CG        CI
GAM164 PTPN12           TGGCACCTGAATTTTCCAG   2358      TG__     CCCACA
                        TGGCACCTG  TTCCAG
                        |||||||||  ||||||
                        ACCGTGGAC  AAGGTC
                             TTAA    IIITAC
GAM164 PTPN12           TGGCACCTGAATTTTCCAG   2358      TG__     III
                        TGGCACCTG  TTCCA
                        |||||||||  |||||
                        ACCGTGGAC  AAGGT
                             TTAA    CII
GAM164 SMTN            TGGCACCTGT-CACCAGCTCA   2360       GTT    C CA
                       TGGCACCTGT  CCAGC CA
                       ||||||||||  ||||| ||
                       ACCGTGGACA  GGTCG GT
                              GT_    A II
GAM164 SMTN            TGGCACCTGT-CACCAGCTCA   2360 _     GTT    CCI
                        GGCACCTGT  CCAGC
                        |||||||||  |||||
                        CCGTGGACA  GGTCG
                         A       GT_   AGI
GAM164 STUB1           CACCTGCTTTTCCAGCCCACA   2348 A   G_        I
                        CCTGT  TTCCAGCCCAC
                        |||||  ||||||||||||
                        GGACG  AAGGTCGGGTG
                         _    AA          I
GAM164 STUB1           CACCTGCTTTTCCAGCCCACA   2348 TGGCAC  G_        T
                         CTGT  TTCCAGCCCACA
                         ||||  |||||||||||||
                         GACG  AAGGTCGGGTGT
                        _____    AA       T
GAM164 TSSC4          CCAGTGCTTCCAGCCCACA     2351 T   _      II
                       CC GTGTT CCAGCCCAC
                       || ||||| |||||||||
                       GG CACGA GGTCGGGTG
                         T   A    TI
GAM164 UBE3A          CTGCTGTTCCAGCCCACAT     2353 _         II
                       CTG TGTTCCAGCCCACA
                       ||| ||||||||||||||
                       GAC ACAAGGTCGGGTGT
                          G      AI
GAM165 ANGPT2        GCAAACTTGAGGGCAAACA      2370   AGGC     II
                      GCAGAC  GGGCAAAC
                      ||||||  ||||||||
                      CGTTTG  CCCGTTTG
                         AACT      TI
GAM165 CALD1         GCAAGCAGGCGGGCAGGCAG     2371 GA       AACAI
                      CA CAGGCGGGCA
                      || ||||||||||
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                        GT  GTCCGCCGT
                        TC       CCGTI
GAM165 CALD1            GCAAGCAGGCGGGCAGGCAG     2371 TGGC A      AA  T
                          AG CAGGCGGGCA  CAG
                          II IIIIIIIII III
                          TC GTCCGCCCGT GTC
                        T___ _       CC  C
GAM165 CARD12          CACACAGG---GCAAACAG      2367 CAGA G  _
                          CA GC GGGCAAACA
                          II II IIIIIIIII
                          GT TG CCCGTTTGT
                        ____  G T
GAM165 CDK5R2          GGCAGACAGGAGGGAAGATGGTG   2379      C  CAAACAGTI
                          GCAGACAGG GGG
                          IIIIIIIII III
                          CGTCTGTCC CCC
                             T  TTCTACCAI
GAM165 CDK5R2          GGCAGACAGGAGGGAAGATGGTG   2379 TG    C  CAAACA  I
                          GCAGACAGG GGG     GTG
                          IIIIIIIII III     III
                          CGTCTGTCC CCC    CAC
                          __      T  TTCTAC  T
GAM165 DDX6            AGACAGTGTGGCAGCAAACAGT    2365 ____  G    III
                          AGACA  GGCGG CAAACAG
                          IIIII  IIIII IIIIIII
                          TCTGT  CCGTC GTTTGTC
                          CACA   _      AII
GAM165 DDX6            AGACAGTGTGGCAGCAAACAGT    2365 ____   A   _ AACAGTG
                          TGGCAG CAGGCGG GCA
                          IIIIII IIIIIII III
                          ACCGTC GTTTGTC TGT
                        TCAC    _     A  AIIIGTG
GAM165 DFFB            TGGGAGACCGAGGCGGGCA       2380  C  __      AACAGT
                          TGG AGAC AGGCGGGCA
                          III IIII IIIIIIIII
                          ACC TCTG TCCGCCCGT
                          C   GC       IIIGTG
GAM165 DFFB            TGGGAGACCGAGGCGGGCA       2380  C  __      III
                          TGG AGAC AGGCGGGC
                          III IIII IIIIIIIII
                          ACC TCTG TCCGCCCG
                          C   GC       TII
GAM165 EIF2C1          GGCAGACAGGCAGGCAGGCAG     2374            AACAI
                          GCAGACAGGCGGGCA
                          IIIIIIIIIIIIII
                          CGTCTGTCCGTCCGT
                             CCGTI
GAM165 EIF2C1          GGCAGACAGGCAGGCAGGCAG     2374 TG        AA  TG
                          GCAGACAGGCGGGCA CAG
                          IIIIIIIIIIIIII III
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                              CGTCTGTCCGTCCGT GTC
                              __            CC  CI
GAM165 FEZ1           TGGGAGGCCAAGGCGGGCAAA   2381 T____   AGAC        CAGTG
                              GGC  AGGCGGGCAAA
                              |||  |||||||||||
                              CCG  TCCGCCCGTTT
                       ACCCT  GT__        IIIGT
GAM165 FEZ1           TGGGAGGCCAAGGCGGGCAAA   2381 T____   AGAC        III
                              GGC  AGGCGGGCAA
                              |||  ||||||||||
                              CCG  TCCGCCCGTT
                       ACCCT  GT__       TII
GAM165 GLRX2          TGGCAGACATGCTGGGGAAAC   2383       G _ C   AGTG
                              TGGCAGACA GC GGG AAAC
                              ||||||||| || ||| ||||
                              ACCGTCTGT CG CCC TTTG
                               A  A  C   IIIG
GAM165 GLRX2          TGGCAGACATGCTGGGGAAAC   2383 G    G _ CAAAI
                              GCAGACA GC GGG
                              ||||||| || |||
                              CGTCTGT CG CCC
                              _    A  A  CTTTI
GAM165 GRLF1          GGCAGA--GGCGGGCACAGAGTG   2378    CA   AA  I
                              GGCAGA GGCGGGC ACAG
                              |||||| ||||||| ||||
                              CCGTCT CCGCCCG TGTC
                              __    __    T
GAM165 GRLF1          GGCAGA--GGCGGGCACAGAGTG   2378 TG   CA   AAC
                              GCAGA GGCGGGCA AGTG
                              ||||| |||||||| ||||
                              CGTCT CCGCCCGT TCAC
                              __    __       GTC
GAM165 GRM4          GGCGGGCAGGCGGGCAAGACAG    2372 _ GACA       ACI
                              GGCA  GGCGGGCAA
                              ||||  |||||||||
                              CCGT  CCGCCCGTT
                       C    ____        CTG
GAM165 GRM4          GGCGGGCAGGCGGGCAAGACAG    2372 T_ CAGA      _ TG
                              GG  CAGGCGGGCAA ACAG
                              ||  ||||||||||| ||||
                              CC  GTCCGCCCGTT TGTC
                       CG C___        C  TI
GAM165 HAS3          GCAGACAGGCAGTCTGAAAACA    2369        GCAAACIII
                              GCAGACAGGCGG
                              ||||||||||||
                              CGTCTGTCCGTC
                              AGACTTTTG
GAM165 HAS3          GCAGACAGGCAGTCTGAAAACA    2369 TGGC      GC___  GTG
                              AGACAGGCGG  AAACA
                              ||||||||||  |||||
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                      TCTGTCCGTC    TTTGT
                      ____        AGACT    GTI
GAM165 IGF1           TGGGAGGCTGAGGCGGGCAAA    2382 T____    AGAC        CAGTG
                      GGC   AGGCGGGCAAA
                      |||   |||||||||||
                      CCG   TCCGCCCGTTT
                      ACCCT AC__          IIIGT
GAM165 IGF1           TGGGAGGCTGAGGCGGGCAAA    2382 T____    AGAC        III
                      GGC   AGGCGGGCAA
                      |||   ||||||||||
                      CCG   TCCGCCCGTT
                      ACCCT AC__         TII
GAM165 JAM3           TGGCAGACA-GCGAGGC-AACAGTG 2384        G _    A   I
                      TGGCAGACAG CG GGCAA CAGTG
                      ||||||||| || ||||| |||||
                      ACCGTCTGTC GC CCGTT GTCAC
                       _  T  _   I
GAM165 JAM3           TGGCAGACA-GCGAGGC-AACAGTG 2384 _      G _    A   I
                      GGCAGACAG CG GGCAA CAGT
                      ||||||||| || ||||| ||||
                      CCGTCTGTC GC CCGTT GTCA
                      A    _  T  _   I
GAM165 KRT8           TGG-AGGCAGGCGGGCCGAACCAG  2385  C A      AAA__  TGI
                      TGG AG CAGGCGGGC   CAG
                      ||| || |||||||||    |||
                      ACC TC GTCCGCCCG    GTC
                       _  C      GCTTG  III
GAM165 KRT8           TGG-AGGCAGGCGGGCCGAACCAG  2385 C A      A_  AI
                      AG CAGGCGGGC  AAC
                      || |||||||| |||
                      TC GTCCGCCCG  TTG
                      C C      GC  II
GAM165 LILRA1         TGGCAGACAGTCCAGATAACA    2387       G_  CA  GTG
                      TGGCAGACAG CGGG AACA
                      ||||||||| |||| ||||
                      ACCGTCTGTC GTCT TTGT
                       AG  A_  III
GAM165 LILRA1         TGGCAGACAGTCCAGATAACA    2387       G_  GC ACI
                      GGCAGACAG CGG AA
                      ||||||||| ||| ||
                      CCGTCTGTC GTC TT
                       AG  TA GII
GAM165 MAML1          GGCAGACAGAAAGGCCAACGGT   2377       C  A AGI
                      GCAGACAGG GGGC AAC
                      ||||||||| |||| |||
                      CGTCTGTCT TCCG TTG
                       T  G  CCI
GAM165 MAML1          GGCAGACAGAAAGGCCAACGGT   2377 TG    C  A  A
                      GCAGACAGG GGGC AAC GTG
                      ||||||||| |||| ||| |||
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                        CGTCTGTCT TCCG TTG CAT
                        __       T   G   C
GAM165 NFE2L1       GGCAG-CAGT--GGCAAACAGT   2376   A   GCG      I
                        GGCAG CAG  GGCAAACA
                        ||||| |||  ||||||||
                        CCGTC GTC  CCGTTTGT
                        _   A__      C
GAM165 NFE2L1       GGCAG-CAGT--GGCAAACAGT   2376 TG   A   GCG
                         GCAG CAG  GGCAAACAGT
                         |||| |||  ||||||||||
                         CGTC GTC  CCGTTTGTCA
                        __  _  A__
GAM165 Nrap         GACATGAACGGGCAAACAG      2368  __        III
                        GACA GGCGGGCAAACA
                        |||| ||||||||||||
                        CTGT TTGCCCGTTTGT
                            AC        CII
GAM165 Nrap         GACATGAACGGGCAAACAG      2368 TGGCAGACA
                            GGCGGGCAAACAGT
                            ||||||||||||||
                            TTGCCCGTTTGTCG
                        C_____
GAM165 SF3A2        TGGCGAAC-GGCGGGCAAA      2386   AG  A      CAG
                        TGGC  AC GGCGGGCAAA
                        ||||  || ||||||||||
                        ACCG  TG CCGCCCGTTT
                         CT  _        III
GAM165 SF3A2        TGGCGAAC-GGCGGGCAAA      2386   AG  A      I
                        TGGC  AC GGCGGGCAA
                        ||||  || |||||||||
                        ACCG  TG CCGCCCGTT
                         CT  _        T
GAM165 SLC17A5      AGACAGACTGAACAAACAGTG    2366 G    _        I
                        ACAGGC GGGCAAACAGT
                        |||||| |||||||||||
                        TGTCTG CTTGTTTGTCA
                         _    A    I
GAM165 SLC17A5      AGACAGACTGAACAAACAGTG    2366 TGGCAGAC   _
                        AGGC GGGCAAACAGTG
                        |||| ||||||||||||
                        TCTG CTTGTTTGTCAC
                        _____   A
GAM165 SLC29A1     GGCAGACAGTCTGACAGACA     2373          AAACI
                        GCAGACAG  GCGGGC
                        ||||||||  ||||||
                        CGTCTGTC  TGTCTG
                         AGAC   IIICA
GAM165 SLC29A1     GGCAGACAGTCTGACAGACA     2373 TG    GCG  A GT
                        GCAGACAG  GGCA ACA
                        ||||||||  |||| |||
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                              CGTCTGTC  CTGT TGT
                              __     AGA  C  GI
GAM165 SLC29A1        GGCAGACAGGGAGGGAGGCAG    2375      C____     AACAI
                        GCAGACAGG   GGGCA
                        |||||||||   |||||
                        CGTCTGTCC   TCCGT
                              CTCCC   IIIAC
GAM165 SLC29A1        GGCAGACAGGGAGGGAGGCAG    2375 TG     C  CAAA  TG
                        GCAGACAGG GGG   CAG
                        ||||||||| |||   |||
                        CGTCTGTCC TCC   GTC
                        __      C  CTCC  CI
GAM165 TEM6          TGGCTTAGATGATGGCAAACAGTG  2388  __  CAGGCG        I
                        TGGC AGA    GGCAAACAGTG
                        |||| |||    ||||||||||
                        ACCG TCT    CCGTTTGTCAC
                          AA  ACTA__         I
GAM165 TEM6          TGGCTTAGATGATGGCAAACAGTG  2388  __  CAGGCG        I
                         GGC AGA    GGCAAACAGT
                         ||| |||    ||||||||||
                         CCG TCT    CCGTTTGTCA
                          AA  ACTA__         I
GAM166 ADORA2B        TATTTGTCAATCC-TTGGAGC   2397  A  CACC      TA
                         TATT GTC   CCTTGGAGC
                         |||| |||   |||||||||
                         ATAA CAG   GGAACCTCG
                          A  TTA_       II
GAM166 ADORA2B        TATTTGTCAATCC-TTGGAGC    2397 ATTA_  CACC     I
                           GTC   CCTTGGAG
                           |||   ||||||||
                           CAG   GGAACCTC
                         ATAAA  TTA_    I
GAM166 IGF1       TTATACCACCCCTTTGAGGTAG    2399 TAGT     G  CI
                         CCACCCCTT GAG
                         ||||||||| |||
                         GGTGGGGAA CTC
                         AT__     A  CA
GAM166 IGF1       TTATACCACCCCTTTGAGGTAG    2399 TATTAGT     G  C
                          CCACCCCTT GAG TAG
                          ||||||||| ||| |||
                          GGTGGGGAA CTC ATC
                         TAT____     A  C
GAM166 NOS1         TCCAGGCCCCTTGGATGCTA     2398  __      _  III
                         TCCA CCCCTTGGA GCT
                         |||| ||||||||| |||
                         AGGT GGGGAACCT CGA
                          CC      A  TII
GAM166 PIGA         TATTAGTCCAGGCACCCCGTGG    2394           T  AGCTAG
                         TATTAGTCC  ACCCC TGG
                         |||||||||  ||||| |||
```

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                    ATAATCAGG   TGGGG ACC
                     TCCG    C  IIIGAT
GAM166 PIGA          TATTAGTCCAGGCACCCCGTGG   2394        ____     TTGIIIC
                     TATTAGTCC  ACCCC
                     IIIIIIIII  IIIII
                     ATAATCAGG   TGGGG
                      TCCG    CACCIII
GAM166 PITX3         TAGTCCACCCCTCAGGGCT      2393        TG A II
                     TAGTCCACCCCT G GC
                     IIIIIIIIIII I II
                     ATCAGGTGGGGA C CG
                       GT C  AI
GAM166 PITX3         TAGTCCACCCCTCAGGGCT      2393 TATTAG      TG A  A
                       TCCACCCCT G GCT
                       IIIIIIIII I III
                       AGGTGGGGA C CGA
                       _____      GT C  C
GAM166 POLG          TATT--TCCACTGCCTTGGAGC   2395 ATTAG    C_      I
                       TCCAC CCTTGGAG
                       IIIII IIIIIIIII
                       AGGTG GGAACCTC
                      ATAA_   AC     I
GAM166 POLG          TATT--TCCACTGCCTTGGAGC   2395 TATTAG    C_      TA
                       TCCAC CCTTGGAGC
                       IIIII IIIIIIIII
                       AGGTG GGAACCTCG
                      ATAA__  AC      II
GAM166 SLC18A1       ATGAGTC-ACCCCTTGCAG      2391 ATT  C     GAI
                      AGTC ACCCCTTG
                      IIII IIIIIIIII
                      TCAG TGGGGAAC
                     TAC   _    GTC
GAM166 SLC18A1       ATGAGTC-ACCCCTTGCAG      2391 TATT  C     G CT
                      AGTC ACCCCTTG AG
                      IIII IIIIIIIII II
                      TCAG TGGGGAAC TC
                     AC__   _     G TI
GAM166 TGFBR3        ATTGGTCCTGCCCTTGGAG-TAG  2392 TA  AC     CI
                      GTCC CCCTTGGAG
                      IIII IIIIIIIIII
                      CAGG GGGAACCTC
                     AC  AC     AI
GAM166 TGFBR3        ATTGGTCCTGCCCTTGGAG-TAG  2392 TATTA AC      C
                      GTCC CCCTTGGAG TAG
                      IIII IIIIIIIIII III
                      CAGG GGGAACCTC ATC
                     AAC__  AC       _
GAM166 ZNF146        TATTTTTCC--CCCTTGGAG     2396 ATTAGTCCA       I
                       CCCCTTGGA
                       IIIIIIIII
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                           GGGGAACCT
                           ATAAAAAG_        I
GAM166 ZNF146          TATTTTTCC--CCCTTGGAG    2396 TATTAGTCCA        CT
                           CCCCTTGGAG
                           ||||||||||
                           GGGGAACCTC
                           ATAAAAAG__       II
GAM167 ADAMTS13          GCAGTGGCAGTG           2407        II
                           GCGGTGGCAGT
                           |||||||||||
                           CGTCACCGTCA
                              CI
GAM167 APPBP2          GCGGTGGCAGCCACGCGGGC-GCAC  2405 C_ TG AG  T  A  I
                         GG  GC  TGC GGC GCA
                         ||  ||  ||| ||| |||
                         CC  CG  GCG CCG CGT
                         CA  GT  GT  C  _  I
GAM167 APPBP2          GCGGTGGCAGCCACGCGGGC-GCAC  2405 GTGC        ___  T  A  I
                         GGTGGCAGT  GC GGC GCAC
                         |||||||||  || ||| ||||
                         CCACCGTCG  CG CCG CGTG
                            ____      GTG C _  C
GAM167 ASS            GCGGTGGCAG-GC-GGCAG      2408      T T  I
                         GCGGTGGCAG GC GGCA
                         |||||||||| || ||||
                         CGCCACCGTC CG CCGT
                            _ _    C
GAM167 ASS            GCGGTGGCAG-GC-GGCAG      2408 GTGC    T T  C
                         GGTGGCAG GC GGCAG
                         |||||||| || |||||
                         CCACCGTC CG CCGTC
                            ____     _ _   T
GAM167 AVPR2           GTGCGGTGGCAGT-ATGGC      2415         C  AGC
                         GTGCGGTGGCAGTG TGGC
                         ||||||||||||| ||||
                         CACGCCACCGTCAT ACCG
                              _   |||
GAM167 AVPR2           GTGCGGTGGCAGT-ATGGC      2415        C  I
                         GTGCGGTGGCAGTG TGG
                         ||||||||||||| |||
                         CACGCCACCGTCAT ACC
                              _  G
GAM167 BSN           GCGGTGACTCACCTGGCAGCA     2410      AGTG   I
                         CGGTGGC  CTGGCAGC
                         |||||||  ||||||||
                         GCCACTG  GACCGTCG
                           AGTG      I
GAM167 CALCA          GCGGTGGCAGCGGCGGCGGC      2409      C  AGI
                         CGGTGGCAGTG TGGC
                         |||||||||| ||||
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                        GCCACCGTCGC GCCG
                           C   CCI
GAM167 CALCA            GCGGTGGCAGCGGCGGCGGC   2409 GTGC      C   A  A
                        GGTGGCAGTG TGGC GC
                        |||||||||| |||| ||
                        CCACCGTCGC GCCG CG
                           ____        C   C  C
GAM167 CDKN2C           GTGCCCTGGAGCAGAGCCTGGCAGCAC2413   ___ T   T _      III
                        GTGC  GG GGCAG GC TGGCAGCAC
                        ||||  || ||||| || |||||||||
                        CACG  CC TCGTC CG ACCGTCGTG
                         GGA _   T G      III
GAM167 CDKN2C           GTGCCCTGGAGCAGAGCCTGGCAGCAC2413 TGC T   T _     I
                        GG GGCAG GC TGGCAGCA
                        || ||||| || |||||||||
                        CC TCGTC CG ACCGTCGT
                         GGA _   T G     I
GAM167 COL6A1           CGGGGTCAGTGCTGGTCAGCA    2402 GGT _     _  I
                        GG CAGTGCTGG CAGC
                        || |||||||||| ||||
                        CC GTCACGACC GTCG
                         C__ A     A  I
GAM167 COL6A1           CGGGGTCAGTGCTGGTCAGCA    2402 GTGCGGT _    _   C
                        GG CAGTGCTGG CAGCA
                        || |||||||||| |||||
                        CC GTCACGACC GTCGT
                        _____  A     A   C
GAM167 CSNK2A2         GTGGCAGCTGCTTGAAGG        2418          I
                        GTGCGGTGGCAGT
                        |||||||||||||
                        CACGTCACCGTCA
                              I
GAM167 CXCR4          TGCGGTGGC--TACTGG-AGCAC  2421 _     AG    C
                        GCGGTGGC TGCTGG AGCA
                        |||||||| |||||| ||||
                        CGCCACCG ATGACC TCGT
                          A      __    _
GAM167 CXCR4          TGCGGTGGC--TACTGG-AGCAC  2421 GT     AG    C
                        GCGGTGGC TGCTGG AGCA
                        |||||||| |||||| ||||
                        CGCCACCG ATGACC TCGT
                          __      __     _
GAM167 DFFB            GCGGTGGCACCTGCTGCCCAGC    2404 CG    G_   G_  I
                        GTGGCA TGCTG CAG
                        ||||||  ||||| |||
                        CACCGT ACGAC GTC
                          __    GG   GG  I
GAM167 DFFB            GCGGTGGCACCTGCTGCCCAGC    2404 GTGC    G_   G_  AC
                        GGTGGCA TGCTG CAGC
                        |||||||  ||||| ||||
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                              CCACCGT ACGAC GTCG
                              ____       GG    GG   AC
GAM167 EMP1          GTGGCAGGTGCTGGCAGCA      2419   _       II
                              GTGGCAG TGCTGGCAGC
                              |||||||| ||||||||||
                              CACCGTC ACGACCGTCG
                                   C        TI
GAM167 FGD1         GCGGTGGCAGTAGCAGCAGCAGCA 2406 _         _ T  GI
                              GCGGTGGCAGT GC GGCA
                              ||||||||||| || ||||
                              CGTCATCGTCG CG TCGT
                                   C      T _   II
GAM167 FGD1         GCGGTGGCAGTAGCAGCAGCAGCA 2406 _ _       _ T  ACI
                              GTG CGGTGGCAGT GC GGCAGC
                              ||| ||||||||| || ||||||
                              CAC GTCATCGTCG CG TCGTCG
                               C  C      T _     III
GAM167 GAL          GTGCGGTGGCGGGTCTGGGCGGCA 2414       A_ G  _ A  CI
                              GTGCGGTGGC GT CTGG C GCA
                              |||||||||| || |||| | |||
                              CACGCCACCG CA GACC G CGT
                                   CC _    C C  II
GAM167 GAL          GTGCGGTGGCGGGTCTGGGCGGCA 2414 T     A_ G  _ A  I
                              GCGGTGGC GT CTGG C GC
                              |||||||| || |||| | ||
                              CGCCACCG CA GACC G CG
                               _       CC _    C C  I
GAM167 GPR4         GTG-GGTGGGAGTGCTGGCA    2416   C   C       GCA
                              GTG GGTGG AGTGCTGGCA
                              ||| ||||| ||||||||||
                              CAC CCACC TCACGACCGT
                                   _    C       III
GAM167 GPR4         GTG-GGTGGGAGTGCTGGCA    2416 _ C   C      I
                              TG GGTGG AGTGCTGGC
                              || ||||| |||||||||
                              AC CCACC TCACGACCG
                               C _    C       I
GAM167 LANGERIN      GCAGTGCTG              2403      II
                              GCAGTGCT
                              ||||||||
                              CGTCACGA
                                   CI
GAM167 MAF         TGCGGTGGCGGCGGTGGTGGCTGC 2420 GC    A  C  AI
                              GGTGGC GTG TGGC
                              |||||| ||| ||||
                              CCGCCG CAC ACCG
                               A_    C C  AC
GAM167 MAF         TGCGGTGGCGGCGGTGGTGGCTGC 2420 GT     A___ C  A  ACI
                              GCGGTGGC  GTG TGGC GC
                              ||||||||  ||| |||| ||
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                              CGCCACCG   CAC ACCG CG
                               __    CCGC  C   A CII
GAM167 PAX8          GCAGTGCTG            2403      II
                              GCAGTGCT
                              IIIIIIII
                              CGTCACGA
                                 CI
GAM167 PPP1R12B      GTGCGGT--CAGTGCTGGCA    2417    GG       GC
                              GTGCGGT CAGTGCTGGCA
                              IIIIIII IIIIIIIIIII
                              CACGCCA GTCACGACCGT
                                 __         II
GAM167 PPP1R12B      GTGCGGT--CAGTGCTGGCA    2417 _   GG       I
                              TGCGGT CAGTGCTGGC
                              IIIIII IIIIIIIIII
                              ACGCCA GTCACGACCG
                                C   __      I
GAM167 TNNI1         GGTGGCAGTG-AGACAGCAC    2411 _    CT     I
                              GTGGCAGTG GGCAGCA
                              IIIIIIIII IIIIIII
                              CACCGTCAC CTGTCGT
                                C     T_   I
GAM167 TNNI1         GGTGGCAGTG-AGACAGCAC    2411 GTGCGGTG    CT
                              GCAGTG GGCAGCA
                              IIIIII IIIIIII
                              CGTCAC CTGTCGT
                              _____      T_
GAM167 WEE1        GTGGGCGTGGCAGTG--GGCAGC   2412 __ T G     CT    AC
                              G GCG TGGCAGTG GGCAGC
                              I III IIIIIIIII IIIIII
                              C CGC ACCGTCAC CCGTCG
                              CA C  _      __      II
GAM167 WEE1        GTGGGCGTGGCAGTG--GGCAGC   2412 T___  G     CT    I
                              GCG TGGCAGTG GGCAG
                              III IIIIIIIII IIIII
                              CGC ACCGTCAC CCGTC
                              CACC  _      __      I
GAM168 ABCC3        ATGAGGTTGGCTGGAGAAT      2425 TATGA_ AT       CTGC
                              TG CTGGAGAATT
                              II IIIIIIIIII
                              AC GACCTCTTAG
                              ACTCCA C_        IIIT
GAM168 CLN5      ATGTTAATATGCAGCAATTCTGCT    2426 TA A   C G _      I
                              TG TGAT TG AG AATTCTGCT
                              II IIII II II IIIIIIIII
                              AC ATTA AC TC TTAAGACGA
                              __  A  T G G       C
GAM168 EVA1       TGATGATCTGG-GAGTCCT        2431 TATG       A A   G
                              ATGATCTGG GA TTCT
                              IIIIIIIII II IIII
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                              TACTAGACC CT AGGA
                        ____         _ C  G
GAM168 LDB3             TGA-GTTCTTG-GAATTCTGCT   2432 TATGATGA  GGA
                             TCT   GAATTCTGC
                             ||| |||||||||
                             AGA   CTTAAGACG
                        TCA_____   AC_
GAM168 MPP3             ATGATGGAATTTGTGGAGAATTCT  2424 TA   ATC____       GCTI
                             TGATG    TGGAGAATTCT
                             |||||    |||||||||||
                             ACTAC    ACCTCTTAAGA
                         __   CTTAAAC      GIII
GAM168 PXF              GATGATCTGCAGACTTGTGCT   2429 TATGAT    G  A  C
                             GATCTG AGA TT TGCT
                             |||||| ||| || ||||
                             CTAGAC TCT AA ACGA
                        _____     G  G C
GAM168 ST7             GATGATCTGAATGATTTCT       2428 TATGAT    _ A  GC
                             GATCTGGA GA TTCT
                             |||||||| || ||||
                             CTAGACTT CT AAGA
                        _____     A  A  AT
GAM168 TCF12           GATGTAACTGGAGAATATATGC   2427 TATGA  T    TC_  T
                             TGA CTGGAGAAT  TGC
                             ||| |||||||||  |||
                             ATT GACCTCTTA  ACG
                        C____  _      TAT  T
GAM168 VSX1            TATGATGATAT-CAG-ATTCTTCT 2430     CT_ GAA   GCT
                             TATGATGAT  GGA  TTCT
                             |||||||||  |||  ||||
                             ATACTACTA  TCT  AAGA
                             TAG AAG   III
GAM168 ZNF193          TGGTGATCTGGAAAACT-TGCT   2433 TATGA          C
                             TGATCTGGAGAATT TGCT
                             |||||||||||||| ||||
                             ACTAGACCTTTTGA ACGA
                        C____            _
GAM169 ARNTL           CAGATCCAGCTTGGGAGGA       2441 TAGCAG    ___ T AGCG
                             ATCCAGC  GGA GA
                             |||||||  ||| ||
                             TAGGTCG  CCT CT
                        _____     AAC  C CAAI
GAM169 CTNND2          AGAGTCACAACGGATGAAG       2436 TAGCAGA _       C
                             TC CAGCGGATGAAG G
                             || ||||||||||| |
                             AG GTTGCCTACTTC C
                        _____  T        T
GAM169 CYP3A4          GCAG-TCCATTGGATGAAGC      2445 TAGC A  GC      G
                             AG TCCA GGATGAAGC
                             || |||| |||||||||
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                          TC AGGT  CCTACTTCG
                         ____  _   AA      G
GAM169 GNLY          GCAGATCCA-CCGATGAGGC    2446 TAGC    G G   A G
                        AGATCCA C GATGA GC
                        ||||||| | ||||| ||
                        TCTAGGT G CTACT CG
                        ____      _G   C G
GAM169 GRAF          CAGATCCAGCTGCCTGTAGC    2442 TAGCAG   GGA_ A
                        ATCCAGC  TG AGCG
                        |||||||  || ||||
                        TAGGTCG  AC TCGT
                        _____      ACGG A
GAM169 GRIK3         AGAAGATCTGAGGAGGATGAAGC  2439 TAGC   C_ C_    GGI
                        AGATC AG GGATGAAGC
                        ||||| || |||||||||
                        TCTAG TC CCTACTTCG
                     CT__   AC CT      GII
GAM169 GUCA2B        TACCAGATCCAGCTGCTCAGGC   2447 G      GGATGAA GG
                        TA CAGATCCAGC    GC
                        || ||||||||||    ||
                        AT GTCTAGGTCG    CG
                         G         ACGAGTC II
GAM169 IMPA1         CAGAATCCAGCGGCAATGAAG    2440 TAGCA     __    CGG
                        GATCCAGCGG ATGAAG
                        |||||||||| ||||||
                        TTAGGTCGCC TACTTC
                        _____        GT   AAT
GAM169 JAM3          AGCAGTGTCTCCGGCGGATGAA   2437 TA  A___ A      CGG
                        GCAG  TCC GCGGATGAAG
                        ||||  ||| ||||||||||
                        CGTC  AGG CGCCTACTTT
                         __   ACAG  C       III
GAM169 PYGB          CAGATCCAGC--ATGCAAG     2443 TAGCAG   GG _ C
                        ATCCAGC ATG AAG
                        ||||||| ||| |||
                        TAGGTCG TAC TTC
                        _____     __ G  C
GAM169 TBX6          CAGATCCA--GGATCACAGC    2444 TAGCAG   GC  GA_
                        ATCCA GGAT AGC
                        ||||| |||| |||
                        TAGGT CCTA TCG
                        _____      __  GTG
GAM169 TNR           AGCAGATGTTAGCCAGCGGAT   2438 TA  _____     GAAGCGG
                        GCAGAT  CCAGCGGAT
                        ||||||  |||||||||
                        CGTCTA  GGTCGCCTA
                        __    CAATC      AIIIGGC
GAM170 CKTSF1B1      AACAGGTCTCT--TGCCCTCAG   2453        GTGA   I
                        AACAGGTCT TGCCCTT
                        ||||||||| |||||||
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                         TTGTCCAGA   ACGGGAG
                           GA__      T
GAM170  CKTSF1B1       AACAGGTCTCT--TGCCCTCAG   2453 TA      GTGA
                         ACAGGTCT   TGCCCTTAG
                         |||||||    |||||||||
                         TGTCCAGA   ACGGGAGTC
                           __        GA__
GAM170  DYRK2          AACAGGTCTGAGCTACTCCTT    2451 A      TGA  _  I
                         CAGGTCTG   TGC CCT
                         ||||||||   ||| |||
                         GTCCAGAC   ATG GGA
                          _         TCG  A  I
GAM170  DYRK2          AACAGGTCTGAGCTACTCCTT    2451 TA      TGA  _  AGT
                         ACAGGTCTG  TGC CCTT
                         |||||||||  ||| ||||
                         TGTCCAGAC  ATG GGAA
                          __        TCG  A  AII
GAM170  EMP1           AGGTCTGTG--GACCTCAGT     2455 _      ATGC   I
                         GGTCTGTG   CCTTAG
                         ||||||||   ||||||
                         CCAGACAC   GGAGTC
                          T    CT__      I
GAM170  ENTPD5         ACAGGGCTCTCTGTGATGCTCT   2454       ____      CCIIIA
                         ACAGG   TCTGTGATGC
                         |||||   ||||||||||
                         TGTCC   AGACACTACG
                           CGAG        AGAIII
GAM170  ENTPD5         ACAGGGCTCTCTGTGATGCTCT   2454 TAAC  ____      C TAGT
                         AGG   TCTGTGATGC CT
                         |||   |||||||||| ||
                         TCC   AGACACTACG GA
                         ____     CGAG      A CCII
GAM170  GFER           AACAGGCTCTGGCTGTGATGCACTT 2450 ACA_ T      C I
                         GG CTGTGATGC CT
                         || |||||||| ||
                         CC GACACTACG GA
                          GAGA  _        T I
GAM170  GFER           AACAGGCTCTGGCTGTGATGCACTT 2450 TA    _____      C AGTII
                         ACAGGT   CTGTGATGC CTT
                         ||||||   |||||||||| |||
                         TGTCCG   GACACTACG GAA
                          __      AGACC     T AIIIT
GAM170  NUFIP1         CAGGTCTGTGACGTCACTAG     2456         CCCTTAI
                         AGGTCTGTGATG
                         ||||||||||||
                         TCCAGACACTGC
                            AGTGATI
GAM170  NUFIP1         CAGGTCTGTGACGTCACTAG     2456 TAACAG      CCC
                         GTCTGTGATG  TTAG
                         ||||||||||  ||||
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                            CAGACACTGC  GATC
                            _____         AGT
GAM170  OAS3          GTCTAAGAAGGTGCCCTTAG    2457    T  ___        III
                            GTCTG GA  TGCCCTTA
                            |||||  ||  |||||||||
                            CAGAT CT  ACGGGAAT
                             T  TCC      CII
GAM170  PCDHGA1       AAGAGGTCA-TGATGCCCTT     2452 AC_    T       I
                            AGGTC GTGATGCCCT
                            ||||| |||||||||||
                            TCCAG TACTACGGGA
                            TTC   _       I
GAM170  PCDHGA1       AAGAGGTCA-TGATGCCCTT     2452 TAAC   T        AG
                            AGGTC GTGATGCCCTT
                            ||||| ||||||||||||
                            TCCAG TACTACGGGAA
                            TC__  _       GI
GAM170  PCDHGA10      AAGAGGTCA-TGATGCCCTT     2452 AC_    T       I
                            AGGTC GTGATGCCCT
                            ||||| |||||||||||
                            TCCAG TACTACGGGA
                            TTC   _       I
GAM170  PCDHGA10      AAGAGGTCA-TGATGCCCTT     2452 TAAC   T        AG
                            AGGTC GTGATGCCCTT
                            ||||| ||||||||||||
                            TCCAG TACTACGGGAA
                            TC__  _       GI
GAM170  PCDHGA11      AAGAGGTCA-TGATGCCCTT     2452 AC_    T       I
                            AGGTC GTGATGCCCT
                            ||||| |||||||||||
                            TCCAG TACTACGGGA
                            TTC   _       I
GAM170  PCDHGA11      AAGAGGTCA-TGATGCCCTT     2452 TAAC   T        AG
                            AGGTC GTGATGCCCTT
                            ||||| ||||||||||||
                            TCCAG TACTACGGGAA
                            TC__  _       GI
GAM170  PCDHGA12      AAGAGGTCA-TGATGCCCTT     2452 AC_    T       I
                            AGGTC GTGATGCCCT
                            ||||| |||||||||||
                            TCCAG TACTACGGGA
                            TTC   _       I
GAM170  PCDHGA12      AAGAGGTCA-TGATGCCCTT     2452 TAAC   T        AG
                            AGGTC GTGATGCCCTT
                            ||||| ||||||||||||
                            TCCAG TACTACGGGAA
                            TC__  _       GI
GAM170  PCDHGA2       AAGAGGTCA-TGATGCCCTT     2452 AC_    T       I
                            AGGTC GTGATGCCCT
                            ||||| |||||||||||
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                              TCCAG TACTACGGGA
                              TTC    _       I
GAM170 PCDHGA2      AAGAGGTCA-TGATGCCCTT    2452 TAAC   T      AG
                         AGGTC GTGATGCCCTT
                         ||||| |||||||||||
                         TCCAG TACTACGGGAA
                         TC__   _       GI
GAM170 PCDHGA3      AAGAGGTCA-TGATGCCCTT    2452 AC_    T      I
                         AGGTC GTGATGCCCT
                         ||||| ||||||||||
                         TCCAG TACTACGGGA
                         TTC    _       I
GAM170 PCDHGA3      AAGAGGTCA-TGATGCCCTT    2452 TAAC   T      AG
                          AGGTC GTGATGCCCTT
                          ||||| |||||||||||
                          TCCAG TACTACGGGAA
                          TC__   _       GI
GAM170 PCDHGA4      AAGAGGTCA-TGATGCCCTT    2452 AC_    T      I
                         AGGTC GTGATGCCCT
                         ||||| ||||||||||
                         TCCAG TACTACGGGA
                         TTC    _       I
GAM170 PCDHGA4      AAGAGGTCA-TGATGCCCTT    2452 TAAC   T      AG
                         AGGTC GTGATGCCCTT
                         ||||| |||||||||||
                         TCCAG TACTACGGGAA
                         TC__   _       GI
GAM170 PCDHGA5      AAGAGGTCA-TGATGCCCTT    2452 AC_    T      I
                          AGGTC GTGATGCCCT
                          ||||| ||||||||||
                          TCCAG TACTACGGGA
                          TTC    _       I
GAM170 PCDHGA5      AAGAGGTCA-TGATGCCCTT    2452 TAAC   T      AG
                          AGGTC GTGATGCCCTT
                          ||||| |||||||||||
                          TCCAG TACTACGGGAA
                          TC__   _       GI
GAM170 PCDHGA6      AAGAGGTCA-TGATGCCCTT    2452 AC_    T      I
                         AGGTC GTGATGCCCT
                         ||||| ||||||||||
                         TCCAG TACTACGGGA
                         TTC            I
GAM170 PCDHGA6      AAGAGGTCA-TGATGCCCTT    2452 TAAC   T      AG
                          AGGTC GTGATGCCCTT
                          ||||| |||||||||||
                          TCCAG TACTACGGGAA
                          TC__   _       GI
GAM170 PCDHGA7      AAGAGGTCA-TGATGCCCTT    2452 AC_    T      I
                         AGGTC GTGATGCCCT
                         ||||| |||||||||||
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                         TCCAG TACTACGGGA
                         TTC     _      I
GAM170  PCDHGA7          AAGAGGTCA-TGATGCCCTT    2452 TAAC   T       AG
                          AGGTC GTGATGCCCTT
                          ||||| |||||||||||
                         TCCAG TACTACGGGAA
                         TC__   _      GI
GAM170  PCDHGA8          AAGAGGTCA-TGATGCCCTT    2452 AC_    T       I
                          AGGTC GTGATGCCCT
                          ||||| |||||||||
                         TCCAG TACTACGGGA
                         TTC    _      I
GAM170  PCDHGA8          AAGAGGTCA-TGATGCCCTT    2452 TAAC   T       AG
                          AGGTC GTGATGCCCTT
                          ||||| |||||||||||
                         TCCAG TACTACGGGAA
                         TC__   _      GI
GAM170  PCDHGA9          AAGAGGTCA-TGATGCCCTT    2452 AC_    T       I
                          AGGTC GTGATGCCCT
                          ||||| |||||||||
                         TCCAG TACTACGGGA
                         TTC    _      I
GAM170  PCDHGA9          AAGAGGTCA-TGATGCCCTT    2452 TAAC   T       AG
                          AGGTC GTGATGCCCTT
                          ||||| |||||||||||
                         TCCAG TACTACGGGAA
                         TC__   _      GI
GAM170  PCDHGB1          AAGAGGTCA-TGATGCCCTT    2452 AC_    T       I
                          AGGTC GTGATGCCCT
                          ||||| |||||||||
                         TCCAG TACTACGGGA
                         TTC    _      I
GAM170  PCDHGB1          AAGAGGTCA-TGATGCCCTT    2452 TAAC   T       AG
                          AGGTC GTGATGCCCTT
                          ||||| |||||||||||
                         TCCAG TACTACGGGAA
                         TC__   _      GI
GAM170  PCDHGB2          AAGAGGTCA-TGATGCCCTT    2452 AC_    T       I
                          AGGTC GTGATGCCCT
                          ||||| |||||||||
                         TCCAG TACTACGGGA
                         TTC         I
GAM170  PCDHGB2          AAGAGGTCA-TGATGCCCTT    2452 TAAC   T       AG
                          AGGTC GTGATGCCCTT
                          ||||| |||||||||||
                         TCCAG TACTACGGGAA
                         TC__   _      GI
GAM170  PCDHGB3          AAGAGGTCA-TGATGCCCTT    2452 AC_    T       I
                          AGGTC GTGATGCCCT
                          ||||| |||||||||
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```
                              TCCAG TACTACGGGA
                              TTC    _      I
GAM170  PCDHGB3        AAGAGGTCA-TGATGCCCTT    2452 TAAC   T      AG
                              AGGTC GTGATGCCCTT
                              ||||| |||||||||||
                              TCCAG TACTACGGGAA
                              TC__   _      GI
GAM170  PCDHGB4        AAGAGGTCA-TGATGCCCTT    2452 AC_   T      I
                              AGGTC GTGATGCCCT
                              ||||| ||||||||||
                              TCCAG TACTACGGGA
                              TTC    _      I
GAM170  PCDHGB4        AAGAGGTCA-TGATGCCCTT    2452 TAAC   T      AG
                              AGGTC GTGATGCCCTT
                              ||||| |||||||||||
                              TCCAG TACTACGGGAA
                              TC__   _      GI
GAM170  PCDHGB5        AAGAGGTCA-TGATGCCCTT    2452 AC_   T      I
                              AGGTC GTGATGCCCT
                              ||||| ||||||||||
                              TCCAG TACTACGGGA
                              TTC    _      I
GAM170  PCDHGB5        AAGAGGTCA-TGATGCCCTT    2452 TAAC   T      AG
                              AGGTC GTGATGCCCTT
                              ||||| |||||||||||
                              TCCAG TACTACGGGAA
                              TC__   _      GI
GAM170  PCDHGB6        AAGAGGTCA-TGATGCCCTT    2452 AC_   T      I
                              AGGTC GTGATGCCCT
                              ||||| ||||||||||
                              TCCAG TACTACGGGA
                              TTC    _      I
GAM170  PCDHGB6        AAGAGGTCA-TGATGCCCTT    2452 TAAC   T      AG
                              AGGTC GTGATGCCCTT
                              ||||| |||||||||||
                              TCCAG TACTACGGGAA
                              TC__   _      GI
GAM170  PCDHGB7        AAGAGGTCA-TGATGCCCTT    2452 AC_   T      I
                              AGGTC GTGATGCCCT
                              ||||| ||||||||||
                              TCCAG TACTACGGGA
                              TTC    _      I
GAM170  PCDHGB7        AAGAGGTCA-TGATGCCCTT    2452 TAAC   T      AG
                              AGGTC GTGATGCCCTT
                              ||||| |||||||||||
                              TCCAG TACTACGGGAA
                              TC__   _      GI
GAM170  PCDHGC3        AAGAGGTCA-TGATGCCCTT    2452 AC_   T      I
                              AGGTC GTGATGCCCT
                              ||||| ||||||||||
```

```
                              TCCAG TACTACGGGA
                              TTC    _      I
GAM170  PCDHGC3        AAGAGGTCA-TGATGCCCTT    2452 TAAC   T       AG
                              AGGTC GTGATGCCCTT
                              ||||| |||||||||||
                              TCCAG TACTACGGGAA
                              TC__   _       GI
GAM170  PCDHGC4        AAGAGGTCA-TGATGCCCTT    2452 AC_   T       I
                              AGGTC GTGATGCCCT
                              ||||| ||||||||||
                              TCCAG TACTACGGGA
                              TTC    _      I
GAM170  PCDHGC4        AAGAGGTCA-TGATGCCCTT    2452 TAAC   T       AG
                              AGGTC GTGATGCCCTT
                              ||||| |||||||||||
                              TCCAG TACTACGGGAA
                              TC__   _       GI
GAM170  PCDHGC5        AAGAGGTCA-TGATGCCCTT    2452 AC_   T       I
                              AGGTC GTGATGCCCT
                              ||||| ||||||||||
                              TCCAG TACTACGGGA
                              TTC    _      I
GAM170  PCDHGC5        AAGAGGTCA-TGATGCCCTT    2452 TAAC   T       AG
                              AGGTC GTGATGCCCTT
                              ||||| |||||||||||
                              TCCAG TACTACGGGAA
                              TC__   _       GI
GAM171  ANK1          GGGGGCTCTGACGTGGAGGGGGCT 2476    ACCC  CT      I
                              GGGGGC  ATG GAGGGGGCT
                              ||||||   |||  ||||||||||
                              CCCCCG  TGC CTCCCCCGA
                               AGAC  AC      I
GAM171  ANKRD3        GGTGCACTCCAGCGACCTGAGGGGGCT2463 GGGG   _  _ __       III
                              GCAC CCA TG  CTGAGGGGGCT
                              |||| ||| ||  |||||||||||
                              CGTG GGT GC  GACTCCCCCGA
                              CA__   A  C  TG       GII
GAM171  BCL11B        GGGTCACCCATGCTAGAGG    2468 G  GG      GA
                              GG CACCCATGCT GGGGGC
                              || |||||||||| ||||||
                              CC GTGGGTACGA TCTCCG
                              _  A_         __
GAM171  BMP1          GGGGGCGTCC---CCGAGGGGGCT  2475    AC  ATG
                              GGGGGC CC  CTGAGGGGGCT
                              |||||| ||  ||||||||||
                              CCCCCG GG  GGCTCCCCCGA
                               CA  ___
GAM171  ESPN          GGGGGCTGC-ATCCTGGAGGGGGCT 2471    ACC  G  _     I
                              GGGGGC  CAT CTG AGGGGGCT
                              ||||||   ||| ||| ||||||||
```

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                         CCCCCG  GTA GAC TCCCCCGA
                         AC_  G  C       I
GAM171 GNA11         GGGGC-CCCATGCTGGCTGGCGGGGGCT2467 GG    A       A_____        III
                         GGGC CCCATGCTG    GGGGGCT
                         IIII IIIIIIIII    IIIIIII
                         CCCG GGGTACGAC    CCCCCGA
                              __  _    CGACCG    GII
GAM171 GTF2I         GGAGCAGCCTCGGCTGAGGGGAGCT 2466 GG    C  AT_      _  II
                         GGGCA CC  GCTGAGGGG GCT
                         IIIII II  IIIIIIIII III
                         CTCGT GG  CGACTCCCC CGA
                         __   C AGC      T  CI
GAM171 HTR6          GGGGCACCCGATGAGCCGAGG    2464 GG      AT___       GGGCT
                         GGGCACCC   GCTGAGG
                         IIIIIIII   IIIIIII
                         CCCGTGGG   CGGCTCC
                         __      CTACT    GIIIT
GAM171 NELL1         GGGGGCACCGAAGCT-AGGTGG    2473      CAT  G  _  GCT
                         GGGGGCACC  GCT AGG GG
                         IIIIIIIII  III III II
                         CCCCCGTGG  CGA TCC CC
                         CTT  _  A III
GAM171 NR1I2         GGGGGCACCCATGTCCTTCCTGAGG 2469              _____     GGGCTII
                         GGGGGCACCCATG    CTGAGG
                         IIIIIIIIIIII     IIIIII
                         CCCCCGTGGGTAC    GACTCC
                         AGGAAG    IIITCGG
GAM171 PACE          GGGGGCACCCCTGGGCAGATGGCT 2474        A CTG GG  I
                         GGGGGCACCC TG  AG GGCT
                         IIIIIIIIII II  II IIII
                         CCCCCGTGGG AC  TC CCGA
                         G  CCG TA  I
GAM171 RFP           GGGAGCCATGCTGACAGGGC      2460 GGGGGCAC      G
                         CCATGCTGA GGGGC
                         IIIIIIIII IIIII
                         GGTACGACT TCCCG
                         TC_____        G
GAM171 SCRT1         GGGGGCACCC-TG--GAGGGG     2472        A CT    G
                         GGGGGCACCC TG GAGGGG
                         IIIIIIIIII II IIIIII
                         CCCCCGTGGG AC CTCCCC
                         _  __    I
GAM171 SLC2A6        GGGGCACCCGCTGCTGAGG       2465 GG      A_     GGGC
                         GGGCACCC TGCTGAGG
                         IIIIIIII IIIIIIII
                         CCCGTGGG ACGACTCC
                         __       CG     GIII
GAM171 TARBP2        GGGGTTGCACTCAGACTGCTGAGGGG 2462   __  C ___        GCTII
                         GGGG GCAC CA TGCTGAGGGG
                         IIII IIII II IIIIIIIIII
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                         CCCC CGTG GT  ACGACTCCCC
                          AA   A CTG        IIITC
GAM171 XRCC3        GGGCACGGTCCCAAGGCTGAGGGGG 2461 GGG_ CA  T_      CTII
                          GG CCCA GCTGAGGGGG
                          II IIII IIIIIIIIII
                          CC GGGT CGACTCCCCC
                         CGTG A_  TC       AGII
GAM171 ZNF205      GGGGGCACC--TGCGGCAGTGGG 2470      CA  TGA _ CT
                        GGGGGCACC TGC  GG GGG
                        IIIIIIIII III  II III
                        CCCCCGTGG ACG  TC CCC
                           __  CCG A  II
GAM172 ABL2          CGGCTCCGCACCCGGCCTC    2497        __  III
                         CGGCTCCGCGCC GCCT
                         IIIIIIIIIII IIII
                         GCCGAGGCGTGG CGGA
                            GC   GII
GAM172 ABL2          CGGCTCCGCACCCGGCCTC    2497 TCA     _ G  CGCCT
                          CACTCGGC TCC CGC
                          IIIIIIII III III
                          GTGGGCCG AGG GTG
                          C__     G A  CCIII
GAM172 ADAM12         TCGCGCACGGC-CCGCGCCGCC  2515 CACACT_  T      I
                          CGGC CCGCGCCGC
                          IIII IIIIIIIIII
                          GCCG GGCGCGGCG
                         AGCGCGT  _      I
GAM172 ADAM12         TCGCGCACGGC-CCGCGCCGCC  2515 TCACACT  T     TC
                          CGGC CCGCGCCGCC
                          IIII IIIIIIIIII
                          GCCG GGCGCGGCGG
                         AGCGCGT  _      II
GAM172 ADPRT        CACGCTTGCCGCCTCGCCGCCTC  2490  A CG  _ G     I
                        AC CT  GCT CC CGCCGCCT
                        II II  III II IIIIIIIII
                        TG GA  CGG GG GCGGCGGA
                         C A_  C A     I
GAM172 ADPRT        CACGCTTGCCGCCTCGCCGCCTC  2490 TC A CG  _ G     I
                        AC CT  GCT CC CGCCGCCTC
                        II II  III II IIIIIIIIII
                        TG GA  CGG GG GCGGCGGAG
                        __ C A_  C A     C
GAM172 ARHGAP6      CACTGCCCTCCGCGCCCGCCTC  2492 ACTCGG       _  I
                         CTCCGCGCC GCCT
                         IIIIIIIII IIII
                         GAGGCGCGG CGGA
                        GACGG_    G  I
GAM172 ARHGAP6      CACTGCCCTCCGCGCCCGCCTC  2492 TCACACTCGG      _
                         CTCCGCGCC GCCTC
                         IIIIIIIII IIIII
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                          GAGGCGCGG CGGAG
                      ACGG_____        G
GAM172 ARIH1          TCAGACGCGGCTCCGCTCCGGCCTC 2513   C T      G _  II
                          TCA AC CGGCTCCGC CCG CCTC
                          ||| || ||||||||| ||| ||||
                          AGT TG GCCGAGGCG GGC GGAG
                            C C      A C   II
GAM172 ARIH1          TCAGACGCGGCTCCGCTCCGGCCTC 2513 CAC T      G _  I
                            AC CGGCTCCGC CCG CCT
                            || ||||||||| ||| |||
                            TG GCCGAGGCG GGC GGA
                      TC_  C      A C    I
GAM172 ARSB           CTCGGCCCC-CGCCGCCTC      2507       G      I
                          CTCGGCTCC CGCCGCCT
                          ||||||||| |||||||||
                          GAGCCGGGG GCGGCGGA
                             _     G
GAM172 ASCL2           ACCCTC--CTCCGCGCCGCC     2480 C   GG       I
                          ACTC  CTCCGCGCCGC
                          ||||  ||||||||||||
                          TGGG  GAGGCGCGGCG
                           _   AG       I
GAM172 ASCL2           ACCCTC--CTCCGCGCCGCC     2480 TCACA  GG
                            CTC  CTCCGCGCCGCC
                            |||  |||||||||||
                            GAG  GAGGCGCGGCGG
                      G____   __
GAM172 BRCA2          CACAG-CGGCTCCGCCTCTGCCGCCT 2489 ACACT        ____    I
                          CGGCTCCGC  GCCGCC
                          |||||||||  ||||||
                          GCCGAGGCG  CGGCGG
                      C____      GAGA   I
GAM172 BRCA2          CACAG-CGGCTCCGCCTCTGCCGCCT 2489 TC  CT       ____    CII
                          ACA CGGCTCCGC   GCCGCCT
                          ||| |||||||||   ||||||
                          TGT GCCGAGGCG   CGGCGGA
                      __  C_     GAGA   TII
GAM172 CACNA1S        CACTCGGCTCCCCGCTGCC      2493       G C II
                          CACTCGGCTCC CGC GC
                          ||||||||||| ||| ||
                          GTGAGCCGAGG GCG CG
                           G  A GI
GAM172 CACNA1S        CACTCGGCTCCCCGCTGCC      2493 TCACAC   G C T
                          TCGGCTCC CGC GCC
                          |||||||| ||| |||
                          AGCCGAGG GCG CGG
                      _____       G A C
GAM172 CD81           CAGACTCGGCTCTCGAACCG     2488 C     _ C II
                          CA ACTCGGCTC CG GCC
                          || ||||||||| || |||
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                              GT TGAGCCGAG GC TGG
                              C       A T  CI
GAM172 CD81          CAGACTCGGCTCTCGAACCG    2488 TCAC     _  C   CCT
                         ACTCGGCTC CG GCCG

                         |||||||| || ||||
                         TGAGCCGAG GC TGGC
                       TC__       A T  CII
GAM172 CDR2          CAGACTCCGCT--GCGCCGCCTC   2491 AC_  G  CC       I
                         ACTC GCT  GCGCCGCCT

                         |||| ||| |||||||||
                         TGAG CGA  CGCGGCGGA
                       GTC  G   __       I
GAM172 CDR2          CAGACTCCGCT--GCGCCGCCTC   2491 TCAC   G  CC
                         ACTC GCT  GCGCCGCCTC

                         |||| ||| ||||||||||
                         TGAG CGA  CGCGGCGGAG
                       TC__  G   __
GAM172 CRAT         CACACCGGGCAAAGTCCGCGCCGCC 2487 ACACTC  ____       I
                         GGC   TCCGCGCCGC

                         |||   ||||||||||
                         CCG   AGGCGCGGCG
                       GC____  TTTC        I
GAM172 CRAT         CACACCGGGCAAAGTCCGCGCCGCC 2487 TC   C  ____        TCII
                         ACACT GGC   TCCGCGCCGCC

                         ||||| |||   |||||||||||
                         TGTGG CCG   AGGCGCGGCGG
                       __   C  TTTC       CIII
GAM172 DYRK1A       TCAGCCTCGGGCTCCCGCGCCGCGCTC2510   CA   _  _    _  III
                         TCA  CTCGG CTCC GCGCCGC CTC

                         |||  ||||| |||| ||||||| |||
                         AGT  GAGCC GAGG CGCGGCG GAG
                       CG   C   G    C  III
GAM172 DYRK1A       TCAGCCTCGGGCTCCCGCGCCGCGCTC2510 CACA   _  _     _ I
                         CTCGG CTCC GCGCCGC CT

                         ||||| |||| ||||||| ||
                         GAGCC GAGG CGCGGCG GA
                       G___   C   G    C I
GAM172 FGF18       CACATGTCCGCTCCGCGCGGCC    2484 ACAC  G     C I
                         TC GCTCCGCGC GC

                         || |||||||||| ||
                         AG CGAGGCGCG CG
                       GTAC  G       C I
GAM172 FGF18       CACATGTCCGCTCCGCGCGGCC    2484 TC  C_ G     C  TC
                         ACA  TC GCTCCGCGC GCC

                         ||| || |||||||||| |||
                         TGT  AG CGAGGCGCG CGG
                       __  AC G      C CI
GAM172 FGFR4       TCAC-CT-GGCTCCTCCGCCGCCTC 2512 CA  TC    G_     I
                         CAC  GGCTCC  CGCCGCCT

                         ||| |||||| |||||||||
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                         GTG  CCGAGG  GCGGCGGA
                         A_   GA    AG       I
GAM172 FGFR4             TCAC-CT-GGCTCCTCCGCCGCCTC  2512 TCA   TC     G_       I
                         CAC  GGCTCC  CGCCGCCTC
                         III  IIIIII  IIIIIIIII
                         GTG  CCGAGG  GCGGCGGAG
                         A__  GA    AG       I
GAM172 FOXD2             CACTCTCCGGCTCCGCTCCG     2485  A  _      G  II
                         CAC CTC GGCTCCGC CC
                         III III IIIIIIIII II
                         GTG GAG CCGAGGCG GG
                          A  G    A CI
GAM172 FOXD2             CACTCTCCGGCTCCGCTCCG     2485 TC A  _      G  CCT
                         AC CTC GGCTCCGC CCG
                         II III IIIIIIIII III
                         TG GAG CCGAGGCG GGC
                         __ A  G    A CII
GAM172 GCN5L1           TCAC-CTCGGCTCCCCGGGGCC    2514    A     G  CC  TC
                        TCAC CTCGGCTCC CG GCC
                        IIII IIIIIIIII II III
                        AGTG GAGCCGAGG GC CGG
                         _       G CC II
GAM172 GCN5L1           TCAC-CTCGGCTCCCCGGGGCC    2514_ A      G  CC  I
                         CAC CTCGGCTCC CG GC
                         III IIIIIIIII II II
                         GTG GAGCCGAGG GC CG
                         A  _     G CC I
GAM172 GUCY1A2            CTGGGGGCCGCCGCCGCCTC     2503 CTC  CT  _     II
                          GG  CCGC  GCCGCCT
                          II  IIII  IIIIIII
                          CC  GGCG  CGGCGGA
                         GAC CC  G     GI
GAM172 GUCY1A2            CTCG-CGCGGCGCCGCCTC      2506  _ TCC      I
                         CTCG GC  GCGCCGCCT
                         IIII II  IIIIIIIII
                         GAGC CG  CGCGGCGGA
                          G C__     G
GAM172 HDAC4            ACTCGGCTCTGGGTC-CCTC       2482 _      CGCG_ GCCTI
                        CTCGGCTC    CC
                        IIIIIIII    II
                        GAGCCGAG    GG
                        T     ACCCA GAIII
GAM172 HIC1            CTCGCGCTCAGCCAGCGGCC        2498 _____    CC  _ GCIII
                         CTCGGCT  GCG CC
                         IIIIIII  III II
                         GAGTCGG  CGC GG
                        GAGCGC    T_ C IIICG
GAM172 HIC1            CTCGCGCTCAGCCAGCGGCC        2498 TCACA      CC  _  _
                        CTCGGCT  GCG CCGC CT
                        IIIIIII  III IIII II
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                      GAGTCGG CGC GGCG GA
                      C____     T_  C   A
GAM172 IL6R           CTCGGCCCCGCGCCGCGCTC    2505          _ II
                      CTCGGCTCCGCGCCGC CT
                      ||||||||||||||| ||
                      GAGCCGGGGCGCGGCG GA
                              C GI
GAM172 IL6ST          CACTCAGG-CCGCGCCGCCTC    2494 _     CT         I
                      ACTCGG CCGCGCCGCCT
                      |||||| ||||||||||
                      TGAGTC GGCGCGGCGGA
                      G    C_    I
GAM172 IL6ST          CACTCAGG-CCGCGCCGCCTC    2494 TCACAC  CT
                      TCGG CCGCGCCGCCT
                      |||| ||||||||||
                      AGTC GGCGCGGCGGA
                      _____   C_
GAM172 LDB1           CTCGGCTCTCCCCGCCGCCGCCTC 2501      __ G      TIIIG
                      CTCGGC TCC CGCCGCC
                      |||||| ||| |||||||
                      GAGCCG AGG GCGGCGG
                           AG  G    CGGAG
GAM172 LDB1           CTCGGCTCTCCCCGCCGCCGCCTC 2501 TCACA  GG    _      I
                      CTC CTCCGC GCCGCCTC
                      ||| |||||| ||||||||
                      GAG GGGGCG CGGCGGAG
                      _____   A_   G     A
GAM172 MAN2A2         TCAGCGCCCGGCCTCCGCGCCGC  2509   CA_  _       CTCI
                      TCA CTCGGC TCCGCGCCGC
                      ||| |||||| |||||||||||
                      AGT GGGCCG AGGCGCGGCG
                          CGC    G    IIIC
GAM172 MAN2A2         TCAGCGCCCGGCCTCCGCGCCGC  2509 CACA     _      I
                      CTCGGC TCCGCGCCG
                      |||||| |||||||||
                      GGGCCG AGGCGCGGC
                      CGC_   G    I
GAM172 MAP3K5         CACAGCTCGGGGCTGCTCCGCGCCCGCC2483 ACACTCG       _ I
                      GCTCCGCGCC GC
                      |||||||||| ||
                      CGAGGCGCGG CG
                      CCCCGA_    G I
GAM172 MAP3K5         CACAGCTCGGGGCTGCTCCGCGCCCGCC2483 TC _ _____      _ TCIII
                      ACA CTCG   GCTCCGCGCC GCC
                      ||| ||||   |||||||||| |||
                      TGT GAGC   CGAGGCGCGG CGG
                      __  C  CCCGA      G  CIIIC
GAM172 MAP3K7IP2      CTCGGCCGCCGCCGCCGCCTC    2500        _ _       III
                      CTCGGCT CCGC GCCGCCT
                      ||||||| |||| |||||||
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                         GAGCCGG GGCG CGGCGGA
                            C   G     GII
GAM172 MET          CACACGCGCGCTCCGCGCCTCC   2486 A  T _       GCI
                         CAC CG GCTCCGCGCC
                         III II IIIIIIIIII
                         GTG GC CGAGGCGCGG
                          _   C  G      AGI
GAM172 MET          CACACGCGCGCTCCGCGCCTCC   2486 TC  T _      G  C
                         ACAC CG GCTCCGCGCC CCT
                         IIII II IIIIIIIIII III
                         TGTG GC CGAGGCGCGG GGG
                          __   C  G     A  I
GAM172 MLF2         CTCGGCCTTCCACGCCGCCTC   2499    __       III
                         CTCGGC TCCGCGCCGCCT
                         IIIIII IIIIIIIIIII
                         GAGCCG AGGTGCGGCGGA
                            GA         GII
GAM172 MLF2         CTCGGCCTTCCACGCCGCCTC   2499 TCACACTCGGC
                             TCCGCGCCGCCTC
                             IIIIIIIIIIII
                             AGGTGCGGCGGAG
                         GGA_____
GAM172 NEO1         CTCGGCTCCCGGGCGCCGC    2502      ___     III
                         CTCGGCTCC  GCGCCG
                         IIIIIIIII  IIIIII
                         GAGCCGAGG  CGCGGC
                            GCC    GII
GAM172 NEO1         CTCGGCTCCCGGGCGCCGC      2502 TCACA    CTCC    __
                         CTCGG  GCGCCGC  CT
                         IIIII  IIIIIII II
                         GGGCC  CGCGGCG GA
                         GA___  ____     AC
GAM172 PTPRF        TCCCACTCCTCTGCCGCCGCCGCCTC 2511  A    GG _  _     II
                         TC CACTC  CT CCGC GCCGCCTC
                         II IIIII  II IIII IIIIIIII
                         AG GTGAG  GA GGCG CGGCGGAG
                          G  GA C  G      II
GAM172 PTPRF        TCCCACTCCTCTGCCGCCGCCGCCTC 2511 CA   GG _  _     I
                         CACTC  CT CCGC GCCGCCT
                         IIIII  II IIII IIIIIII
                         GTGAG  GA GGCG CGGCGGA
                          __   GA C  G     I
GAM172 SMURF1       CGGCCCCGCCGCCGCCGCCTC    2495    _      TIIIG
                         CGGCTCCGC GCCGCC
                         IIIIIIIII IIIIII
                         GCCGGGGCG CGGCGG
                           G    CGGAG
GAM172 SRRM2        CGCCTCCGCCCGCCGCCTC    2496 G   __       III
                         CG CTCCGC GCCGCCT
                         II IIIIII IIIIIII
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                        GC GAGGCG  CGGCGGA
                         G   GG    GII
GAM172  TEF             ACTCGGCTCGCGCACCTCGCCTC  2481 CTC    _   __    I
                         GGCTC CGCGCC GCCT
                         IIIII IIIIII IIII
                         CCGAG GCGTGG CGGA
                         ___   C   AG  I
GAM172  TNFRSF1B        CTCGGCTCCCTGCAACCTC     2508      GC C   II
                         CTCGGCTCC GC GCCT
                         IIIIIIIII II IIII
                         GAGCCGAGG CG TGGA
                          GA  T  GI
GAM172  TNFRSF1B        CTCGGCTCCCTGCAACCTC      2508 TCACA  G T_  GCG
                         CTC GC CC  CCGCCT
                         III II II  IIIIII
                         GGG CG GG  GGTGGA
                         GA___  A TT A__
GAM172  YY1            CTCGGCTCCCCGCCTCGCCTC    2504       G  __    III
                         CTCGGCTCC CGCC  GCCT
                         IIIIIIIII IIII  IIII
                         GAGCCGAGG GCGG  CGGA
                          G   AG   GII
GAM172  YY1            CTCGGCTCCCCGCCTCGCCTC    2504 TCACA  G TC  GC
                         CTC GC CGC  CGCCTC
                         III II III  IIIIII
                         GGG CG GCG  GCGGAG
                         GA___  G GA  GA
GAM172  ZNF18          ACACTCGGC-CCGCGGCGCC     2479 _     T   C I
                         CACTCGGC CCGCG CGC
                         IIIIIIII IIIII III
                         GTGAGCCG GGCGC GCG
                         T   _   C I
GAM172  ZNF18          ACACTCGGC-CCGCGGCGCC     2479 TCAC    T   C T
                         ACTCGGC CCGCG CGCC
                         IIIIIII IIIII IIII
                         TGAGCCG GGCGC GCGG
                         ____    _   C  C
GAM173  ABCB9          TCGCTCCGCTCTTCCCGCT      2522      G_  G  TTCGA
                         TCGCTCCGC TTC CGCT
                         IIIIIIIII III IIII
                         AGCGAGGCG AAG GCGA
                          AG  G  IIICA
GAM173  ABCB9          TCGCTCCGCTCTTCCCGCT      2522      G_  G  II
                         TCGCTCCGC TTC CGC
                         IIIIIIIII III III
                         AGCGAGGCG AAG GCG
                          AG  G  AI
GAM173  EN2            CGCTC-GCC--CGCGCTTTC     2519 _    CGC
                         GCTC  GTTCGCGCTTT
                         IIII  IIIIIIIIII
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                          CGAG  CGGGCGCGAAA
                            G    ___
GAM173 EN2          CGCTC-GCC--CGCGCTTTC     2519 TC   CGC        G
                          GCTC  GTTCGCGCTTTC
                          ||||  ||||||||||||
                          CGAG  CGGGCGCGAAAG
                            __   ___        G
GAM173 NPTX2        CGCTCCGCGGGAGGCGCCTTCG   2518 G     TTC_      I
                       CTCCGCG  GCGCTTTC
                       |||||||  ||||||||
                       GAGGCGC  CGCGGAAG
                       _       CCTC     I
GAM173 NPTX2        CGCTCCGCGGGAGGCGCCTTCG   2518 TC    TTC_      AC
                       GCTCCGCG  GCGCTTTCG
                       ||||||||  |||||||||
                       CGAGGCGC  CGCGGAAGC
                       __       CCTC     GI
GAM173 PDE5A        GCTCCAGTCGGGCCGGCTTTCGAC 2521 CTC__  C T C     I
                      CG GT CG GCTTTCGA
                      || || || |||||||||
                      GC CG GC CGAAAGCT
                      GGTCA  C  _  _     I
GAM173 PRKAB1       GCTCTCGCAATCGCGCTTT      2520   _  T     II
                      GCTC CGCG TCGCGCTT
                      |||| |||| |||||||||
                      CGAG GCGT AGCGCGAA
                        A    T    AI
GAM173 PRKAB1       GCTCTCGCAATCGCGCTTT      2520 TCG  C T     CGA
                      CTC GCG TCGCGCTTT
                      ||| ||| ||||||||||
                      GAG CGT AGCGCGAAA
                      A__  _  T    TGI
GAM173 UBTF       TCGCTCCGC-TTCGCCATCTCG     2523      G   GC   AC
                      TCGCTCCGC TTCGC TTTCG
                      ||||||||| ||||| |||||
                      AGCGAGGCG AAGCG AGAGC
                        _    GT    II
GAM173 UBTF       TCGCTCCGC-TTCGCCATCTCG     2523 _     G   GC  I
                      CGCTCCGC TTCGC TTTC
                      |||||||| ||||| ||||
                      GCGAGGCG AAGCG AGAG
                      A     _   GT   I
GAM174 COG3        ATGCCCTCATTTCTTTGGAAAG    2526        G___    III
                      ATGCCCTCAT  TTGGGAA
                      ||||||||||  |||||||
                      TACGGGAGTA  AACCTTT
                        AAGA     CII
GAM174 DYT1        GGGATGCCCTCCTGTTCAGGAA    2529        A  _   GCA
                      GGGATGCCCTC TGTT GGGAA
                      ||||||||||| |||| |||||
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                      CCCTACGGGAG ACAA TCCTT
                        G   G    III
GAM174  DYT1        GGGATGCCCTCCTGTTCAGGAA    2529 G        A    _    I
                      GATGCCCTC TGTT GGGA
                      IIIIIIIII IIII IIII
                      CTACGGGAG ACAA TCCT
                        _    G   G   I
GAM174  IL1RAP        GATGCCTT--TCTTGGGAAGC    2528     CTCATG       I
                      GATGCC    TTGGGAA
                      IIIIII    IIIIIII
                      CTACGG    AACCCTT
                        AAAG__    C
GAM174  IL1RAP       GATGCCTT--TCTTGGGAAGC    2528 GGGA    CTCATG
                       TGCC    TTGGGAAGC
                       IIII    IIIIIIIII
                       ACGG    AACCCTTCG
                       ____    AAAG__
GAM174  RGS14        CCCTCCATGTTGGGCAAGC    2527    _    _    III
                      CCCTC ATGTTGGG AAG
                      IIIII IIIIIIII III
                      GGGAG TACAACCC TTC
                        G      G   GII
GAM174  SLC21A3       GGCATTGCCTCAC-TTGGGAAGC    2530 G GC    G       A
                      GG AT  CCTCAT TTGGGAAGC
                      II II  IIIIII IIIIIIIII
                      CC TA  GGAGTG AACCCTTCG
                       G  AC    _        I
GAM174  SLC21A3       GGCATTGCCTCAC-TTGGGAAGC    2530 GGA__    C    G       I
                        TGCC TCAT TTGGGAAG
                        IIII IIII IIIIIIII
                        ACGG AGTG AACCCTTC
                       CCGTA  _   _      I
GAM174  SOST      GGGAAGCC---AGGCTGGGAAGCA    2531    T    CTCAT
                      GGGA GCC   GTTGGGAAGCA
                      IIII III   IIIIIIIIIII
                      CCCT CGG   CGACCCTTCGT
                       T  TC___
GAM174  SOST      GGGAAGCC---AGGCTGGGAAGCA    2531 _  T    CTCAT
                      GGA GCC   GTTGGGAAGC
                      III III   IIIIIIIIII
                      CCT CGG   CGACCCTTCG
                       C  T  TC___
GAM175  CDS2        CCTGCTCAGTTCTGTTCCT       2536  A  _          II
                      CCT CT AGTTCTGTTCC
                      III II IIIIIIIIIII
                      GGA GA TCAAGACAAGG
                        C  G      AI
GAM175  CDS2        CCTGCTCAGTTCTGTTCCT       2536 TATCCTAC          CT
                      TAGTTCTGTTCCT
                      IIIIIIIIIIIII
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                              GTCAAGACAAGGA
                    CGA_____          CA
GAM175 CRY2          TCCTACCACTACGTTCTGTTC  2538        ____      IIIG
                     TCCTACTA  GTTCTGTT
                     |||||||   ||||||||
                     AGGATGGT  CAAGACAA
                        GATG      GIII
GAM175 CRY2          TCCTACCACTACGTTCTGTTC  2538 TATC   _        CTCTG
                        CTACTA GTTCTGTTC
                        |||||| |||||||||
                        GGTGAT CAAGACAAG
                        GAT_   G    TCIII
GAM175 GPR61          ATCCTGTTGGCTCTGTTCCT     2535   ACTA        I
                        TCCT  GTTCTGTTCC
                        ||||  ||||||||||
                        AGGA  CGAGACAAGG
                         CAAC       I
GAM175 GPR61          ATCCTGTTGGCTCTGTTCCT     2535 TA  ACTA       CT
                        TCCT  GTTCTGTTCCT
                        ||||  |||||||||||
                        AGGA  CGAGACAAGGA
                         __  CAAC       CI
GAM175 OTX1          TATCTTAA-AGTTCTGTTTCCT  2537   C CT      _  CTG
                     TATC TA  AGTTCTGTT CCT
                     |||| ||  |||||||||| |||
                     ATAG AT  TCAAGACAA GGA
                       A T_       A  III
GAM175 OTX1          TATCTTAA-AGTTCTGTTTCCT  2537   C CT      _  I
                     ATC TA  AGTTCTGTT CC
                     ||| ||  |||||||||| ||
                     TAG AT  TCAAGACAA GG
                       A T_      A I
GAM175 POP4          TCCTGCCAGT-CTGTTCCTC    2539 _  A   T    I
                     CCT CTAGT CTGTTCCT
                     ||| ||||| ||||||||
                     GGA GGTCA GACAAGGA
                      A C   _    I
GAM175 POP4          TCCTGCCAGT-CTGTTCCTC    2539 TATC A   T
                     CT CTAGT CTGTTCCTCT
                     || ||||| |||||||||||
                     GA GGTCA GACAAGGAGG
                      ____  C   _
GAM175 TFE3          ATCCT-C-ACTTCTGTTCCT    2534 _  AC G      I
                     TCCT  TA TTCTGTTCC
                     ||||  || |||||||||
                     AGGA  GT AAGACAAGG
                      T  __  G    I
GAM175 TFE3          ATCCT-C-ACTTCTGTTCCT    2534 TA  AC G       C
                     TCCT  TA TTCTGTTCCT
                     ||||  || ||||||||||
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                              AGGA  GT AAGACAAGGA
                              __   __ G       A
GAM176 ADCY6          TACCCTCACCCCTACCCCATGGCACC 2562        _  A __    CII
                      TACCCTCACCCC ATC CA  GCACC
                      |||||||||| ||| || |||||
                      ATGGGAGTGGGG TGG GT CGTGG
                              A  G AC    III
GAM176 ASPH          ACCCTCA-CCAATCAGAGCA      2546 TA     CC   C   CC
                      CCCTCACC  ATCA AGCA
                      |||||||| |||| ||||
                      GGGAGTGG  TAGT TCGT
                              __      T_  C   TI
GAM176 ATF5        CCCTCACCCAGACACAGCCCC      2557 TACC    CAT   A
                      CTCACCC  CACAGC CCC
                      |||||||  |||||| |||
                      GAGTGGG  GTGTCG GGG
                              ___       TCT      _
GAM176 CDKN1A        ACCCTCACCCC--CACAGC      2545 TA      AT    AC
                      CCCTCACCCC CACAGC
                      |||||||||| ||||||
                      GGGAGTGGGG GTGTCG
                              __      __   AI
GAM176 CELSR2        CCCCCACCCACATCACAGCA      2553 TACC    _       CC
                      CTCACCC CATCACAGCA
                      ||||||| ||||||||||
                      GGGTGGG GTAGTGTCGT
                              ___       T      TT
GAM176 ENO2        ACCCTGACGCTCCCATCACAG      2542 TA   C ___        CACCC
                      CCCT AC  CCCATCACAG
                      |||| ||  ||||||||||
                      GGGA TG  GGGTAGTGTC
                              __   C  CGA       TIIIC
GAM176 FADD        CCTCTCCCCACCACAGCACCC      2561 TACCCTCA
                      CCCCATCACAGCACCC
                      ||||||||||||||||
                      GGGGTGGTGTCGTGGG
                          GA_____
GAM176 FLNA        CCCTCACCCC-TCCCAGAACC      2558 TACC     A A  C
                      CTCACCCC TC CAG ACC
                      |||||||| || ||| |||
                      GAGTGGGG AG GTC TGG
                              ___      _  G   T
GAM176 FUT1        CCCTCACCCCACGTTCACA      2555 TACC       ___   GCACC
                      CTCACCCCA TCACA
                      ||||||||| |||||
                      GAGTGGGGT AGTGT
                          ___        GCA   AAIII
GAM176 GAS1        ACCCTCACCCC--CACGTCAC      2547 TA      AT AG  C
                      CCCTCACCCC CAC CAC
                      |||||||||| ||| |||
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                              GGGAGTGGGG GTG GTG
                              __       __  CA  A
GAM176  GJB1          CCCTCACCCCA-GACACCTCC    2559 TACC      TCACA
                              CTCACCCCA    GCACC
                              |||||||||    |||||
                              GAGTGGGGT    TGTGG
                              ____         C____
GAM176  GJB1          CACCCACATGTCCACAGCACCC   2550 TACCCTCACCCCA
                                  TCACAGCACCC
                                  |||||||||||
                                  GGTGTCGTGGG
                          GTACA_____
GAM176  GYPC          CCCTCACCCTCAACA-AGGAC    2554 TACC    _ T  C  C  C
                              CTCACCC CA CA AG AC
                              ||||||| || || || ||
                              GAGTGGG GT GT TC TG
                              ____      A  T _  C  A
GAM176  HAP1          CCCTCACCCACCCACA-CAC     2556 TACC    CA   G   C
                              CTCACCC TCACA CAC
                              ||||||| ||||| |||
                              GAGTGGG GGTGT GTG
                              ____      TG   _  T
GAM176  HMGE           ACACCCACCCCATCAACAGCA    2543 TACC       _   CCC
                              CTCACCCCATCA CAGCA
                              |||||||||||| |||||
                              GGGTGGGGTAGT GTCGT
                          GT__         T  CII
GAM176  LRP5          CCCTGCCCACCCCATCACAG     2551 TACC          CACC
                              CTCACCCCATCACAG
                              |||||||||||||||
                              GGGTGGGGTAGTGTC
                          GAC_           AAII
GAM176  LTB          CCCTCACCCCACCATCACGGCCCC  2552 TACC          _ __ A  I
                              CTCACCCCATCA CA GC CCC
                              |||||||||||| || || |||
                              GAGTGGGGTGGT GT CG GGG
                              ____         A GC _  T
GAM176  MTNR1A         TACTCTCACCCCAGCCCTGAACC   2563  C      _ ACAGC  CI
                              TAC CTCACCCCA TC    ACC
                              ||| ||||||||| ||     |||
                              ATG GAGTGGGGT GG    TGG
                               A     C GACT_  II
GAM176  PDYN          ACCCTT-CCCCATCACAG-ACCC   2549 TA  CA      C
                              CCCT CCCCATCACAG ACCC
                              |||| |||||||||| ||||
                              GGGA GGGGTAGTGTC TGGG
                              __  A_       _
GAM176  SGCA          ACTCTCACCCCACCCCACCCCC    2548 TACC       ACA  A
                              CTCACCCCATC  GC CCC
                              |||||||||||  || |||
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                        GAGTGGGGTGG  TG GGG
                 GA__          GG_ G
GAM176  SLC6A8          ACCCTCACCCAGCCCCAGC      2544 TA       CA  A   ACC
                        CCCTCACCC  TC CAGC
                        |||||||||  ||  ||||
                        GGGAGTGGG  GG GTCG
                          __        TC  G   GII
GAM176  ZNF205          CCTCACCCCATGCCCTCACC     2560     CAC  A   A  ACC
                        TACCCT  CCC TCAC GC
                        ||||||   |||  ||||  ||
                        GTGGGG  GGG AGTG CG
                          TAC  _   G  GII
GAM177  ACADS           GGGACAGGTGTGTTTATTA      2575  A       ATTII
                         GGGA AGGTGTGTT
                         |||| |||||||||
                         CCCT TCCACACAA
                           G     ATAAT
GAM177  ATBF1           ATTTTTGAAATTGGTTTGTTATTAA 2572   GG AA  G     I
                        TTTG  A  GGT TGTTATTA
                        ||||  |  |||  ||||||||
                        AAAC  T  CCA ACAATAAT
                          TT AA  A       I
GAM177  ATBF1           ATTTTTGAAATTGGTTTGTTATTAA 2572 AA   GG AA  G      II
                         TTTG  A  GGT TGTTATTAA
                         ||||  |  |||  |||||||||
                         AAAC  T  CCA ACAATAATT
                          AA  TT AA  A       AI
GAM177  CANX            ATTTGGGAAA-GTCTGCTAT      2573 _        G G    I
                         TTTGGGAAAG T TGTTA
                         |||||||||| |  |||||
                         AAACCCTTTC A ACGAT
                           T     _G   I
GAM177  CANX            ATTTGGGAAA-GTCTGCTAT      2573 AA       G G    TA
                         TTTGGGAAAG T TGTTAT
                         |||||||||| |  |||||
                         AAACCCTTTC A ACGATA
                           __      _G   CI
GAM177  DAPP1           AATTCTGGGAAAGGGATTGTTAT   2566 A        TG_    I
                         TTTGGGAAAGG TGTTA
                         ||||||||||  |||||
                         AGACCCTTTCC ACAAT
                           _        CTA   I
GAM177  DAPP1           AATTCTGGGAAAGGGATTGTTAT   2566 AA_      TG_    TAAI
                         TTTGGGAAAGG TGTTAT
                         ||||||||||  |||||
                         AGACCCTTTCC ACAATA
                          TTA      CTA   IIIA
GAM177  DIBD1           TTTGGGGCCACAGGTGTGTT      2580     AA___      III
                         TTTGGG  AGGTGTGT
                         ||||||   ||||||||
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                        AAACCC    TCCACACA
                         CGTG        AII
GAM177 DIBD1        TTTGGGGCCACAGGTGTGTT    2580 AATTT  AA__        ATTA
                       GGG    AGGTGTGTT
                       III   IIIIIIIII
                       CCC   TCCACACAA
                      AC___    GGTG        CIII
GAM177 FBXL7        AATCTGGGAAAGGGCCATGTGTTTATTA2568          ____   _   AIII
                     AATTTGGGAAAGG   TGTGTT ATTA
                     IIIIIIIIIIII    IIIIII IIII
                     TTAGACCCTTTCC   ACACAA TAAT
                          CGGT    A   IIIA
GAM177 FBXL7        AATCTGGGAAAGGGCCATGTGTTTATTA2568 TG       ____     ATTI
                         GGAAAGG   TGTGTT
                         IIIIIII   IIIIII
                         CCTTTCC   ACACAA
                         __        CGGT    AIII
GAM177 FNTB         TGCACCAAGCGTGG-CCTTG    2576 _   A        CGTI
                        GCG  CAAGCGTGGTC
                        III  IIIIIIIIIII
                        CGT  GTTCGCACCGG
                        A   G       AAII
GAM177 FNTB         TGCACCAAGCGTGG-CCTTG    2576 TGTTGCGA        CGTG
                            CAAGCGTGGTC
                            IIIIIIIIIII
                            GTTCGCACCGG
                        TG_____         AACC
GAM177 GPR85        AATATGG-AATTCTGTGTTATTA   2570 AATTTG   AGG       A
                            GGAA   TGTGTTATTA
                            IIII   IIIIIIIIII
                            CCTT   ACACAATAAT
                        TTATA_   AAG        I
GAM177 GPR85        AATATGG-AATTCTGTGTTATTA   2570 ATTTG   AGG       I
                            GGAA   TGTGTTATT
                            IIII   IIIIIIIII
                            CCTT   ACACAATAA
                        TTATA   AAG        I
GAM177 KCNK4        TGGGACA-GCGTGGT-CGTG    2578 C   A       CGI
                        TG DACA GCGTGGTC
                        II IIII IIIIIIII
                        AC CTGT CGCACCAG
                        C   _    CAC
GAM177 KCNK4        TGGGACA-GCGTGGT-CGTG    2578 TGTTGC   A     C
                         GACA GCGTGGTC GT
                         IIII IIIIIIII II
                         CTGT CGCACCAG CA
                        _____   _   __
GAM177 KPNA1        ATTTGGGAAAATTGGAGGGTTTTT 2571 AA        ___  TGT  ATTAAI
                         TTTGGGAAA GG GTT
                         IIIIIIIII II III
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                        AAACCCTTT  CC  CAA
                        __      TAA  TCC  AAAAII
GAM177 LDB3        TTTGGGAAAGCTGCTTGTT    2582       G  GTIII
                        TTTGGGAAAG TGT
                        |||||||||| |||
                        AAACCCTTTC ACG
                             G   AACAA
GAM177 LDB3        TTTGGGAAAGCTGCTTGTT    2582 AATT      G  __   ATTA
                        TGGGAAAG TGT  GTT
                        |||||||| ||| |||
                        ACCCTTTC ACG  CAA
                        ____        G  AA  CGII
GAM177 MAP3K4        GACAGAGGCGATGGTCCGTG     2574  A__  _       III
                        GACA  GCG TGGTCCGT
                        ||||  ||| ||||||||
                        CTGT  CGC ACCAGGCA
                        CTC  T    CII
GAM177 MLN      AATTTGCTTTGGAAAGGTGTTTT   2567   ____        GTIIIA
                        AATTTG  GGAAAGGTGT
                        ||||||  ||||||||||
                        TTAAAC  CCTTTCCACA
                        GAAA      AAAIII
GAM177 MLN      AATTTGCTTTGGAAAGGTGTTTT   2567   ____        GTTATTAAI
                        AATTTG  GGAAAGGTGT
                        ||||||  ||||||||||
                        TTAAAC  CCTTTCCACA
                        GAAA        AAAIIIAAT
GAM177 SHOX        TTTGGGAAACGGTGTGTGATT    2581 AATT    _    T  AA
                        TGGGAAA GGTGTGT ATT
                        ||||||| ||||||| |||
                        ACCCTTT CCACACA TAA
                        ____      G    C  AC
GAM177 SHOX        TTTGGGAAACGGTGTGTGATT    2581 T    _    TATI
                        TGGGAAA GGTGTGT
                        ||||||| |||||||
                        ACCCTTT CCACACA
                        _     G    CTAI
GAM177 SORBS1      TGAGATAAGATAGTGTTATTAA    2579 AATTTGGGA   _
                        AAGGT GTGTTATTAA
                        ||||| ||||||||||
                        TTCTA CACAATAATT
                        TA_____   T
GAM177 SORBS1      TGAGATAAGATAGTGTTATTAA    2579 GGGA    _       I
                        AAGGT GTGTTATTA
                        ||||| |||||||||
                        TTCTA CACAATAAT
                        CTA_  T    I
GAM177 TPMT       AATTTGGG-AATGTTTGTT    2569       AG  G   ATT
                        AATTTGGGAA GT TGTT
                        |||||||||| || ||||
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                              TTAAACCCTT CA ACAA
                                 A_  A   III
GAM177  TPMT          AATTTGGG-AATGTTTGTT    2569       AGG_  GTI
                         AATTTGGGAA  TGT
                         IIIIIIIIII  III
                         TTAAACCCTT  ACA
                                 ACAA  AII
GAM177  YWHAG           TGCTA-AAGA-TGGTCCGTG    2577 _ GAC  C      I
                          GC  AAG GTGGTCCGT
                          II  III IIIIIIIII
                          CG  TTC TACCAGGCA
                          A AT_  _      I
GAM178  CPD           TATAAGCAGC-AGCACCTGT     2591 ATCATCATC      I
                          TAGCACCTG
                          IIIIIIIII
                          GTCGTGGAC
                          ATATTCGTC      I
GAM178  CPD           TATAAGCAGC-AGCACCTGT     2591 TATCATCATC      CCG
                          TAGCACCTGT
                          IIIIIIIIII
                          GTCGTGGACA
                          ATATTCGTC_     III
GAM178  CTSL          TCTTCCAGTCCCTGTCCGG      2594 A   CA      II
                          TC TCTAG  CCTGTCCG
                          II IIIII  IIIIIIIII
                          AG AGGTC  GGACAGGC
                           A   AG     CI
GAM178  MTMR3        TATCATAACCTCTTGGCACCTGTC 2590    C  A___      CGGI
                         TATCAT ATCT   GCACCTGTC
                         IIIIII IIII   IIIIIIIII
                         ATAGTA TGGA   CGTGGACAG
                            T  GAAC        IIIG
GAM178  MTMR3        TATCATAACCTCTTGGCACCTGTC 2590 ATC  A  A_       I
                         ATC TCT  GCACCTGT
                         III III  IIIIIIII
                         TGG AGA  CGTGGACA
                         TAT  _  AC     I
GAM178  NFKB2         TCCTCCAGCCGCCTGTCCGG     2593 A   A_      II
                         TC TCTAGC  CCTGTCCG
                         II IIIIII  IIIIIIII
                         AG AGGTCG  GGACAGGC
                           G   GC     CI
GAM178  RFC4         ATCATCATCCAG--CTTGTCC     2586 _        ACC  I
                          TCATCATCTAGC  TGTC
                          IIIIIIIIIIII  IIII
                          AGTAGTAGGTCG  ACAG
                          T       A__ I
GAM178  RFC4         ATCATCATCCAG--CTTGTCC     2586 TA       ACC   G
                          TCATCATCTAGC  TGTCC
                          IIIIIIIIIIII  IIIII
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                        AGTAGTAGGTCG  ACAGG
                        __         A__    A
GAM178 SCD              ATCATCATCTTTAGCATCCTG   2585        __  _  III
                        ATCATCATCT AGCA CCT
                        IIIIIIIII IIII III
                        TAGTAGTAGA TCGT GGA
                                  AA   A  CII
GAM178 SCD              ATCATCATCTTTAGCATCCTG   2585 TA     __  _   TCCGG
                        TCATCATCT AGCA CCTG
                        IIIIIIII IIII IIII
                        AGTAGTAGA TCGT GGAC
                        __        AA   A   CIIIG
GAM178 SLC7A7           TATTGTCATCCAGCACCTGT   2592  CA          CCG
                        TAT TCATCTAGCACCTGT
                        III IIIIIIIIIIIIIII
                        ATA AGTAGGTCGTGGACA
                          AC          III
GAM178 SLC7A7           TATTGTCATCCAGCACCTGT   2592 ATCA        I
                        TCATCTAGCACCTG
                        IIIIIIIIIIIIII
                        AGTAGGTCGTGGAC
                        TAAC          I
GAM178 TDG             ATCCT-TACCGCCTGTCCGG    2587 TCA  A A_    I
                        TCT GC  CCTGTCCG
                        III II  IIIIIIII
                        GGA TG  GGACAGGC
                        TA_  A GC    I
GAM178 TSNAX           CAACATCTGGGCACCTGTC     2588  T   A_     II
                        CA CATCT GCACCTGT
                        II IIIII IIIIIIII
                        GT GTAGA CGTGGACA
                          T   CC     GI
GAM178 TSNAX           CAACATCTGGGCACCTGTC     2588 TATCAT   A_      CG
                        CATCT GCACCTGTC
                        IIIII IIIIIIIII
                        GTAGA CGTGGACAG
                        _____     CC      TT
GAM178 WRN            CATCTTCC--CACCTGTCC      2589   A AG     I
                        CATC TCT CACCTGTC
                        IIII III IIIIIIII
                        GTAG AGG GTGGACAG
                            A  __     G
GAM178 WRN            CATCTTCC--CACCTGTCC      2589 TATCATCA AG
                        TCT CACCTGTCC
                        III IIIIIIIII
                        AGG GTGGACAGG
                        GA_____   __
GAM179 MKKS          TTTTTATTTTGTAAACCACAT     2598 TATTTT   GC__    GA
                        TTATTT AACTACAT
                        IIIIII IIIIIIII
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                              AATAAA   TTGGTGTA
                              _____      ACAT      AA
GAM179 NDP          TTTTATATTTGCAAC-ACA       2599 TATTTTT        T
                              TATTTGCAAC ACAT
                              |||||||||| ||||
                              ATAAACGTTG TGTG
                         AAT____       _
GAM179 PCDHGA8      ATTGTTTTATTTGGTTTAAACTAC  2597 TATT       C____      ATGAI
                              TTTTATTTG   AACTAC
                              |||||||||   ||||||
                              AAAATAAAC   TTGATG
                         AAC_        CAAAT    AIIIA
GAM180 ADORA2B      ATTTGTCAATCCTTGGAGCCTA    2606 ATTTCTG            GC
                              GATCCTTGGAGCTTA
                              |||||||||||||||
                              TTAGGAACCTCGGAT
                    TAAACAG              II
GAM180 BRCA1        TTTCTGGATGCCTCTCAGCT      2615 AT      _   GG    TAG
                              TTCTGGAT CCTT  AGCT
                              |||||||| |||| ||||
                              AAGACCTA GGAG  TCGA
                         __       C   AG   CII
GAM180 CRY2         CTGAGTCCTTGGAGCTCAGC      2608 ATTTCTGGA
                              TCCTTGGAGCTTAG
                              ||||||||||||||
                              AGGAACCTCGAGTC
                    C_____
GAM180 DRD3         ATTTCTGGAGACCGAGGAGTTTA   2602      T_ TT  C  GCI
                              ATTTCTGGA CC GGAG TTA
                              ||||||||| || |||| |||
                              TAAAGACCT GG  CCTC AAT
                         CT CT   A  III
GAM180 GIP          ATTTCTGGA-CCTTCTGAGC      2603        T  G_  TTAG
                              ATTTCTGGA CCTT GAGC
                              ||||||||| |||| ||||
                              TAAAGACCT GGAA  CTCG
                         _   GA   IIIC
GAM180 GRF2         TTCAGGGACCCTGGAGCTTAG     2611 ATTTCT    T      C
                              GGATCCT GGAGCTTAG
                              ||||||| |||||||||
                              CCTGGGA CCTCGAATC
                    GTC___        _       C
GAM180 HUNK         TTTTGGGATCCTTGGA-CTGAG    2618 ATTTCT       G T C
                              GGATCCTTGGA CT AG
                              ||||||||||| || ||
                              CCTAGGAACCT GA TC
                         AAAC__        _ C T
GAM180 ITGA5        TTCTGATTCCCCTTGGAGCT      2610 ATTT  A__      TAG
                              CTGG  TCCTTGGAGCT
                              ||||  ||||||||||
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                              GACT  GGGAACCTCGA
                    ____      AAG          CCI
GAM180 NOV          TTTCCTTGGAT--TTGGAGCTT   2614 A TC   CC      AG
                       TT TGGAT TTGGAGCTT
                       II IIIII IIIIIIIII
                       AG ACCTA AACCTCGAA
                          A  GA      __      CI
GAM180 PCDHA9       ATCTCTGGATCCCTGTGAG      2604          _  CTTAG
                       ATTTCTGGATCCTTG GAG
                       IIIIIIIIIIIIII III
                       TAGAGACCTAGGGAC CTC
                              A  IIICG
GAM180 PCDHB16        TTGCTGGATCC-TGGAGCT       2616 ATTT     T   TA
                        CTGGATCCT GGAGCT
                        IIIIIIIII IIIIII
                        GACCTAGGA CCTCGA
                     AC__      _     CI
GAM180 PIK3C2B       TTTCTG-ATCCTTGGA-ATTAG   2617 AT   G      C
                       TTCTG ATCCTTGGAG TTAG
                       IIIII IIIIIIIIII IIII
                       AAGAC TAGGAACCTT AATC

                        __    _     __
GAM180 PIK3C2B       TTCGGGCTCCT--GAGCTTAGC   2613 ATTTCT A_   TG
                         GG TCCT GAGCTTAG
                         II IIII IIIIIIII
                         CC AGGA CTCGAATC
                     G_____   CG    __
GAM180 PTTG1         TCTGGATTATTGCAGGTCTTA    2609 ATTTCT   CC  G __
                         GGAT TTG AG CTTAGC
                         IIII III II IIIIII
                         CCTA AAC TC GAATTG
                         _____   AT  G  CA
GAM180 SLC21A9       ATCTCAGGA-CCT-GGAGCTTAGC 2607    T T T
                        ATTTC GGA CCT GGAGCTTAGC
                        IIIII III III IIIIIIIIII
                        TAGAG CCT GGA CCTCGAATCG
                        T  _  _
GAM180 TGFBR2        ATTTGGGG---CTTGGAGCTTA   2605 ATTTC ATC      G
                          TGG CTTGGAGCTTA
                          III IIIIIIIIIII
                          ACC GAACCTCGAAT
                     TAA__  CC_          I
GAM180 ZNF26         TTCTG----CTTGGAGCTGAG    2612 ATTT GATC     T
                        CTG  CTTGGAGCT A
                        III  IIIIIIIII I
                        GAC  GAACCTCGA T
                     ____  ____            C
GAM181 ADCY6         GGGTGGCAGAGGTTGCAGTGA   2634 TG G T CAG     AGTG
                        GG GG GG  GCAGTGA
                        II II II  IIIIIII
```

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                        CC TC CC  CGTCACT
                        __ G T AA_    CGTT
GAM181 CAMLG            GGGGTGGCAGTGGCGGTGATGT   2632 TGGGGG    __  A  A  G
                        GTGGCA  GGC GTGA GT
                        |||||| ||| |||| ||
                        CACCGT CCG CACT CA
                        _____      CA  C   A  A
GAM181 CASP8           TGGCGGGGTACAGGCAGGCAG-GAAG 2635  _  ___      T TGII
                        TGG GGGGT  GGCAGGCAG GAAG
                        ||| |||||  ||||||||| ||||
                        ACC CCCCA  CCGTCCGTC CTTC
                          G   TGT      _   IIIG
GAM181 CSF1R           TGGGGAAGTGGCAGGCAGGTGCAG  2637     _       _ A TGI
                        TGGGGG GTGGCAGGCAG TG AG
                        |||||| ||||||||||| || ||
                        ACCCCT CACCGTCCGTC AC TC
                          T        C G III
GAM181 EFNB1          TGGGGGGTGG--GG--GTGAA    2642      CA  CA   G
                        TGGGGGGTGG GG GTGAA
                        |||||||||| || |||||
                        ACCCCCCACC CC CACTT
                                __  __   I
GAM181 FOXD2          GGGGGACTGAGGCAGGCAGGGA   2621 T  G __      T AGTG
                        GGGGG T GGCAGGCAG GA
                        ||||| | ||||||||| ||
                        CCCCT A CCGTCCGTC CT
                          _   G CT      C CIII
GAM181 GAS11          TGGGCGGTGGCAGGTAGGTGA   2640   G     CA_   AGTG
                        TGGG GGTGGCAGG GTGA
                        |||| ||||||||| ||||
                        ACCC CCACCGTCC CACT
                          G    ATC  IIIG
GAM181 GPT          GGAGGTGGCAGGACCAGAAGTG   2628 TGGG       _ AGT
                        GGGTGGCAGG C  GAAGTG
                        |||||||||| |  ||||||
                        TCCACCGTCC G  CTTCAC
                        ____        T GT_
GAM181 HHLA1         TGGGGGGTGGTATGGAGAGA    2641      CA_ C T AGT
                        TGGGGGGTGG  GG AG GA
                        ||||||||||  || || ||
                        ACCCCCCACC  CC TC CT
                         ATA _ T III
GAM181 KRTHB1        TGTGGGGTGGCAGAGCCCAGAAGTG 2639 TGG      _ AGT   II
                        GGGGTGGCAG GC  GAAGTG
                        |||||||||| || |||||
                        CCCCACCGTC CG  CTTCAC
                         ACA     T GGT   II
GAM181 MASP1         TGGGGTGTGCCCAGGCAGTG    2638   G G_      AAGT
                        TGGGG GTG CAGGCAGTG
                        ||||| ||| |||||||||
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                          ACCCC CAC  GTCCGTCAC
                             A  GG      IIIG
GAM181  MGAT4B            GGGGGGTGGCTGCTGCAGT    2622 TG       AG__     GAAGT
                             GGGGGTGGC  GCAGT
                             |||||||||  |||||
                             CCCCCACCG  CGTCA
                                   ACGA    AIIIG
GAM181  MPP2              GGGGTGGCAGGGGGCAGTG    2631 TGGGGG    ___     AAGT
                             GTGGCA  GGCAGTG
                             ||||||  |||||||
                             CACCGT  CCGTCAC
                            _____     CCC      ACGI
GAM181  NDRG3             GGGGGTGGGCAGGCAGAGA    2626 TGGG    _     T  AGT
                             GGGTGG CAGGCAG GA
                             |||||| ||||||| ||
                             CCCACC GTCCGTC CT
                            ____     C   T CTI
GAM181  NFE2L1           GGAGTGGCAAGGCAGTGAA    2633 TGGGGG    _       GT
                             GTGGCA GGCAGTGAA
                             |||||| |||||||||
                             CACCGT CCGTCACTT
                            _____      T      AC
GAM181  NIPSNAP1        GGAGGGAGGCAGGCAGGGAA    2624 TG   T      T  T
                             GGGGG GGCAGGCAG GAAG
                             ||||| ||||||||| ||||
                             CTCCC CCGTCCGTC CTTT
                            __     T      C   I
GAM181  PLXNB3           GGGAGGTGGCAGGCAGGGA    2623 TG          T  AGT
                             GGGGGTGGCAGGCAG GA
                             ||||||||||||||| ||
                             CCTCCACCGTCCGTC CT
                            __           C  CII
GAM181  RGS14           GGTGGCGGGCAGGCAGTGGAG    2625 TGGGG    _      A  TG
                             GGTGG CAGGCAGTG AG
                             ||||| |||||||||| ||
                             CCGCC GTCCGTCAC TC
                            CA___     C      C  TI
GAM181  RNF26          TGGAGGGGTGGGCAGGCAGGGAAG    2636 _    _       T  TGI
                             TGG GGGGTGG CAGGCAG GAAG
                             ||| ||||||| ||||||| ||||
                             ACC CCCCACC GTCCGTC CTTC
                              T      C       C   III
GAM181  SRC            GGGGGTGGCA--CA--GAAGTG    2629 TGGG     AG  GT
                             GGGTGGC GCA  GAAG
                             ||||||| |||  ||||
                             CCCACCG TGT  CTTC
                            ____      __    __
GAM181  TNNI3          GGGGGTGGCGGGTACTG-AGTG    2630 TGGG     A CAG  A
                             GGGTGGC GG  TGA GTG
                             ||||||| ||  ||| |||
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                        CCCACCG CC  ACT CAC
                        ____      C ATG  _
GAM181  TUBA2           GGGGGTGGCAGTGGAGTGGAG   2627 TGGG      GC_  A TG
                        GGGTGGCAG  AGTG AG
                        ||||||||| |||| ||
                        CCCACCGTC  TCAC TC
                                  ACC   C TT
GAM182  BMP4            TGCCACACTCACCT-AGCTTCC   2663      GT CT   CG
                        TGCCACACT CCT GCTTCC
                        ||||||||| ||| ||||||
                        ACGGTGTGA GGA CGAAGG
                                GT  T_    ||
GAM182  BMP4            TGCCACACTCACCT-AGCTTCC   2663 _    GT CT   I
                         GCCACACT CCT GCTTC
                         |||||||| ||| |||||
                         CGGTGTGA GGA CGAAG
                              A   GT T_  I
GAM182  CAPN10          TGCCAAACTGGGTCCTCTGCT    2658   C __      TCCCG
                        TGCCA ACT GTCCTCTGCT
                        ||||| ||| ||||||||||
                        ACGGT TGA CAGGAGACGA
                            T CC      |||GC
GAM182  CAPN10          TGCCAAACTGGGTCCTCTGCT    2658   C __      |||
                        TGCCA ACT GTCCTCTGC
                        ||||| ||| |||||||||
                        ACGGT TGA CAGGAGACG
                            T CC     A||
GAM182  CLASP1          TGGCACCCAG-CCTCTGCTT     2662  C A T     CCC
                        TG CAC CTG CCTCTGCTT
                        || ||| ||| ||||||||||
                        AC GTG GGT GGAGACGAA
                           C   _ C     |||
GAM182  CLASP1          TGGCACCCAG-CCTCTGCTT     2662 _C A T    I
                         G CAC CTG CCTCTGCT
                         | ||| ||| |||||||||
                         C GTG GGT GGAGACGA
                          A C  _ C   I
GAM182  FCMD            TGGCTCACTGCAGACTCTGCTTCCCG 2659 GCCA    C__       I
                           CACTGT CTCTGCTTCCC
                           |||||| |||||||||||
                           GTGACG GAGACGAAGGG
                          GA__   TCT      I
GAM182  FCMD            TGGCTCACTGCAGACTCTGCTTCCCG 2659 T_ CA    C__       II
                         GC CACTGT CTCTGCTTCCCG
                         || |||||| |||||||||||
                         CG GTGACG GAGACGAAGGGC
                          AC A_   TCT      II
GAM182  GAA             CACACAGGC-TCTGCTTCCC     2646 _  TGTC     I
                         ACAC  CTCTGCTTCC
                         ||||  |||||||||
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                        TGTG   GAGACGAAGG
                       G    TCC_          I
GAM182 GAA             CACACAGGC-TCTGCTTCCC    2646 TGCCACACTGTC
                            CTCTGCTTCCC
                            |||||||||||
                            GAGACGAAGGG
                        TGTCC_____
GAM182 GAA             CACTGTCCTACCTGCTGCC    2649        __    TCIII
                         CACTGTCCT  CTGCT
                         |||||||||  |||||
                         GTGACAGGA  GACGA
                          TG    CGGII
GAM182 GAA             CACTGTCCTACCTGCTGCC     2649 TGCCACA   T  _    CC
                            CTG CCT CTGCTTC
                            ||| ||| ||||||
                            GAT GGA GACGGAG
                        AG_____  _  C    TA
GAM182 GJB3           TGCCACACTG-CC-CTGCATTTCCC 2660      T  T  __   GI
                         TGCCACACTG CC CTGC  TTCCC
                         |||||||||| || |||| |||||
                         ACGGTGTGAC GG GACG  AAGGG
                            _ _   TA    II
GAM182 GJB3           TGCCACACTG-CC-CTGCATTTCCC 2660      T  T  __   I
                          GCCACACTG CC CTGC  TTCC
                          ||||||||| || |||| ||||
                          CGGTGTGAC GG GACG  AAGG
                            _ _   TA    I
GAM182 GNA11          TGCAACACCTACCTCTGCTT    2661  C   GT      CCC
                         TGC ACACT CCTCTGCTT
                         ||| ||||| ||||||||||
                         ACG TGTGG GGAGACGAA
                           T   AT      III
GAM182 GNA11          TGCAACACCTACCTCTGCTT     2661  C   GT    I
                          GC ACACT CCTCTGCT
                          || ||||| |||||||||
                          CG TGTGG GGAGACGA
                           T   AT    I
GAM182 GNGT2          GCCACACTGTCCTCAGAGTGTTCCC 2656 CCA        ____ C  I
                          CACTGTCCTC  TG TTCC
                          ||||||||||  || ||||
                          GTGACAGGAG  AC AAGG
                            ___    TCTC _  I
GAM182 GNGT2          GCCACACTGTCCTCAGAGTGTTCCC 2656 TG          ____ C  II
                          CCACACTGTCCTC  TG TTCCCG
                          |||||||||||||  || ||||||
                          GGTGTGACAGGAG  AC AAGGGT
                            __      TCTC _  II
GAM182 KITLG         CACTGTCC-CTGCTTCCCG      2650      T      I
                          CACTGTCC CTGCTTCCC
                          |||||||| |||||||||
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                        GTGACAGG GACGAAGGG
                           _        C
GAM182 MYO1D    TGCCCCGCT-TCCT--GCTTCCCG  2665   ACA   CC
                        TGCC  CTGT  TCTGCTTCCCG
                        ||||  ||||  |||||||||||
                        ACGG  GGCG  GGACGAAGGGC
                           ___       AA
GAM182 MYO1D    TGCCCCGCT-TCCT--GCTTCCCG  2665_  ACA   CC
                         GCC  CTGT  TCTGCTTCCC
                         |||  ||||  ||||||||||
                         CGG  GGCG  GGACGAAGGG
                         A    ___    AA
GAM182 MYO1F    CCACGCCG--CTCTGCTTCACG    2654   A TC    CI
                        CCAC CTG  CTCTGCTTC
                        |||| |||  |||||||||
                        GGTG GGC  GAGACGAAG
                         C   __       TG
GAM182 MYO1F    CCACGCCG--CTCTGCTTCACG    2654 TGCCACACT  _      C
                         GTC CTCTGCTTC C
                         ||| ||||||||| |
                         CGG GAGACGAAG G
                        TG_____   C        T
GAM182 PLCB4    CCTCAGTGTCCTCTG-TTCCC     2652 CA_ C      C  I
                         CA TGTCCTCTG TTCC
                         || |||||||||| ||||
                         GT ACAGGAGAC AAGG
                         GGA C      _    I
GAM182 PLCB4    CCTCAGTGTCCTCTG-TTCCC     2652 TGCCA C      C
                         CA TGTCCTCTG TTCCC
                         || |||||||||| |||||
                         GT ACAGGAGAC AAGGG
                         A____ C      _
GAM182 RARB     CCACAGCTTTCACTCTGCTTC     2651   _ G _     III
                        CCACA CT TC CTCTGCTT
                        ||||| || || |||||||||
                        GGTGT GA AG GAGACGAA
                          C A T     GII
GAM182 RARB     CCACAGCTTTCACTCTGCTTC     2651 TGCC _ G _     CCG
                        ACA CT TC CTCTGCTTC
                        ||| || || ||||||||||
                        TGT GA AG GAGACGAAG
                         ____  C A T    TAI
GAM182 SCN2B    CACTGCAACCTCTGCTTCCCG     2648   __        III
                        CACTGT CCTCTGCTTCCC
                        |||||| |||||||||||
                        GTGACG GGAGACGAAGGG
                          TT     CII
GAM182 SCN2B    CACTGCAACCTCTGCTTCCCG     2648 TGCCACACTGT
                         CCTCTGCTTCCCG
                         |||||||||||||
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                        GGAGACGAAGGGC
                     GTT_____
GAM182 SMG1          CACACGG-CCACTGCTTCCC    2647 _   T T T        I
                        ACAC G CC CTGCTTCC
                        IIII I II IIIIIIII
                        TGTG C GG GACGAAGG
                        G   C _ T     I
GAM182 SYNGR1        TGCCACACTCTCCCCTACAGCCC  2664      G    TT GI
                     TGCCACACT TCCTCTGC CCC
                     IIIIIIIII IIIIIIII III
                     ACGGTGTGA AGGGGATG GGG
                        G    TC  II
GAM182 SYNGR1        TGCCACACTCTCCCCTACAGCCC  2664      G    TT I
                      GCCACACT TCCTCTGC CC
                      IIIIIIII IIIIIII  II
                      CGGTGTGA AGGGGATG GG
                        G    TC I
GAM182 TLX1          CCTCTCTGGCTTCTGCTTCCC    2653 CACA  TCC      I
                        CTG  TCTGCTTCC
                        III  IIIIIIIII
                        GAC  AGACGAAGG
                     GAGA  CGA       I
GAM182 TLX1          CCTCTCTGGCTTCTGCTTCCC    2653 TGCCACA  TCC     G
                        CTG  TCTGCTTCCC
                        III  IIIIIIIIII
                        GAC  AGACGAAGGG
                     AGA____  CGA        G
GAM182 TOP3A         GCCAACACTGTCCTCTAAGTTTCC  2655 C        CTTCI
                        ACACTGTCCTCTG
                        IIIIIIIIIIIII
                        TGTGACAGGAGAT
                        _      TCAAA
GAM182 TOP3A         GCCAACACTGTCCTCTAAGTTTCC  2655 TG _       C__  CGI
                        CCA CACTGTCCTCTG  TTCC
                        III IIIIIIIIIIII  IIII
                        GGT GTGACAGGAGAT  AAGG
                        __  T       TCA  TII
GAM182 TRAP100       TGCCTCATCTTTCCTCACTGCTTCCC 2657   A _ G  __      GII
                        TGCC CA CT TCCTC  TGCTTCCC
                        IIII II II IIIII  IIIIIIII
                        ACGG GT GA AGGAG  ACGAAGGG
                        A  A A  TG       III
GAM182 TRAP100       TGCCTCATCTTTCCTCACTGCTTCCC 2657 GCCA _ G  __      I
                        CA CT TCCTC  TGCTTCC
                        II II IIIII  IIIIIII
                        GT GA AGGAG  ACGAAGG
                        A___ A A  TG    I
GAM182 ZNF289        CACA---TCCTCTGCTTCCC     2645 A  T
                        CAC GTCCTCTGCTTCC
                        III IIIIIIIIIIIII
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GTG TAGGAGACGAAGG

GAM182 ZNF289         CACA---TCCTCTGCTTCCC     2645 TGCCACACT
                         GTCCTCTGCTTCC
                         |||||||||||
                         TAGGAGACGAAGG

GAM183 ADAM19         ACAGCAGTGGCTGGCTTGA     2671 A     A GII
                        ACA CAGTGGCTGG CT
                        ||| |||||||||| ||
                        TGT GTCACCGACC GA
                          C   _ ACT

GAM183 ADCY6          ACAGTGGCTTACACCTGTAATCC  2673 CA    GGA__ A  I
                        GTGGCT    CTG AATC
                        ||||||   ||| ||||
                        CACCGA   GAC TTAG
                        __    ATGTG A  I

GAM183 CBFA2T2       ACAGTGGCTCATGCCTGTAATCC  2676 CA    GGA__ A  I
                        GTGGCT    CTG AATC
                        ||||||   ||| ||||
                        CACCGA   GAC TTAG
                        __    GTACG A  I

GAM183 CHST6          ACAGTGGCTCATGCCTGTAATCC  2676 CA    GGA__ A  I
                        GTGGCT    CTG AATC
                        ||||||   ||| ||||
                        CACCGA   GAC TTAG
                        __    GTACG A  I

GAM183 CIAS1          ACAGTGGCTCACGCCTGTAATCC  2675 CA    GGA__ A  I
                        GTGGCT    CTG AATC
                        ||||||   ||| ||||
                        CACCGA   GAC TTAG
                        __    GTGCG A  I

GAM183 CYP8B1         ACAGTGGCTCATGCCTGTAATCC  2676 CA    GGA__ A  I
                        GTGGCT    CTG AATC
                        ||||||   ||| ||||
                        CACCGA   GAC TTAG
                        __    GTACG A  I

GAM183 DSCR3          ACAGTGGCTCACACCTGTAATC  2677 CA    _ G  GAAATI
                        GTGGCT G ACT
                        |||||| | |||
                        CACCGA T TGG
                        __    G G ACATTA

GAM183 DSCR3          AACAGTGGCAGGATTTGAA     2668     T CTGAII
                        AACAGTGGC GGA
                        ||||||||| |||
                        TTGTCACCG CCT
                        T AAACTT

GAM183 GALR1          AACAG---CTCGGCTGAAATCC  2670 AC TG _ A
                        AG GCT GG CTGAAATC
                        || ||| || ||||||||

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                              TT  CGA CC GACTTTAG
                              __   GT   G _
GAM183  GPRK5         AACAGTGGCTGCACAGAAA    2669        G  T  II
                      AACAGTGGCTG AC GAA
                      |||||||||| || |||
                      TTGTCACCGAC TG CTT
                          G  T  TI
GAM183  HTR1D         ACAGTGGCTCATGCCTGTAATCC  2676 CA    GGA__  A  I
                      GTGGCT    CTG AATC
                      ||||||    ||| ||||
                      CACCGA    GAC TTAG
                        __    GTACG  A   I
GAM183  MEFV          ACAGTGGCTCATGCCTGTAATCC  2676 CA    GGA__  A  I
                      GTGGCT    CTG AATC
                      ||||||    ||| ||||
                      CACCGA    GAC TTAG
                        __    GTACG  A   I
GAM183  PRIM2A        ACAGTGGCTCACAACTGTAATCC  2674 CA    G__   A  I
                      GTGGCT  GACTG AATC
                      ||||||  ||||| ||||
                      CACCGA  TTGAC TTAG
                        __   GTG   A   I
GAM183  RAD54B        CAGTGGCTGGATTCCAATC     2680        __ TG AATII
                      CAGTGGCTGGA C A
                      ||||||||||| | |
                      GTCACCGACCT G T
                        AA GT AGIII
GAM183  RTN4          ACAACAGTGCATGG-CTAAAA    2672 _     G _  A  I
                      CAACAGTG C TGG CTGAA
                      |||||||| | ||| |||||
                      GTTGTCAC G ACC GATT
                        T    _ T _   I
GAM183  SCA1          CATCCGTG-CAGG-CTGAAATCC  2679 AACA_  G T A    I
                      GTG C GG CTGAAATC
                      ||| | || |||||||||
                      CAC G CC GACTTTAG
                      GTAGG  _ T _    I
GAM183  SH3BP2        ACAGTGGCTCATGCCTGTAATCC  2676 CA    GGA__  A  I
                      GTGGCT    CTG AATC
                      ||||||    ||| ||||
                      CACCGA    GAC TTAG
                        __    GTACG  A   I
GAM183  SH3GL3        ACAGTGGCTCACACCTGTAATCC  2678 CA    GGA__  A  I
                      GTGGCT    CTG AATC
                      ||||||    ||| ||||
                      CACCGA    GAC TTAG
                        __    GTGTG  A   I
GAM183  SNAP23        ACAGTGGCTCACGCCTGTAATCC  2675 CA    GGA__  A  I
                      GTGGCT    CTG AATC
                      ||||||    ||| ||||
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                        CACCGA    GAC TTAG
                        __    GTGCG  A    I
GAM183 UBE2I            GGCTGGACTCCGAAACTCC    2681      __    CIII
                        GGCTGGACT GAAAT
                        |||||||| |||||
                        CCGACCTGA CTTTG
                          GG    AGGI
GAM184 DLC1             TGAGCCGGC-GCTCCTGATGC    2691    AG  A       AG
                        TGAG GGC GCTCCTGATGC
                        |||| ||| ||||||||||
                        ACTC CCG CGAGGACTACG
                          GG    _       II
GAM184 DLC1             TGAGCCGGC-GCTCCTGATGC    2691 _ AG  A       I
                         GAG GGC GCTCCTGATG
                         ||| ||| |||||||||
                         CTC CCG CGAGGACTAC
                          A  GG   _        I
GAM184 IGJ             GAGACGCCAGCTCCTGCTCCA    2686  GGG       ATGCI
                        AGA  CAGCTCCTG
                        |||  |||||||||
                        TCT  GTCGAGGAC
                          GCG       GAGGI
GAM184 IGJ             GAGACGCCAGCTCCTGCTCCA    2686 TG  GGG      ATG GC
                        AGA  CAGCTCCTG  CA
                        |||  ||||||||| ||
                        TCT  GTCGAGGAC  GT
                          __  GCG       GAG GI
GAM184 INS             GATGGCCTCTTCTGATGCAGC    2689 AG  AG  C      I
                          GGC CT CTGATGCAG
                          ||| || |||||||||
                          CCG GA GACTACGTC
                          TA  GA  A       I
GAM184 POU3F2          AGCGGGCAGCTCC-GACGC      2684  A        T  I
                        AG GGGCAGCTCC GATG
                        || ||||||||| ||||
                        TC CCCGTCGAGG CTGC
                          G     _    G
GAM184 POU3F2          AGCGGGCAGCTCC-GACGC      2684 TGAGA       T  A
                          GGGCAGCTCC GATGC
                          |||||||||| |||||
                          CCCGTCGAGG CTGCG
                          G___      _  G
GAM184 RRP22          GAGAGGGCAG-GCCCGAGGCAG    2687 _      CT   T  I
                        AGAGGGCAG CCTGA GCA
                        ||||||||| ||||| |||
                        TCTCCCGTC GGGCT CGT
                          C     C_   C  I
GAM184 RRP22          GAGAGGGCAG-GCCCGAGGCAG    2687 TG       CT   T  C
                        AGAGGGCAG CCTGA GCAG
                        ||||||||| ||||| ||||
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                        TCTCCCGTC  GGGCT CGTC
                           C_     C   C
GAM184  SNCAIP          AGGGCCAAGCTCCTGAGGC    2685   __      TGIII
                        AGGGC AGCTCCTGA
                        ||||| |||||||||
                        TCCCG TCGAGGACT
                          GT       CCGII
GAM184  SNCAIP          AGGGCCAAGCTCCTGAGGC    2685 TGAGAGGGC     T AG
                            AGCTCCTGA GC
                            ||||||||| ||
                            TCGAGGACT CG
                        GGT_____        C AC
GAM184  TP73            GAGGGCAGCTCGCT-CTGCAGC   2688        _ GA   I
                        AGGGCAGCTC CT TGCAG
                        |||||||||| || |||||
                        TCCCGTCGAG GA ACGTC
                             C G_    I
GAM184  TP73            GAGGGCAGCTCGCT-CTGCAGC   2688 TGAGAG     _ GA
                          GGCAGCTC CT TGCAGC
                          |||||||| || ||||||
                          CCGTCGAG GA ACGTCG
                        _____        C G_
GAM184  VCAM1           TGGGAGGGTATTCAGCTCCTGAAGC 2690 A  ____        T AGCII
                        TG GAGGG   CAGCTCCTGA GC
                        || |||||   |||||||||| ||
                        AC CTCCC   GTCGAGGACT CG
                          C  ATAA       T IIICG
GAM184  VCAM1           TGGGAGGGTATTCAGCTCCTGAAGC 2690 AGA  ____       TGI
                           GGG   CAGCTCCTGA
                           |||   ||||||||||
                           CCC   GTCGAGGACT
                        ___  ATAA       TII
GAM185  AQP6            GACACATGAGGCCAAGAGG      2702          AAAAGII
                        GACACATGAGGC
                        ||||||||||||
                        CTGTGTACTCCG
                           GTTCTCC
GAM185  AQP6            GACACATGAGGCCAAGAGG      2702 TG      AAA_ CTCC
                          ACACATGAGGC   AGG
                          |||||||||||   |||
                          TGTGTACTCCG   TCC
                             __    GTTC TIII
GAM185  B4GALT1         ACACAT-AGGCAAAAGG-TCC    2695     G     _ I
                        ACACAT AGGCAAAAGG CT
                        |||||| ||||||||||| ||
                        TGTGTA TCCGTTTTCC GG
                           _      A I
GAM185  B4GALT1         ACACAT-AGGCAAAAGG-TCC    2695 TGAC  G      C
                          ACAT AGGCAAAAGG TCC
                          |||| ||||||||||| |||
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                       TGTA TCCGTTTTCC AGG
                       ___   _     _
GAM185 B4GALT3     TGTCACA-GAGGGCAGAGAAAGGCTCC2705 GAC  T  _ ___        I
                       ACA GAGG CA  AAAGGCTC
                       ||| |||| ||  ||||||||
                       TGT CTCC GT  TTTCCGAG
                       ___   _   C  CTC        I
GAM185 B4GALT3     TGTCACA-GAGGGCAGAGAAAGGCTCC2705 TGA  T  _ ___        GII
                       CACA GAGG CA  AAAGGCTCC
                       |||| |||| ||  ||||||||||
                       GTGT CTCC GT  TTTCCGAGG
                       ACA   _   C CTC       III
GAM185 EPS15       CACAGGCAGGCAAAA-GCTC    2701  TG_      G II
                       CACA   AGGCAAAAG CT
                       ||||   |||||||||| ||
                       GTGT   TCCGTTTTC GA
                       CCG        _  GI
GAM185 EPS15       CACAGGCAGGCAAAA-GCTC    2701 TGACACATG     G  _
                       AGGCAAAAG CTC C
                       ||||||||| ||| |
                       TCCGTTTTC GAG G
                       TCCG_____        _ T
GAM185 KIAA0442    ACATTACACAAGAAGGCTCCG   2697 ____ TG  CAAA      I
                       CA  AGG  AGGCTCC
                       ||  |||   |||||||
                       GT  TCT   TCCGAGG
                       TAAT  GT  ____        I
GAM185 KIAA0442    ACATTACACAAGAAGGCTCCG   2697 TGAC  TG  CAAA
                       ACA  AGG   AGGCTCCG
                       |||  |||    ||||||||
                       TGT  TCT   TCCGAGGC
                       A___  GT  ____
GAM185 LIMD1       CACAATGAGGCAAAGGCCT     2699  _       A  II
                       CACA TGAGGCAAA GGC
                       |||| |||||||||| |||
                       GTGT ACTCCGTTT CCG
                       T      _  GA
GAM185 LIMD1       CACAATGAGGCAAAGGCCT     2699 TGACAC     A  CC
                       ATGAGGCAAA GGCT
                       |||||||||| ||||
                       TACTCCGTTT CCGG
                       T_____        _ AT
GAM185 P53AIP1     ACAGGAGGAACAAAAGGCTCC   2696  T  __        III
                       ACA GAGG  CAAAAGGCTC
                       ||| ||||  ||||||||||
                       TGT CTCC  GTTTCCGAG
                       C  TT    GII
GAM185 PFKFB4      CACAGGCCAGG--AAAGGCTCCG  2700 ACATG  A___        I
                       AGGC  AAAGGCTCC
                       ||||   |||||||||
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                        TCCG   TTTCCGAGG
                   TG___   GTCC        I
GAM185 SLC8A2      TGGCAC-TGAGGGCAAAAGG    2704  A  A   _      CTCC
                   TG CAC TGAGG CAAAAGG
                   || ||| ||||| |||||||
                   AC GTG ACTCC GTTTCC
                    C  _   C   IIIG
GAM185 SLC8A2      TGGCAC-TGAGGGCAAAAGG    2704  A  A   _      II
                   TG CAC TGAGG CAAAAG
                   || ||| ||||| ||||||
                   AC GTG ACTCC GTTTC
                    C  _   C   CI
GAM185 TDG         ACAGATGAGTGGCAAAAGG      2694  C  ___      III
                   ACA ATGA  GGCAAAAG
                   ||| ||||  ||||||||
                   TGT TACT  CCGTTTTC
                    C  CA     CII
GAM185 TDG         ACAGATGAGTGGCAAAAGG      2694 TGACAC  __      C  C
                     ATGA  GGCAAAAGG TC
                     |||| ||||||||| ||
                     TACT  CCGTTTTCC AG
                   TC____   CA     _  I
GAM185 USH2A       TGAAACAATCAGGCAAAAG      2703  C  _G      GCTCC
                   TGA ACA T AGGCAAAAG
                   ||| ||| | |||||||||
                   ACT TGT A TCCGTTTTC
                    T   T G     IIIGC
GAM185 USH2A       TGAAACAATCAGGCAAAAG      2703  C  _G      II
                   TGA ACA T AGGCAAAA
                   ||| ||| | ||||||||
                   ACT TGT A TCCGTTTT
                    T   T G    CI
GAM185 WHSC1       CACACTAAGGCAAAAGGGCTC    2698  _       _ III
                   CACA TGAGGCAAAAGG CT
                   |||| |||||||||||| ||
                   GTGT ATTCCGTTTTCC GA
                    G        C GII
GAM185 WHSC1       CACACTAAGGCAAAAGGGCTC    2698 TGACACA       _  CG
                     TGAGGCAAAAGG CTC
                     |||||||||||| |||
                     ATTCCGTTTTCC GAG
                   TG_____        C  AG
GAM186 ACCN1       TGACTT--TGGACCTGGAATCTGGT 2713    GT   G_       I
                   TGACTT TGGAC GGAATCTGGT
                   |||||| ||||| ||||||||||
                   ACTGAA ACCTG CCTTAGACCA
                    __      GA        I
GAM186 ADAMTS13      CTTGGTG-ACTGGGAATCTGGT    2708 TGACTTGTTG  _
                     GAC GGGAATCTGGT
                     ||| |||||||||||
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                          CTG CCCTTAGACCA
                     CCA_____    A
GAM186 GAD1          GAGTTGTTGGAC---AAGCTGGT  2710 TGAC        AAT
                        TTGTTGGACGGG  CTGG
                        ||||||||||| ||||
                        AACAACCTGTTC  GACC
                     TC__          ___
GAM186 GLUD1         TGACTTGTTGAGAATGGTATC   2712      _ CG A  TGGT
                        TGACTTGTTG GA  GG ATC
                        ||||||||| || || |||
                        ACTGAACAAC CT  CC TAG
                      T  TA A  IIIT
GAM186 LNK           TTGGACGGGAAGCAGTCTGG    2714 TGACTTG__    _ AATCTGG
                        TTGGACG GG
                        ||||||| ||
                        GACCTGC CC
                     CCTTCGTCA     A CIIITGG
GAM186 NEBL          TGACTTTTATGCTCAGTGAATCTGGT 2711   GT_ GA _      II
                        TGACTT  TG CGG GAATCTGGT
                        ||||||  ||  ||| |||||||||
                        ACTGAA  AC GTC CTTAGACCA
                      AAT GA  A       II
GAM186 TEC           CTTGT-GCTTGGGAATCTGG    2709 TGACTTGTTGGAC
                              GGGAATCTGG
                              ||||||||||
                              CCCTTAGACC
                     CACGAA_____
GAM187 ABCB4         AATTCCCTCTTGCATTCCT     2717 TGAGAATT        G  T
                        TCTCTTGCAT CCT
                        |||||||||| |||
                        GGAGAACGTA GGA
                     G_____        A  C
GAM187 AFG3L2        GAGAATTTCTGCTGGC---CCTT  2725 TG       C  CAT
                        AGAATTTCT TTG  GCCTT
                        ||||||||| ||| |||||
                        TCTTAAAGA GAC  CGGGA
                     __         C ___
GAM187 AKAP2         TGAGAATTTTAGTC-TCCATGCC  2730     C__  G    TTA
                        TGAGAATTT TCTT CATGCC
                        ||||||||| |||| ||||||
                        ACTCTTAAA AGAG GTACGG
                      ATC   _  III
GAM187 ATF4          TGAGAATTTCATCCTTCCA---CTTA 2732       __ G  GCCTTAI
                        TGAGAATTTC TCTT CAT
                        |||||||||| |||| |||
                        ACTCTTAAAG GGAA GTG
                       TA  G  AATIIIA
GAM187 BCAS1         AGCATTTCTCTTCTATAACTTA   2724 TGAGA        GC C
                        ATTTCTCTT ATG CTTA
                        ||||||||| ||| ||||
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                          TAAAGAGAA  TAT GAAT
                          G____        GA  T
GAM187 DIRC1          AGAATTTCTACTCCA-GCC      2723 TGAG      C  G  T  T
                          AATTTCT TT CA GCC
                          |||||||| || || |||
                          TTAAAGA GA GT CGG
                              ___      T  G  _  T
GAM187 EPHA3          TGAGAAATTTCTCT--CCTG-CTTA 2729      ___         ATGCCTTA
                          TGAGAA  TTTCTCTTGC
                          ||||||  ||||||||||
                          ACTCTT  AGAGAGGACG
                          TAA          AATIIIAT
GAM187 FGA            AGAATGTTTCTCTTGCCTTCCT    2720 TGAGAA       ATG  TA
                          TTTCTCTTGC  CCT
                          |||||||||| |||
                          AAAGAGAACG  GGA
                          TTAC__       GAA  CC
GAM187 FGFR1          AGAAAGCTCTCACTTGCATGCCT   2719 T  AA  T       TAI
                          GAG  TTTC CTTGCATGCCT
                          ||| |||| |||||||||||
                          TTC  AGAG GAACGTACGGA
                          T  G_  T       CAI
GAM187 FUT6          AGAATTTCTACCTTCC--GCCTT    2721 TGAG      _  GCA    A
                          AATTTCT CTT  TGCCTT
                          |||||||| ||| ||||||
                          TTAAAGA GGA  GCGGAA
                          ____        T  AG_    A
GAM187 NOTCH2        TGACGAATTGCTTCTCTTGCAT     2727 _  ___        GCCTTA
                          TGA GAATT  TCTCTTGCAT
                          ||| |||||  ||||||||||
                          ACT CTTAA  AGAGAACGTA
                          G   CGA       IIIATT
GAM187 PPP1R2        TGAGCATG-CTGCTTGGCATGCCTTA 2733    AATTT  _  _       II
                          TGAG    CT CTTG CATGCCTTA
                          ||||    || |||| |||||||||
                          ACTC    GA GAAC GTACGGAAT
                          GTAC_  C   C       II
GAM187 PRDM2        TGAGAATTTCAAGTCTGGAAATGCCT 2731          ___   TGC_    TAII
                          TGAGAATTTC  TCT  ATGCCT
                          ||||||||||  |||  ||||||
                          ACTCTTAAAG  AGA  TACGGA
                          TTC  CCTT    IIIA
GAM187 PTPN1        AGAATTTCTCTGTAC-TGGCTT     2722 TGAG      _  A  C  A
                          AATTTCTCT TGC TG CTT
                          ||||||||| ||| || |||
                          TTAAAGAGA ATG AC GAA
                          ____         C  _  C  G
GAM187 SH3GL2        GAGAATTTCT-TTTCAGTCCCT    2726 TG       C  G  TG   A
                          AGAATTTCT TT CA  CCTT
                          |||||||||| || || ||||
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                       TCTTAAAGA AA GT  GGGA
                    __        A _ CA   G
GAM187 SPK          AATGTCTCGCTTGCATGCCT    2718 TGAGAA   T
                    TTTC CTTGCATGCCTT
                    |||| |||||||||||
                    AGAG GAACGTACGGAG
                    _____       C
GAM187 TNFSF15        TGAAATATTTCTCTTTCAATCCT  2728     _      G TG  TAI
                    TGAGA ATTTCTCTT CA  CCT
                    ||||| ||||||||| || |||
                    ACTTT TAAAGAGAA GT  GGA
                         A     A TA  III
GAM188 NCOR2          CATCG---AATTCATTCTGC     2736    GCG      GI
                    CATC  GAATTCATTC
                    ||||  ||||||||||
                    GTAG  CTTAAGTAAG
                    ___          AC
GAM188 NCOR2          CATCG---AATTCATTCTGC  2736 TATCATCGCG      G
                       GAATTCATTC G
                       |||||||||| |
                       CTTAAGTAAG C
                    G_____       A
GAM189 CYBB          AAAGGCTATA--TTCGCACAG   2739 TCAA  AGACT       G
                       AGGT   TTCGCACAG
                       ||||   |||||||||
                       TCCG   AAGCGTGTC
                    ____     ATAT_      G
GAM189 MECP2          TCAAAGGTAGGATTTCCTCCAGG  2743        AC  GCA  TI
                    TCAAAGGTAG TTTC  CAGG
                    |||||||||| |||| ||||
                    AGTTCCATC AAAG  GTCC
                         CT  GAG  II
GAM189 TCEA1          AAATGTAGACTTT-GCAACAG    2740 TCAAAG      C _ G
                       GTAGACTTT GCA CAG
                       ||||||||| ||| |||
                       CATCTGAAA CGT GTC
                    TA____      _ T A
GAM189 TEM8          TCAAAGGTATACATTTGGAAC    2742     G TTTCGCACAGGT
                    TCAAAGGTA AC
                    |||||||| ||
                    AGTTTCCAT TG
                      A TAAACCTTGIII
GAM189 TRIM14        CAAAGGTAGACTCAAGTCTCGCAGAG 2741 TC          _____  C GTII
                    AAAGGTAGACTT   TCGCA AG
                    |||||||||||    ||||| ||
                    TTTCCATCTGAG   AGCGT TC
                    __         TTCAG   C AIII
GAM190 HNRPDL        CAAAATCAACTGTGCCTTAATT    2747 TGCCAAT       _
                    GTCGATTG GCCTTAATT
                    |||||||| |||||||||
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                          TAGTTGAC CGGAATTAA
                        T_____        A
GAM190 MKI67            TGCAGATGTCCAATAGCCTTAATT  2751  CA    GAT        I
                        TGC ATGTC  TGGCCTTAATT
                        III IIIII  IIIIIIIIIII
                        ACG TACAG  ATCGGAATTAA
                         TC  GTT         I
GAM190 MS4A4A           TGCCAATGT-AAT--GCCTTTAT   2750      CGATTG    AAT
                        TGCCAATGT    GCCTT
                        IIIIIIIII    IIIII
                        ACGGTTACA    CGGAA
                          TTA___    ATA
GAM190 PITX1            TGTCGCTCCGTGGCCTTAAT      2752 TGCCAATG  AT
                          TCG TGGCCTTAAT
                          III IIIIIIIIII
                          GGC ACCGGAATTA
                         A_____ __
GAM190 SHANK2           TGCCACTCCC--TTGGCCTTA     2749    ATG GA      AT
                        TGCCA TC TTGGCCTTA
                        IIIII II IIIIIIIII
                        ACGGT GG AACCGGAAT
                         GA_ G_      II
GAM190 SLC9A5           GCCAGAGTAGA--GGCCTTAAT    2748 TG  AT C  TT
                         CCA GT GA GGCCTTAAT
                         III II II IIIIIIIII
                         GGT CA CT CCGGAATTA
                         __ CT T __
GAM190 ZNF265           CAATGTCTCCATTGGCCTT       2746 TGCCAATG G     AAT
                          TC ATTGGCCTT
                          II IIIIIIIII
                          AG TAACCGGAA
                        ACAG____ G    AGT
GAM191 ADRA2A           GCAATTATGCTGTTAGGCA       2758 CAG       TCII
                        GC  TATGCTGTTAG
                        II  IIIIIIIIIII
                        CG  ATACGACAATC
                         TTA        CGTI
GAM191 ADRA2A           GCAATTATGCTGTTAGGCA       2758 TGC  _      T AGA
                         CAGT ATGCTGTTAG CA
                         IIII IIIIIIIIII II
                         GTTA TACGACAATC GT
                          ___  A      C GII
GAM191 BMP6             GTATGCTGTATAGTAAAAAG      2759       _  C  II
                        GTATGCTGT TAGT AAGA
                        IIIIIIIII IIII IIII
                        CATACGACA ATCA TTTT
                           T  T  CI
GAM191 CACNB2           ATGCTGTTAGTTATACAAGA      2755         ____  IIIT
                        ATGCTGTTAGT  CAAG
                        IIIIIIIIIII  IIII
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                        TACGACAATCA  GTTC
                          ATAT   TIII
GAM191 COL9A3        GTATGCTGTCAGGCGACAG      2760        TCAAGAII
                        GTATGCTGTTAG
                        IIIIIIIIIII
                        CATACGACAGTC
                          CGCTGTCI
GAM191 GSTM3         TGCCAGTATCGCAGCGATTCAA  2761    _ T TAG   GAG
                        TGCCAGTAT GC GT  TCAA
                        IIIIIIIII II II   IIII
                        ACGGTCATA CG CG  AGTT
                          G  T CTA   III
GAM191 GSTM3         TGCCAGTATCGCAGCGATTCAA  2761 G     _ T TAG  I
                          CCAGTAT GC GT  TCA
                        IIIIIII II II   III
                        GGTCATA CG CG  AGT
                          _     G T CTA  I
GAM191 PLCB4         CCAG-A-GCTGTTAGTCTAG    2757   TAT      AI
                        CCAG  GCTGTTAGTC
                        IIII  IIIIIIIIII
                        GGTC  CGACAATCAG
                          T__      AT
GAM191 PLCB4         CCAG-A-GCTGTTAGTCTAG    2757 TGCCAGTAT     A
                          GCTGTTAGTC AG
                          IIIIIIIIII II
                          CGACAATCAG TC
                        TCT_____      A
GAM191 PRDM2         TGTCAATATGCTGTTGATTCCCAGAG 2762  C      AG_ A_  II
                        TG CAGTATGCTGTT  TC AGAG
                        II IIIIIIIIIII  II IIII
                        AC GTTATACGACAA  AG TCTC
                          A       CTA GG  II
GAM191 PRDM2         TGTCAATATGCTGTTGATTCCCAGAG 2762 GC      AG_ A_  I
                        CAGTATGCTGTT  TC AGA
                        IIIIIIIIIII  II III
                        GTTATACGACAA  AG TCT
                          __       CTA GG  I
GAM191 STC1          CAGTATAGGTCTAAGTCAAGAG   2756 A   CT __     I
                        GTATG GTT AGTCAAGA
                        IIIII III IIIIIIII
                        CATAT CAG TCAGTTCT
                          _  C_ AT      I
GAM192 ABCG1         GATCCA---ACCCAGCTGG      2771 TGCGAG  TTC
                        CCA ACCCAGCTG
                        III IIIIIIIII
                        GGT TGGGTCGAC
                        _____  __
GAM192 ARHGEF1          TGCGGGGCCAGTAACCCCAGCTGG 2779  A_ TTCA_      TCI
                        TGCG GCCA   CCCAGCTGG
                        IIII IIII   IIIIIIIII
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                    ACGC  CGGT    GGGTCGACC
                     CC   CATTG       III
GAM192 ATP7B        GAGGCCCTCACTCCAGCTGGTC   2770 TGCGA  A    _
                    GCC TTCAC CCAGCTGGTC
                    III IIIII IIIIIIIIII
                    CGG GAGTG GGTCGACCAG
                    _____  _    A
GAM192 COG3         GCTAGAGATCCACACAGCTGGTC   2777 TGC  CC    C       I
                    GAG  ATTCAC CAGCTGGTC
                    III  IIIIII IIIIIIIII
                    CTC  TAGGTG GTCGACCAG
                    GAT __   T    G
GAM192 CYP4F3       AGCTCTTTCACCCAGGCTGG     2765 TGCGAGCCA      _  T
                      TTCACCCAG CTGG
                      IIIIIIIII IIII
                      AAGTGGGTC GACC
                    GA_____      C  T
GAM192 EIF2B1       TGCGAGCCAGTCTGACAGC      2781     T ACC  TGGT
                    TGCGAGCCA TC  CAGC
                    IIIIIIIII II  IIII
                    ACGCTCGGT AG  GTCG
                     C  ACT   IIIC
GAM192 EPRS         GAGCCATATAACCCAGCTG      2768 TGCGAG  TC_       GT
                     CCAT  ACCCAGCTG
                     IIII  IIIIIIIII
                     GGTA  TGGGTCGAC
                    _____     TAT      AT
GAM192 FMR2         GAGGC-TTCCCACAGCTGGTC    2773 TGCGAGCCA  A  _
                     TTC CC CAGCTGGT
                     III II IIIIIIII
                     AAG GG GTCGACCA
                    CG_____  _  T
GAM192 HOXC4        GCGAGGCAGGGTCCCAGCTGG    2776 TG   C TTCA      TC
                    CGAG CA   CCCAGCTGG
                    IIII II   IIIIIIIII
                    GCTC GT   GGGTCGACC
                    __  C  CCCA       TI
GAM192 HTR1D        TGCTGAGACAACTACC-AGCTGGT 2778  _  C TTCAC      CI
                    TGC GAG CA   CCAGCTGGT
                    III III II   IIIIIIIII
                    ACG CTC GT   GGTCGACCA
                    A  T  TGAT_       II
GAM192 KIFC3        GCGAGCCA-TC-CCCGGCT      2775 TG    T A  A  GG
                    CGAGCCAT C CCC GCT
                    IIIIIIII I III III
                    GCTCGGTA G GGG CGA
                    __    __  C  GI
GAM192 KLF8         GAGTCGATTCAGACCCAGCTGG   2767 TG  GC TTC       TC
                    CGA CA  ACCCAGCTGG
                    III II  IIIIIIIII
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                         GCT  GT   TGGGTCGACC
                        A_   AA  C__         CG
GAM192 MSH3        TGCCAG--ATTCACCCAGTTG    2782 TGCGA  __      C  GT
                        GCCA  TTCACCCAG TG
                        IIII  IIIIIIIII II
                        CGGT  AAGTGGGTC AC
                        A____    CT      A  II
GAM192 NFKBIL2       GAGC---TCCCCCAGCTGGT    2772 TGCGAGCCA  A
                          TTC CCCAGCTGG
                          III IIIIIIIII
                          AGG GGGTCGACC
                        G_____  _
GAM192 RARA          GAGCCAGCTCCCCCAGCTGG    2769 TGCGAG  _  A      T
                          CCA TTC CCCAGCTGG
                          III III IIIIIIIII
                          GGT GAG GGGTCGACC
                        _____    C  G     C
GAM192 SCN1B        TGCGAGCCAAGCCCCCTGC      2780        TTCA  A  TGGT
                          TGCGAGCCA  CCC GC
                          IIIIIIIII  III II
                          ACGCTCGGT  GGG CG
                          TCGG   A IIIC
GAM192 TSLP         AGCCCTTATTCACCCATGCTG    2766 TGCGAGCC      _  GTC
                          ATTCACCCA GCTG
                          IIIIIIIII IIII
                          TAAGTGGGT CGAC
                        GAA_____        A  AAC
GAM192 ZNF10        GCGACTCCATTCA-CCAGC      2774 TG G_     C  TGG
                          CGA  CCATTCACC AGC
                          III  IIIIIIIII III
                          GCT  GGTAAGTGG TCG
                        __  GA       _  CII
GAM193 CHST6        TCCCGGGCCT--AGCGCCTGC    2793       AC  G  GG
                          TCCCGGGCCT AGCG CTGC
                          IIIIIIIIII IIII IIII
                          AGGGCCCGGA TCGC GACG
                          __  G  II
GAM193 CSF3         CCAGGGGCTCACAGCGGCT      2785 TCCC  C      GCGG
                          GGGC TACAGCGGCT
                          IIII IIIIIIIIII
                          CCCG GTGTCGCCGA
                        GTC_  A      GIII
GAM193 HK3          CCCGG--CTCCAGCAAGGCTGCGGC 2786 TC  G CTA  __      I
                          CCGG C  CAGC GGCTGCGGC
                          IIII I  IIII IIIIIIIII
                          GGCC G  GTCG CCGACGCCG
                          __  _AG_  TT    C
GAM193 KCNA7        TCCCGCCCCCTACAGCGAGCTGGGG 2791    GG_     _  C CII
                          TCCCG  CCTACAGCG GCTG GG
                          IIIII  IIIIIIIII IIII II
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                          AGGGC  GGATGTCGC CGAC CC
                           GGG       T  _ CII
GAM193 LFG        TCCCGGGCCCCCATCTGCAGC   2792      TA GCGG
                  TCCCGGGCC CA  CTGCGGC
                  |||||||| ||  |||||||
                  AGGGCCCGG GT  GACGTCG
                      GG A___
GAM193 MLC1         TCCCGGGCCAGGACAGAGGC    2790      T__  C TGCGG
                   TCCCGGGCC  ACAG GGC
                   |||||||| |||| |||
                   AGGGCCCGG TGTC CCG
                     TCC  T IIICG
GAM193 PRX        CCCGGGCCTCCA-CCTCTGC     2787 TC     ACA GG   G
                    CCGGGCCT GC CTGCG
                    |||||||| || |||||
                    GGCCCGGA TG GACGT
                      __    GG_ GA  I
GAM193 SHC1        CCCGGGCCTA----GGCTG-GGC  2789 TC     CAGC   C
                   CCGGGCCTA  GGCTG G
                   ||||||||| ||||| |
                   GGCCCGGAT  CCGAC C

                     __      ____   _
GAM193 SURF4      CCCCTGCCCACAGCGGCTGCGGC  2788 T  GG            I
                  CCC GCCTACAGCGGCTGCGGC
                  ||| |||||||||||||||||
                  GGG CGGGTGTCGCCGACGCCG
                    _ A_         A
GAM194 ATP11B     TATAATGGCCTCAGCAACAG    2801       ATT C  GCA
                  TATAATGGCCT CA CAG
                  |||||||||| || |||
                  ATATTACCGGA  GT GTC
                      GTC T  III
GAM194 ATP11B     TATAATGGCCTCAGCAACAG    2801       ATT C  I
                  ATAATGGCCT  CA CA
                  |||||||||| || ||
                  TATTACCGGA  GT GT
                      GTC T  I
GAM194 FGFR2     TAAAATGGCCTACTTATCTGTGCAC 2802 AT      CACCAG_  I
                    AATGGCCTATT    GCA
                    ||||||||||     |||
                    TTACCGGATGA    CGT
                    T_       ATAGACA  I
GAM194 FGFR2     TAAAATGGCCTACTTATCTGTGCAC 2802 TAT     CACCAG_  II
                    AATGGCCTATT    GCAC
                    ||||||||||     ||||
                    TTACCGGATGA    CGTG
                  ATT       ATAGACA  II
GAM194 ICA1      TGGCC----CACCAGGCAC     2805    TATT
                 TGGCC  CACCAGGCA
                 |||||  |||||||||
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                        ACCGG   GTGGTCCGT
                        ‾‾‾‾
GAM194 INMT             TGGCCTATTCCTTGACCAAAGCAC 2803        ‾‾‾‾  _ IIIG
                        TGGCCTATTC   ACCAG GCA
                        IIIIIIIII   IIIII III
                        ACCGGATAAG   TGGTT CGT
                          GAAC   T  GIII
GAM194 INMT             TGGCCTATTCCTTGACCAAAGCAC 2803 TATAATGG  ATTC   _   I
                             CCT   ACCAG GCAC
                             III   IIIII IIII
                             GGA   TGGTT CGTG
                        ATAA‾‾‾‾  AC__   T  T
GAM194 ITPR3            ATCATGG---AGTCACCAGGC   2797 TA_   CCTAT
                          ATGG   TCACCAGG
                          IIII   IIIIIIII
                          TACC   AGTGGTCC
                          TAG   TC___
GAM194 ITPR3            ATCATGG---AGTCACCAGGC   2797 TATA   CCTAT
                          ATGG   TCACCAGGC
                          IIII   IIIIIIIII
                          TACC   AGTGGTCCG
                         AG__   TC___
GAM194 LPIN2            AAAGGCCCA--CACCAGGCA   2796 AT_   TT     I
                          GGCCTA CACCAGGC
                          IIIIII IIIIIIII
                          CCGGGT GTGGTCCG
                         TTT   __   I
GAM194 LPIN2            AAAGGCCCA--CACCAGGCA   2796 TATAAT   TT
                          GGCCTA CACCAGGC
                          IIIIII IIIIIIII
                          CCGGGT GTGGTCCG
                         ‾‾‾‾‾‾   __
GAM194 MEF2C             TATAA---CTTATTCACCA        2800 TATA    C
                          ATGGC TATTCACC
                          IIIII IIIIIIII
                          TATTG ATAAGTGG
                         A___   A
GAM194 MEF2C             TATAA---CTTATTCACCA        2800 TATA    C       GG
                          ATGGC TATTCACCA
                          IIIII IIIIIIIII
                          TATTG ATAAGTGGT
                         A___   A     II
GAM194 NDRG1            TGGCCTTCTGACCAGGCAC        2806    A C     II
                        TGGCCT TT ACCAGGCA
                        IIIIII II IIIIIIII
                        ACCGGA GA TGGTCCGT
                           A C     GI
GAM194 PES1            GGCCTCTTCTGACCAGGCAC   2798    A  ‾‾‾‾     IIIG
                        GGCCT TTC   ACCAGGCA
                        IIIII III   IIIIIIII
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                            CCGGA AAG   TGGTCCGT
                              G  AGAC      GIII
GAM194  PES1        GGCCTCTTCTCTGACCAGGCAC   2798 TATAA   TATT    G C
                              TGGCC   CACCAG CA
                              |||||   |||||| ||
                              ACTGG   GTGGTC GT
                            AAGAG   TCC_   _ C
GAM194  SLC1A4      TAATGGCCTGTT-A-CAGG     2799       ATTCACCAGI
                            TAATGGCCT
                            |||||||||
                            ATTACCGGA
                                CAATGTCCII
GAM194  SLC1A4      TAATGGCCTGTT-A-CAGG       2799 TATA    A CAC   C
                            ATGGCCT TT  CAGG
                            ||||||| ||  ||||
                            TACCGGA AA  GTCC
                            ____      C T__   C
GAM194  TARBP2      TGGACAGTTCCACCAGGCAC     2804  _ CTA        II
                            TGG C  TTCACCAGGCA
                            ||| |  ||||||||||
                            ACC G  AGGTGGTCCGT
                             T TCA         GI
GAM194  TARBP2      TGGACAGTTCCACCAGGCAC     2804 TATAATGGCCTA
                                TTCACCAGGCA
                                |||||||||||
                                AGGTGGTCCGT
                            TCA_____
GAM195  ADCY8       GGGATGGGGAGCAGGGGCGGA      2814        C ____    IIIT
                            GGGATGGGGA C   GCGG
                            |||||||||| |   ||||
                            CCCTACCCCT G   CGCC
                             C TCCC   TIII
GAM195  ADCY8       GGGATGGGGAGCAGGGGCGGA      2814 TG      C ____    AGTTCC
                            GGATGGGGA C   GCGGA
                            ||||||||| |   |||||
                            CCTACCCCT G   CGCCT
                            __      C TCCC   CIIICC
GAM195  ARHGEF1     GGCTGGTGTCCGCGCGGAAGT     2811  A GGAC__       III
                            GG TGG    CGCGGAAG
                            || |||    |||||||||
                            CC ACC    GCGCCTTC
                             G ACAGGC      AII
GAM195  ARHGEF1     GGCTGGTGTCCGCGCGGAAGT     2811 TG A GGGAC        TCC
                            GG TG   CGCGGAAGT
                            || ||   |||||||||
                            CC AC   GCGCCTTCA
                            GA _ AGGC_       CTI
GAM195  CAPN7       GGACTCGGGAGCGCCGCGGAAG     2810 TGGGATG  ___       TTCC
                            GGGA  CCGCGGAAG
                            ||||  |||||||||
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                              CCCT  GGCGCCTTC
                         TGAG___   CGC      CTII
GAM195 CAPN7          GGACTCGGGAGCGCCGCGGAAG   2810   G_  ___        IIIC
                         GGAT GGGA  CCGCGGAA
                         |||| ||||  ||||||||
                         CCTG CCCT  GGCGCCTT
                          AG  CGC     CIII
GAM195 CELSR1        TGGGCGGGGCTGGACCGCGG   2822   A  ____        AAGTTC
                         TGGG TGGGG  ACCGCGG
                         |||| |||||  |||||||
                         ACCC GCCCC  TGGCGCC
                          _   GACC     IIICCT
GAM195 CELSR1        TGGGCGGGGCTGGACCGCGG   2822   A  ____        III
                         TGGG TGGGG  ACCGCG
                         |||| |||||  ||||||
                         ACCC GCCCC  TGGCGC
                          _   GACC     CII
GAM195 CYP1B1        TGGGATGGGGA-CGGAGAAG   2824      C C    TTC
                         TGGGATGGGGAC G GGAAG
                         ||||||||||| | |||||
                         ACCCTACCCCTG C TCTTC
                              _  C    III
GAM195 CYP1B1        TGGGATGGGGA-CGGAGAAG   2824 _      CGC  AI
                          GGGATGGGGAC  GGA
                          |||||||||||  |||
                          CCCTACCCCTG  CCT
                          A       ___  CT
GAM195 DAG1        GGGA---GGACCGCGGCAG   2817   TGG     AA
                          GGGA  GGACCGCGG
                          ||||  |||||||||
                          CCCT  CCTGGCGCC
                          ___      GT
GAM195 DAG1        GGGA---GGACCGCGGCAG   2817 TGGGAT      A T
                           GGGGACCGCGG AG
                           |||||||||| ||
                           CTCCTGGCGCC TC
                          C_____      G C
GAM195 FOXE3        GGGATGGGGGACGGAGAAG   2818      ACC   AII
                          GGGATGGGG  GCGGA
                          ||||||||| |||||
                          CCCTACCCC  TGCCT
                          C__      CTT
GAM195 FOXE3        GGGATGGGGGACGGAGAAG   2818 TG    AC C   TTC
                           GGATGGGG  CG GGAAG
                           |||||||| || |||||
                           CCTACCCC  GC TCTTC
                          __      CT C   CII
GAM195 FXYD6        GATGGGGACTCCTCGTGGAAG   2809       ____  C  IIIC
                          GATGGGGAC  CG GGAA
                          ||||||||| || ||||
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                              CTACCCCTG   GC CCTT
                                AGGA  A   CIII
GAM195 HOXD1          GGGATGGGGGTCGCCTGGGACTTC 2815    AC ___   AGTTI
                       ATGGGG CGC  GGA
                       IIIIII III  III
                       TACCCC GCG  CCT
                         CA  GAC  GIIIT
GAM195 HOXD1          GGGATGGGGGTCGCCTGGGACTTC 2815 TG    AC ___   AG  CI
                        GGATGGGG CGC  GGA  TTC
                        IIIIIIII III  III III
                        CCTACCCC GCG  CCT  AAG
                        __     CA  GAC  G_  AI
GAM195 MYO1D          GGAAGGAGA--GAGGAAGTTCC  2812   T  CCGC    I
                        GGA GGGGA   GGAAGTT
                        III IIIII   IIIIIII
                        CCT CCTCT   CCTTCAA
                         T   CT__      G
GAM195 MYO1D          GGAAGGAGA--GAGGAAGTTCC   2812 TGGGAT   CCGC
                          GGGGA   GGAAGTTC
                          IIIII   IIIIIIII
                          CCTCT   CCTTCAAG
                        TT____    CT__
GAM195 PRKACA         TGGGATGGGGA-----GAAGTT  2825          CCGCG
                        TGGGATGGGGA   GAAGTT
                        IIIIIIIIIII   IIIIII
                        ACCCTACCCCT   CTTCAA
                            _____
GAM195 PRKACA         TGGGATGGGGA-----GAAGTT  2825 _        CCGCG
                        GGGATGGGGA   GAAG
                        IIIIIIIIII   IIII
                        CCCTACCCCT   CTTC
                        A         _____
GAM195 RELA          GGGATGGGGGACC-CCACAGTTCC 2813      _ G GA    I
                        GGATGGGG ACC CG AGTTC
                        IIIIIIII III II IIIII
                        CCTACCCC TGG GT TCAAG
                          C  G G_  I
GAM195 RELA          GGGATGGGGGACC-CCACAGTTCC 2813 TG    _ G GA    I
                         GGATGGGG ACC CG AGTTCC
                         IIIIIIII III II IIIIII
                         CCTACCCC TGG GT TCAAGG
                        __    C  G G_  G
GAM195 RFNG          TGGGATGGGCAGGTCAGCGGAA 2821       GACC___    GTTCC
                        TGGGATGGG   GCGGAA
                        IIIIIIIII   IIIIII
                        ACCCTACCC   CGCCTT
                         GTCCAGT   IIICC
GAM195 RFNG          TGGGATGGGCAGGTCAGCGGAA 2821       GACC___   III
                        TGGGATGGG   GCGGA
                        IIIIIIII   IIIII
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                              ACCCTACCC    CGCCT
                              GTCCAGT   TII
GAM195 TBX6          GGGATGGGGCCGGTGGAGGT    2820       A  C_   AGI
                         GGATGGGG CCG GGA
                         ||||||||| ||| |||
                         CCTACCCC GGC  CCT
                             _   CA   CCI
GAM195 TBX6          GGGATGGGGCCGGTGGAGGT    2820 TG      A  C_  A TC
                         GGATGGGG CCG GGA GT
                         ||||||||| ||| ||| ||
                         CCTACCCC GGC  CCT CA
                          __     _   CA  C CI
GAM195 TCIRG1          GGGCTTGGGACTGTGGGAAGTTCC  2816 GGATG    CGC_     I
                           GGGAC   GGAAGTTC
                           |||||   ||||||||
                           CCCTG   CCTTCAAG
                          CGAA_    ACAC      I
GAM195 TCIRG1          GGGCTTGGGACTGTGGGAAGTTCC  2816 TG ATG    CGC_     I
                          GG  GGGAC   GGAAGTTCC
                          ||  |||||  |||||||||
                          CC  CCCTG   CCTTCAAGG
                          __  GAA   ACAC       C
GAM195 THPO          GGGATGGGGGCGTTGGAAG       2819       ACC  GAAII
                         GGGATGGGG  GCG
                         ||||||||| |||
                         CCCTACCCC  CGC
                           ___   AACCT
GAM195 THPO          GGGATGGGGGCGTTGGAAG       2819 TG     AC C_   TTC
                         GGATGGGG  CG GGAAG
                         ||||||||| || |||||
                         CCTACCCC  GC  CCTTC
                           __     C_ AA   CII
GAM195 VASP          TGGGATGGGGAGTG-GGAA       2823        CCGC  GTT
                        TGGGATGGGGA   GGAA
                        ||||||||||   ||||
                        ACCCTACCCCT   CCTT
                          CAC_   III
GAM195 VASP          TGGGATGGGGAGTG-GGAA       2823        CCGC  I
                        TGGGATGGGGA   GGA
                        ||||||||||   |||
                        ACCCTACCCCT   CCT
                          CAC_  T
GAM196 CARD10          CTGGATGGT-GGGAGTCAC     2832    _  T      CTAC
                         CTGG TGGT GGGAGTCAC
                         |||| |||| |||||||||
                         GACC ACCA CCCTCAGTG
                          T   _    IIIG
GAM196 CHS1          TGGTACAGAGGCACCTACTG      2844 CTGGTGGTTG   T
                         GGAG CACCTACT
                         |||| ||||||||
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                              TCTC GTGGATGA
                     TG_____      C
GAM196 FVT1          ACATTCCTGAAGAGCACTGGT   2828 TGAC      CCC__   ATG
                        ATTCCTGAA    CTGGT
                        |||||||||    |||||
                        TAAGGACTT    GACCA
                     ____       CTCGT   GGI
GAM196 GALNT2        ACATTCCTGAGCACCCAGGTA   2829 TGAC    __  CT  TG
                        ATTCCTGA ACCC GGTA
                        |||||||| |||| ||||
                        TAAGGACT TGGG CCAT
                     ____       CG   T_  CT
GAM196 GP9           CTGGTGGTTTGGGCTGACC   2834      _ AGTC TACT
                        CTGGTGGTT GGG   ACC
                        ||||||||| |||   |||
                        GACCACCAA CCC   TGG
                         A  GAC_  IIIG
GAM196 GRLF1         ACACGCCTGAACCCTGGGTTTG   2831 TGACATT     CT ATG
                          CCTGAACCC GGT
                          ||||||||| |||
                          GGACTTGGG CCA
                     TGC____      AC  AAC
GAM196 HD           TGGGGGTGGGG-GACACCTACTG   2842 CT_  TT  GT
                          GGTGG GGGA CACCTACTG
                          ||||| |||| |||||||||
                          CCACC CCCT GTGGATGAC
                     CCC       __   __
GAM196 LARGE        GGTGGTTGGTAGAGGCAGCT   2836 C___    TT G CACCTACT
                          TGGTGG GG AGT
                          |||||| || |||
                          ACCATC CC TCG
                     ACCA     T_ G  ACTIIIGT
GAM196 MMP14        TGACAG--CTGCACCCCTGGT   2841    TTC A     AT
                          TGACA CTG ACCCCTGGT
                          ||||| ||| |||||||||
                          ACTGT GAC TGGGGACCA
                           C__  G     II
GAM196 MYO1D        GGTTGGGAGGCAGCAGCTG    2837 CT____ TG   AGTCACCTACT
                           GG GTTGGG
                           || ||||||
                           TC CGACCT
                     CCTCCG GT    GACIIIGTCAT
GAM196 PARK2        TCCTGGGGAACCCCTGGTATG   2839 TGACATTCCT
                            GAACCCCTGGTATG
                            ||||||||||||||
                            CTTGGGGACCATAC
                     C_____
GAM196 PPIL1        GTAGTAAGTAGTCACCTATTG   2838 CTGGTGGT  _     CTG
                          TGGG AGTCACCTA
                          |||| |||||||||
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                              ATTC TCAGTGGAT
                        C_____    A    AAC
GAM196 PPP4R1           TGAC--TCTTGAAATCCCTGGTAT  2840   AT C  C_        G
                        TGAC TC TGAA  CCCTGGTAT
                        |||| || ||||  |||||||||
                        ACTG AG ACTT  GGGACCATA
                          __  A  TA        I
GAM196 RPH3AL           TGGGGGTTGGGAGTCACAT-CTG  2843 CT  T          CTA
                        GG GGTTGGGAGTCAC  CTG
                        || |||||||||||||  |||
                        CC CCAACCCTCAGTG  GAC
                          C_ _        TA_
GAM196 RPH3AL           CTGGGGGTTGGGAGTCACAT-CTG  2835   T          CTA  I
                        CTGG GGTTGGGAGTCAC  CTG
                        |||| |||||||||||||  |||
                        GACC CCAACCCTCAGTG  GAC
                          C        TA_  I
GAM196 SLC13A3          TTCTAGAACTTCCCCTGGTATG   2845 TGACATTCCTGAA
                              CCCCTGGTATG
                              |||||||||||
                              GGGGACCATAC
                        CTTGAA_____
GAM196 ST3GALVI         CTGGTGGTTATGAATCACC      2833       G     TACT
                        CTGGTGGTTG GAGTCACC
                        |||||||||| ||||||||
                        GACCACCAAT CTTAGTGG
                             A     IIIG
GAM196 TNF              ACATTCCTGAATCCCAGGT      2830 TGAC      C  T  AT
                        ATTCCTGAA CCC GGT
                        ||||||||| ||| |||
                        TAAGGACTT GGG CCA
                          ____      A  T  AA
GAM197 COL19A1          AAGTCACTTTGAATTACAT      2849 TGGCAAGT       CAG
                        CACTTTGA ACAT
                        |||||||| ||||
                        GTGAAACT TGTA
                          _____       TAA
GAM197 FGF12           TGGCAAAAGTCACTT---CAG-CATT 2856    __      TGA  A
                        TGGCA AGTCACTT  CAG CATT
                        ||||| ||||||||  ||| ||||
                        ACCGT TCAGTGAA  GTC GTAA
                        TT        ___  _
GAM197 FMO2            TGGCACCGTCTCTTTGACAGA    2857  A_  A       CATT
                        TGGCA GTC CTTTGACAGA
                        ||||| ||| ||||||||||
                        ACCGT CAG GAAACTGTCT
                          GG  A        IIIT
GAM197 NAPB            AATTCACTTTGACACTCAT      2850 TGGCAAGT       GA
                        CACTTTGACA CAT
                        |||||||||| |||
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                                 GTGAAACTGT  GTA
                                 _____       GA
GAM197 NAT1           AAGTCACTTTTGTGGACATT    2851 TGGCAAGT    GACA
                                 CACTTT   GACAT
                                 ||||||   |||||
                                 GTGAAA   CTGTA
                                 _____       ACAC
GAM197 NRXN1          TCACTTCTACATGACAGACAT    2855 TGGCAAGTC TT
                                 AC TGACAGACATT
                                 || ||||||||||
                                 TG ACTGTCTGTAG
                         A_____    T_
GAM197 PDE1A           GCTATTGACTTTGACAGGCAT    2852 TGGCAAGTC      A T
                                 ACTTTGACAG CAT
                                 |||||||||| |||
                                 TGAAACTGTC GTA
                         ATAAC____        C  T
GAM197 PRKR           AAGTCAACCGCTGGTTGACAGACA  2848 TGGCA GT A __        TTI
                                 A C CT TTGACAGACA
                                 | | || ||||||||||
                                 T G GA AACTGTCTGT
                             G____ TG C CC        CGC
GAM197 SLC29A1        GGCA-GACAGTCTGACAGACA     2854 TG  A T  C
                                 GCA G CA TTTGACAGACAT
                                 ||| | || |||||||||||
                                 CGT C GT AGACTGTCTGTG
                             __  _T C
GAM197 SLC7A6         GGCAAGTCAGCCTTTGCATAAGACA 2853 TG       __      AC__    TII
                                 GCAAGTCA CTTTG  AGACAT
                                 |||||||| |||||  ||||||
                                 CGTTCAGT GAAAC  TCTGTG
                             __      CG   GTAT     III
GAM198 ATBF1          CAGTCGTGCCGGGCGCAGGCC     2866 TC    T C      CC
                                 AGTTGT CC GGCGCAGGCC
                                 |||||| || ||||||||||
                                 TCAGCA GG CCGCGTCCGG
                             __    C C      CI
GAM198 CCNF           CAGT-GTGCAGGGACGCAGGCCCC  2863 TC  _  TCCC        I
                                 AGT TGT  GGCGCAGGCCCC
                                 ||| |||  |||||||||||
                                 TCA ACG  CTGCGTCCGGGG
                             __  C  TCC_       G
GAM198 CLDN5          TCAGCTG---CGGGCGCAGGC     2872      TCCC     C
                                 TCAGTTGT  GGCGCAGGC
                                 ||||||||  ||||||||||
                                 AGTCGACG  CCGCGTCCG
                                   C___      I
GAM198 COX4I1         CAGGTG---CAGGCGCAGGCC     2865 TCAGTTGTTCCC
                                 GGCGCAGGCC
                                 ||||||||||
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                              CCGCGTCCGG
                          TCCACGT_____
GAM198 CST1        TCTGTCTGTCTCTTGGCGCAGGC  2869 TCA _ _ CC      CCCI
                          GT TGT TC GGCGCAGGC
                          II III II IIIIIIIII
                          CA ACA AG CCGCGTCCG
                          AGA G  G  AA      IIIC
GAM198 EZH2        GTTGTTCCCGCGCGTCGCCCCC   2868 TCAGTT    G  AG_
                             GTTCCG CGC  GCCCC
                             IIIIIII III  IIIII
                             CAAGGGC GCG  CGGGG
                          _____    _ CAG
GAM198 FUT3        GTTCCCGGCAGCCCAGGCACC    2867 TCAGTT T_ _   AG_ CC
                          GT CCC GGCGC  GCC
                          II III IIIII  III
                          CG GGG CCGTG  CGG
                          C_____ TC T  GTA CI
GAM198 KCNK10        TCAGTTGTTTATGGCACAG      2871       CCC     GCCC
                          TCAGTTGTT GGCGCAG
                          IIIIIIIII IIIIIII
                          AGTCAACAA CCGTGTC
                             ATA      IIIC
GAM198 KDR         AGTGATGCCCGGCGCAGGC      2862 TCAGTTGTT       CC
                             CCCGGCGCAGGC
                             IIIIIIIIIIII
                             GGGCCGCGTCCG
                          ACTAC____        TC
GAM198 LAD1        TCAGTGGCTG--GGAGCAGGCCCC 2873    T CCC C
                          TCAGT GTT  GG GCAGGCCCC
                          IIIII III  II IIIIIIIII
                          AGTCA CGA  CC CGTCCGGGG
                            C  C__ T
GAM198 MKI67       AGTTGTTCCTGCCACCGTGCCC   2861 TCAG    CG _ AG_  C
                          TTGTTCC GC GC  GCCC
                          IIIIIII II II  IIII
                          AACAAGG CG TG  CGGG
                          ____     A_ G GCA  A
GAM198 MYO1D        CAGTT--TCACGGGCGCAGGCCCC 2864 TC   GTTCCC
                          AGTT    GGCGCAGGCCCC
                          IIII    IIIIIIIIIIII
                          TCAA    CCGCGTCCGGGG
                          __  AGTGC_
GAM198 PTPRG        AGTTGTGGCTCCGGCGCAGGC    2860 TCA T  C      CCC
                          GT GTTCC GGCGCAGGC
                          II IIIII IIIIIIIII
                          CA CGAGG CCGCGTCCG
                          AA_ C  _    ACI
GAM198 TNP2        TCATTTCTGCCCCTGTGCAGGCCCC 2870  GT__ T GGC      II
                          TCA  TGT CCC  GCAGGCCCC
                          III  III III  IIIIIIIII
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                        AGT   ACG GGG   CGTCCGGGG
                          AAAG _  ACA        II
GAM199 ADCY6            CACCCAGTGAGCACAGAGTCCA  2876        ____ T  GIII
                         CACCCAGTGA  AG GTCCA
                         IIIIIIIII   II IIIII
                         GTGGGTCACT   TC CAGGT
                           CGTG  T    IIIG
GAM199 BAIAP3          CACCCAGTG--GTG-CCAG     2877        AA  T
                         CACCCAGTG  GTG CCAG
                         IIIIIIIII  III IIII
                         GTGGGTCAC  CAC GGTC
                               __  _
GAM199 EGFL4           CCAAGTAGACAGTGTCCAG      2879 CACCC  _ _       I
                          AGT GA AGTGTCCAG
                          III II IIIIIIIII
                          TCA CT TCACAGGTC
                         T____  T G        C
GAM199 WT1            CACCCAGTGATGCATCTAG       2878       A    CAGI
                         CACCCAGTGA GTGTC
                         IIIIIIIIII IIIII
                         GTGGGTCACT CGTAG
                           A    ATCI
GAM200 ADRBK1          GGTTGG-GGCAAGAGGGGACAG    2884 TG    T   CC
                          GTTGG GGCA AGGGGACAG
                          IIIII IIII IIIIIIIII
                          CAACC CCGT TCCCCTGTC
                           __   _  TC
GAM200 APOC1          TTGGTGGCACCTGGGGCCA       2895 TGGTTG    A  A
                          GTGGCACC GGGG CA
                          IIIIIIII IIII II
                          CACCGTGG CCCC GT
                          _____    A  G
GAM200 BACE2         GTTGGTGGCACATGTAGACA       2885 TGGT     CAGG   G
                         TGGTGGCAC   GGACA
                         IIIIIIIII   IIIII
                         ACCACCGTG   TCTGT
                          ____      TACA  G
GAM200 CASP2         TTGGTGGCAGCAGCCAACAG        2896 TGGT  TG _ _  CAG
                         TGG  GCA CCAG GGGA
                         III  III IIII IIII
                         ACC  CGT GGTT TCCT
                         C___  GT  C  G  AII
GAM200 DLEC1         TGGTTGGTGTACTCCAGGAG-CAG    2891        _ A    A I
                         TGGTTGGTG GC CCAGGGG CAG
                         IIIIIIIII II IIIIIII III
                         ACCAACCAC TG GGTCCTC GTC
                             A A   _ I
GAM200 EGLN2        TGGTAGGAGGGGAGCAGGGGACAG     2892    T  T CAC_       II
                         TGGT GG GG   CAGGGGACAG
                         IIII II II   IIIIIIIIII
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                    ACCA CC CC   GTCCCCTGTC
                     T T CCTC         II
GAM200  EZH1        GGTGGCACCACAGCCTGGGACAG   2882 TGGTTG TG  ACCAG      I
                     G GC    GGGACAG
                     I II    IIIIIII
                     T CG    CCCTGTC
                    GTGG__ GT GA___        C
GAM200  G6PD        GTTGGTGGGAC-AGGGGACA   2886 TGGT    CAC
                    TGGTGG  CAGGGGACA
                    IIIIII  IIIIIIIII
                    ACCACC  GTCCCCTGT
                    ____      CT_
GAM200  JDP1        TGTTGGCAGCATAGGGGACAG   2889 TGGTT TG  CC
                     GG GCA AGGGGACAG
                     II III IIIIIIIII
                     CC CGT TCCCCTGTC
                    _____ GT  A_
GAM200  KLHL3       TTGGTGGCATCTGTGGGCAG   2897 TGGTTG    CCAG_ A
                     GTGGCA    GGG CAG
                     IIIIII    III III
                     CACCGT    CCC GTC
                    _____    AGACA   _
GAM200  NDST1       TGATGGGTGACGACAGGGGACAG  2893   T   AC      I
                    TGGT GGTGGC CAGGGGACAG
                    IIII IIIIII IIIIIIIIII
                    ACTA CCACTG GTCCCCTGTC
                       C    CT        I
GAM200  NTSR1       GGTTGGTGGCCCTTGGGCAC   2883 TG     A A_ G AG
                     GTTGGTGGC CC GGG AC
                     IIIIIIIII II III II
                     CAACCACCG GG CCC TG
                    __      _ AA  G AI
GAM200  PCTK1       TGTTTGGGCAGGCAGCAGGGGACA  2890 TG __ _  C     GII
                    GTT GGT GGCA CAGGGGACA
                    III III IIII IIIIIIIII
                    CAA CCG CCGT GTCCCCTGT
                    A_ AC  T  C      III
GAM200  PKD2L1      TTGCTGCAAGCCCCAGGGGAC   2894 TGGT GT A     AG
                     TG GGC CCAGGGGAC
                     II III IIIIIIIII
                     AC TCG GGTCCCCTG
                    G___ GT G     GT
GAM200  TUFT1       TGGGTGCAGCCAGGGGACAG   2888 TGGTTGGTG _
                     GCA CCAGGGGACAG
                     III IIIIIIIIII
                     CGT GGTCCCCTGTC
                    A_____   C
GAM200  WHN         TGGCTTAGTGGCAT-AGGGGACAG  2887  _   CC     I
                    TGGTT GGTGGCA AGGGGACAG
                    IIIII IIIIIII IIIIIIIII
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                          ACCGA TCACCGT  TCCCCTGTC
                            A      A_        I
GAM201 BRCA1          TGTCTGTTCATTTGGCTTGTTA   2913       ATG     ATGA
                     TGTCTGTTCAT TTGGTT
                     |||||||||| ||||||
                     ACAGACAAGTA AACCGA
                              ___      ACAA
GAM201 BRCA1          TGTCTGTTCATTTGGCTTGTTA   2913       ATG     I
                      TCTGTTCAT TTGGTT
                      |||||||| ||||||
                      AGACAAGTA AACCGA
                              ___      A
GAM201 BTC           CATTTTCA--AATGAGCAA      2903     AAA        TC
                     CATTT CGAATGAGCAA
                     ||||| |||||||||||
                     GTAAA GTTTACTCGTT
                         A__      II
GAM201 BTC           CATTTTCA--AATGAGCAA      2903     AAA        I
                     CATTT CGAATGAGCA
                     ||||| ||||||||||
                     GTAAA GTTTACTCGT
                         A__      T
GAM201 C18orf1       TGTCTGTTCACATCTCTGTGAT   2915        G G TATGA
                     TGTCTGTTCATAT TT GT
                     ||||||||||||| || ||
                     ACAGACAAGTGTA AG CA
                          G  A  CTAII
GAM201 C18orf1       TGTCTGTTCACATCTCTGTGAT   2915        G G TAI
                      GTCTGTTCATAT TT GT
                      |||||||||||| || ||
                      CAGACAAGTGTA AG CA
                          G  A  CTI
GAM201 C5R1          TGTCAATATCCTGGTTATGA     2917  C  G       I
                     GTT ATAT TTGGTTATG
                     ||| |||| |||||||||
                     CAG TATA GACCAATAC
                       T   G      I
GAM201 C5R1          TGTCAATATCCTGGTTATGA     2917 TGTCTGTTC  G
                         ATAT TTGGTTATG
                         |||| |||||||||
                         TATA GACCAATAC
                     T_____     G
GAM201 COG3          CATTTAAACGAGGCAGTTATCA   2905       ATGA  ___  GI
                     CATTTAAACGA GCA ATCA
                     |||||||||| ||| ||||
                     GTAAATTTGCT CGT TAGT
                           C___  CAA  II
GAM201 COG3          CATTTAAACGAGGCAGTTATCA   2905       ATGA ATCI
                      ATTTAAACGA GCA
                      ||||||||| |||
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                              TAAATTTGCT   CGT
                                C___    CAAT
GAM201 CXCL6          CATTTCTATGTAAATTAGCAATCAG 2901    AAAC__  G      II
                         CATTT    GAAT AGCAATCAG
                         |||||    |||| |||||||||
                         GTAAA    TTTA TCGTTAGTC
                             GATACA   A      II
GAM201 CXCL6          CATTTCTATGTAAATTAGCAATCAG 2901 ATTTAAAC  G      I
                             GAAT AGCAATCA
                             |||| ||||||||
                             TTTA TCGTTAGT
                         AAGATACA   A     I
GAM201 EXT2         TCTGTTCTTAAAATGGTTATGA   2911    A TGT      I
                         CTGTTC TA  TGGTTATG
                         |||||| ||  |||||||||
                         GACAAG AT  ACCAATAC
                          A TTT      I
GAM201 EXT2         TCTGTTCTTAAAATGGTTATGA   2911 TGTC   A TGT
                          TGTTC TA  TGGTTATGA
                          ||||| ||  |||||||||
                          ACAAG AT  ACCAATACT
                         ____     A TTT
GAM201 FBLN1         CATTAAAA--AATGAGCAA       2902 CAT   C      TC
                             TTAAA GAATGAGCAA
                             ||||| ||||||||||
                             AATTT TTTACTCGTT
                         GT_   _         II
GAM201 FBLN1         CATTAAAA--AATGAGCAA       2902 CAT   C      I
                             TTAAA GAATGAGCA
                             ||||| |||||||||
                             AATTT TTTACTCGT
                         GT_   _        T
GAM201 FBXL3A       TCTTCTCATATGTTGCTGTAGGA 2909 TG         GTTATI
                             TTCATATGTTG
                             |||||||||||
                             GAGTATACAAC
                         A_         GACATC
GAM201 FBXL3A       TCTTCTCATATGTTGCTGTAGGA 2909 TGTCTG         GTTATGAI
                             TTCATATGTTG
                             |||||||||||
                             GAGTATACAAC
                         AA____         GACATCCT
GAM201 FGF1         TCAGTATCATATGTTAGAGATGA 2908 CT _         TT I
                             GT TCATATGTTGG ATG
                             || ||||||||||| |||
                             CA AGTATACAATC TAC
                         T_ T        TC I
GAM201 FGF1         TCAGTATCATATGTTAGAGATGA 2908 TGTCT _         TT I
                             GT TCATATGTTGG ATGA
                             || ||||||||||| ||||
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                          CA AGTATACAATC TACT
                          T___ T      TC  T
GAM201 FOXD2      TGTCTGTTCATGGGTCTGG     2914      AT GII
                 TGTCTGTTCAT GTT
                 |||||||||| |||
                 ACAGACAAGTA CAG
                          CC  ACC
GAM201 FOXD2      TGTCTGTTCATGGGTCTGG     2914      ATG_  TTATG
                 TGTCTGTTCAT TTGG
                 |||||||||| ||||
                 ACAGACAAGTA GACC
                          CCCA  IIIAG
GAM201 IDH1    CATTTACCCTTTTGAGCAATC     2904     AACGAA      AG
               CATTTA   TGAGCAATC
               ||||||   |||||||||
               GTAAAT   ACTCGTTAG
                 GGGAAA       II
GAM201 IDH1    CATTTACCCTTTTGAGCAATC     2904     AACGAA    I
               ATTTA   TGAGCAAT
               |||||   ||||||||
               TAAAT   ACTCGTTA
                 GGGAAA     I
GAM201 NEB       TAATAAGCATTAGCAATCAG     2907 TAAACGAATG_     II
                          AGCAATCA
                          ||||||||
                          TCGTTAGT
                 ATTATTCGTAA      CI
GAM201 PTPN7     TGTCTG--CATG-GATGGTTATGA 2916     TCAT T_
                 TGTCTGT  ATG TGGTTATGA
                 |||||||  ||| |||||||||
                 ACAGACG   TAC ACCAATACT
                     ___  CT
GAM201 PTPN7     TGTCTG--CATG-GATGGTTATGA 2916 _   TCAT T_
                  GTCTGT  ATG TGGTTATG
                  ||||||  ||| ||||||||
                  CAGACG   TAC ACCAATAC
                 A   ___   CT
GAM201 RPL5      CTGTTCATAAGTTTATTAT     2906      T  G II
                 CTGTTCATA GTT GTTA
                 ||||||||| ||| ||||
                 GACAAGTAT CAA TAAT
                      T  A  AI
GAM201 RPS19     TTTTTACGAATGAGGCAAT     2919 CATTTAA     _ CA
                    ACGAATGAG CAAT
                    ||||||||| ||||
                    TGCTTACTC GTTA
                 AAA___      C  AA
GAM201 RPS19     TTTTTACGAATGAGGCAAT     2919 TTTAA      _ II
                    ACGAATGAG CAA
                    ||||||||| |||
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                                   TGCTTACTC GTT
                                 AAAAA     C   AI
GAM201  SAR1          TCTGTTCATA-ATT--TTATGA   2910        TGTTGGTTAI
                                 TCTGTTCATA

                                 |||||||||
                                 AGACAAGTAT
                                   TAAAATACTI
GAM201  SAR1          TCTGTTCATA-ATT--TTATGA   2910 TGTC      TGTTGG
                                 TGTTCATA    TTATG

                                 ||||||||   |||||
                                 ACAAGTAT   AATAC
                                 ____      TAA___
GAM201  TDG        ATTATAAAGAGAA-GAGCAATCA   2900 CATTTAAAC  T      GI
                                 GAA GAGCAATCA

                                 ||| |||||||||
                                 CTT CTCGTTAGT
                                 AATATTTCT  _       AI
GAM201  TDG        ATTATAAAGAGAA-GAGCAATCA   2900 TTTAAAC_  T      I
                                 GAA GAGCAATC

                                 ||| ||||||||
                                 CTT CTCGTTAG
                                 ATATTTCT  _        I
GAM201  TNFSF10       TTCACTATGTTGGTCACTATG   2918     _        IIIC
                                 TTCAT ATGTTGGTTAT

                                 ||||| ||||||||||||
                                 AAGTG TACAACCAGTG
                                     A       ATAC
GAM201  TRIM9       TGTCTAGGTCCTTTGTTGGTTA   2912     __  ATA      TGA
                                 TGTCT GTTC  TGTTGGTTA

                                 ||||| ||||  |||||||||
                                 ACAGA CAGG  ACAACCAAT
                                     TC  AA_        III
GAM201  TRIM9       TGTCTAGGTCCTTTGTTGGTTA   2912 G  __  ATA      I
                                 TCT GTTC  TGTTGGTT

                                 ||| ||||  ||||||||
                                 AGA CAGG  ACAACCAA
                                 _  TC  AA_       I
GAM201  ZNF124        TTCAAA--AATGAGCAACCA   2920 CATTTAAAC
                                 GAATGAGCAATCA

                                 ||||||||||||||
                                 TTTACTCGTTGGT
                                 GTT_____
GAM201  ZNF124        TTCAAA--AATGAGCAACCA   2920 TTAAAC          I
                                 GAATGAGCAATC

                                 |||||||||||||
                                 TTTACTCGTTGG
                                 AAGTT_         I
GAM202  ADSL     AACAGGAAAGCACCATGGGAAGA   2923 ACA     _       I
                                 GAGAG GCCATGGGAAG

                                 ||||| ||||||||||||
```

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                          CTTTC TGGTACCCTTC
                          TC_      G          I
GAM202  ADSL         AACAGGAAAGCACCATGGGAAGA  2923 TGAACA    _          TI
                          GAGAG GCCATGGGAAGA
                          ||||| |||||||||||
                          CTTTC TGGTACCCTTCT
                          GTC___    G        TC
GAM202  BAALC          TGTACAGAGAGGCCAAGGGGAAG  2939 A       T_     ATI
                          TG ACAGAGAGGCCA GGGAAG
                          || ||||||||||| ||||||
                          AC TGTCTCTCCGGT CCCTTC
                           A       TC   III
GAM202  BAALC          TGTACAGAGAGGCCAAGGGGAAG  2939 GA       T_    I
                          ACAGAGAGGCCA GGGAA
                          |||||||||||| |||||
                          TGTCTCTCCGGT CCCTT
                          A_         TC   I
GAM202  BRS3          GAACAGAACAGA-ATGGGAAGA  2935 _      A CC      I
                          AACAGAG GG ATGGGAAG
                          ||||||| || |||||||||
                          TTGTCTT TC TACCCTTC
                           C       G T_    I
GAM202  BRS3          GAACAGAACAGA-ATGGGAAGA  2935 T___       GAGGCC      T
                          GAACAGA    ATGGGAAGA
                          |||||||    |||||||||
                          CTTGTCT    TACCCTTCT
                          TTGT       _____        T
GAM202  CARPX        AGGGAATCCCTGGGAAGAT     2930 A  G A     II
                          AG GAG CC TGGGAAGA
                          || ||| || |||||||||
                          TC CTT GG ACCCTTCT
                           C  A  G     AI
GAM202  CBFA2T2       TGCACAGAGAGGCTGTGGG      2940 A     CA   AAGA
                          TG ACAGAGAGGC TGGG
                          || |||||||||| ||||
                          AC TGTCTCTCCG ACCC
                           G       AC   IIIT
GAM202  CBFA2T2       TGCACAGAGAGGCTGTGGG      2940 A     CA  II
                          TG ACAGAGAGGC TGG
                          || |||||||||| |||
                          AC TGTCTCTCCG ACC
                           G       AC  CI
GAM202  HIP1        GAACAGAGATGACCATGGG      2932          _    II
                          GAACAGAGA GGCCATGG
                          ||||||||| ||||||||
                          CTTGTCTCT CTGGTACC
                              A    CI
GAM202  HIP1        GAACAGAGATGACCATGGG      2932 TG      _    AAGA
                          AACAGAGA GGCCATGGG
                          |||||||| |||||||||
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                          TTGTCTCT CTGGTACCC
                            __        A        AIII
GAM202 HOXA7        ACA-AGATGCC-TGGGAAGAT    2928 CA    G   A       I
                          GAGA GCC TGGGAAGA
                          |||| ||| |||||||||
                          TTCT CGG ACCCTTCT
                            TG   A   _        I
GAM202 HOXA7        ACA-AGATGCC-TGGGAAGAT    2928 TGAACAG   G   A
                          AGA GCC TGGGAAGA
                          ||| ||| |||||||||
                          TCT CGG ACCCTTCT
                          _____      A   _
GAM202 HSD17B2       TGAACAGAGAGTCAA---GAAG    2943        GC  T  AI
                        TGAACAGAGAG CA GGG
                        |||||||||| || |||
                        ACTTGTCTCTC GT CTT
                          A_  T  CI
GAM202 HSD17B2       TGAACAGAGAGTCAA---GAAG    2943        GC  TG   A
                        TGAACAGAGAG CA GGAAG
                        |||||||||| || |||||
                        ACTTGTCTCTC GT TCTTC
                          A_  __   I
GAM202 IL1R1        AGAGCGGCATCATGGGAAG     2929    A   __       III
                          AGAG GGC CATGGGAA
                          |||| ||| ||||||||
                          TCTC CCG GTACCCTT
                           G  TA      CII
GAM202 MAGP2        TGAACAGAGCCACTCCCTGGAAAG  2937       AGG__  A    ATI
                        TGAACAGAG   CC TGGGAAG
                        |||||||||   || |||||||
                        ACTTGTCTC   GG ACCTTTC
                          GGTGA  G       III
GAM202 MAGP2        TGAACAGAGCCACTCCCTGGAAAG  2937 GA    AGG__  A    I
                          ACAGAG   CC TGGGAA
                          ||||||   || |||||||
                          TGTCTC   GG ACCTTT
                          __    GGTGA  G    I
GAM202 MAP2K1       TGAACAGAGACAGGCATGGGAAG   2938        __  C     ATI
                        TGAACAGAGA GGC ATGGGAAG
                        |||||||||| ||| |||||||||
                        ACTTGTCTCT CCG TACCCTTC
                          GT  _    III
GAM202 MAP2K1       TGAACAGAGACAGGCATGGGAAG   2938 G     __  C     I
                          AACAGAGA GGC ATGGGAA
                          |||||||| ||| |||||||
                          TTGTCTCT CCG TACCCTT
                          _      GT  _   I
GAM202 MPP3        TGGACAGAGAGG--ATGGGAA     2942 A     CC    GA
                        TG ACAGAGAGG ATGGGAA
                        || ||||||||| |||||||
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                              AC TGTCTCTCC  TACCCTT
                              C        __      II
GAM202 MPP3        TGGACAGAGAGG--ATGGGAA    2942 _ A      CC    I
                        G ACAGAGAGG  ATGGGA
                        I IIIIIIIII IIIIII
                        C TGTCTCTCC  TACCCT
                        A C        __      I
GAM202 MYL3        ACAGAGAGG-GATGTGGAGA    2927 _      CC _ AGI
                        CAGAGAGG  ATG GGA
                        IIIIIIII III III
                        GTCTCTCC  TAC CCT
                        T    C_  A CII
GAM202 MYL3        ACAGAGAGG-GATGTGGAGA        2927 TGAACA    CCA_  GA
                           GAGAGG   TGG AGA
                           IIIIII   III III
                           CTCTCC   ACC TCT
                        _____      CTAC  TC
GAM202 PKP1       GAGCAGAGAGGCGAGGCGA      2934  A     CAT GII
                        GA CAGAGAGGC  GG
                        II IIIIIIIII  II
                        CT GTCTCTCCG  CC
                        C        CT_ GCT
GAM202 PKP1       GAGCAGAGAGGCGAGGCGA      2934 TGAA      CAT _ AGA
                           CAGAGAGGC  GG GA
                           IIIIIIIII  II II
                           GTCTCTCCG  CC CT
                        TC__        CT_ G CII
GAM202 PODXL       GAACATAGAGGG--TGGGAAGAT   2936    G    CCA     I
                        GAACA AGAGG  TGGGAAG
                        IIIII IIIII  IIIIIII
                        CTTGT TCTCC  ACCCTTC
                           A    C__    T
GAM202 PODXL       GAACATAGAGGG--TGGGAAGAT   2936 TG   G    CCA
                           AACA AGAGG   TGGGAAGAT
                           IIII IIIII   IIIIIIIII
                           TTGT TCTCC   ACCCTTCTA
                        __    A   C__
GAM202 PTPRA       AACTGAG-GGCCATGGGCTGAT    2925 ACA_ A     AA I
                        GAG GGCCATGGG GA
                        III IIIIIIIII II
                        CTC CCGGTACCC CT
                        TTGA  _      GA I
GAM202 PTPRA       AACTGAG-GGCCATGGGCTGAT    2925 TGAACA A     AA
                           GAG GGCCATGGG GAT
                           III IIIIIIIII III
                           CTC CCGGTACCC CTA
                        GA____  _      GA
GAM202 RAB38       AACATTCAGGCCATGGCAAG      2924  GAG      G  I
                        ACA  AGGCCATGG AA
                        III  IIIIIIIII II
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                    TGT   TCCGGTACC TT
                    AAG          G  I
GAM202  RAB38       AACATTCAGGCCATGGCAAG     2924 TGAACAGAG       G   A
                       AGGCCATGG AAG
                       |||||||| |||
                       TCCGGTACC TTC
                    GTAAG____        G  A
GAM202  RGS5        TGAGCAAAGCTGCTGTGGGAAGAT 2945  A   AG  CA       I
                    TGA CAGAG GC TGGGAAGAT
                    ||| ||||| || |||||||||
                    ACT GTTTC CG ACCCTTCTA
                      C   GA  AC      I
GAM202  RGS5        TGAGCAAAGCTGCTGTGGGAAGAT 2945  A   AG  CA       I
                    GA CAGAG GC TGGGAAGA
                    || ||||| || ||||||||
                    CT GTTTC CG ACCCTTCT
                     C   GA  AC      I
GAM202  RNF4        GAACAGAGATGGCC-TGGGA      2933       _   A   II
                    GAACAGAGA GGCC TGGG
                    ||||||||| |||| ||||
                    CTTGTCTCT CCGG ACCC
                      A   _   TI
GAM202  RNF4        GAACAGAGATGGCC-TGGGA      2933 TG    _   A   AGA
                     AACAGAGA GGCC TGGGA
                     |||||||| |||| |||||
                     TTGTCTCT CCGG ACCCT
                      __     A  _    CII
GAM202  SNAI1       ACAGAAATGGCCATGGGAAG      2926       _        II
                    ACAGAGA GGCCATGGGAA
                    ||||||| ||||||||||||
                    TGTCTTT CCGGTACCCTT
                         A       CI
GAM202  SNAI1       ACAGAAATGGCCATGGGAAG      2926 TGAACA  _        A
                       GAGA GGCCATGGGAAG
                       |||| |||||||||||
                       CTTT CCGGTACCCTTC
                    _____     A       C
GAM202  TMEPAI      TGAACAGAG----CTTGGGAA     2941        AGGCCA   G
                    TGAACAGAG     TGGGAA
                    |||||||||     ||||||
                    ACTTGTCTC     ACCCTT
                       GA____      I
GAM202  TMEPAI      TGAACAGAG----CTTGGGAA     2941 _      AGGCCA
                     GAACAGAG     TGGGA
                     ||||||||     |||||
                     CTTGTCTC     ACCCT
                      A   GA____
GAM202  TNFSF4      AGAGGCCAACATGGGAAGA       2931      ___       III
                    AGAGGCCA  TGGGAAG
                    ||||||||  |||||||
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                        TCTCCGGT  ACCCTTC
                           TGT      TII
GAM202 TP63         TGACCAGA-ATGC-ATGGGAAGAT  2944   A    AG  C
                       TGA CAGAG  GC ATGGGAAGAT
                       ||| ||||| || ||||||||||
                       ACT GTCTT  CG TACCCTTCTA
                         G     A_  _
GAM202 TP63         TGACCAGA-ATGC-ATGGGAAGAT  2944 _  A    AG  C        I
                        GA CAGAG  GC ATGGGAAGA
                        || ||||| || |||||||||
                        CT GTCTT  CG TACCCTTCT
                         A  G    A_ _        I
GAM203 CHGB           TGTGATGGCTGCTTCTTAAC      2950        _  AA_     GTTTC
                      TGTGATGGC GC  TTAAC
                      ||||||||| ||   |||||
                      ACACTACCG CG  AATTG
                         A  AAG    IIICC
GAM203 LZTFL1        TGTGATGGC-C-ATCAATGT      2951      G  A   C  TT
                     TGTGATGGC CA TTAA GT
                     ||||||||| || |||| ||
                     ACACTACCG GT AGTT CA
                         _  _   A II
GAM203 MUCDHL         TGTGATGGCCGAGTTGAGGT      2952       GCAATTAACGTTTC
                      TGTGATGGC
                      |||||||||
                      ACACTACCG
                         GCTCAACTCCAIII
GAM203 PPL         TGGTGGCTGACAATTAACGT      2948 TGTGA   __        C
                      TGGC  GCAATTAACGTTT
                      ||||  |||||||||||||
                      ACCG  TGTTAATTGCAGG
                         C____  AC         I
GAM203 STAT1        TGTGATGGCGATAGCAATTA      2949      ____      ACGTTTC
                     TGTGATGGC  GCAATTA
                     |||||||||  |||||||
                     ACACTACCG  CGTTAAT
                        CTAT     IIICCTT
GAM204 ABCC3         TGAGGATGACAGGGG-CCAG      2963 TGTGA      A    TCC
                       GTGACAGGGG CCAG
                       |||||||||| ||||
                       TACTGTCCCC GGTC
                       TCC__       _  TTI
GAM204 FE65L2       GAGGGGCAGGGGACC--TCCT     2958 TGTGAGTGA       AG
                        CAGGGGACC TCC
                        ||||||||| |||
                        GTCCCCTGG AGG
                       CCC_____      __
GAM204 GLTSCR1       TGAGGTGACAGGGCAGCCA      2964 TGTGA      GAC   C
                        GTGACAGGG CAGTC
                        ||||||||| |||||
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                          CACTGTCCC  GTCGG
                     TC___        ___     T
GAM204  GPC1         GTGAGTGACAGGAGGTCACCAG   2960 TG          ___    TCCT
                       TGAGTGACAGGGG  ACCAG
                       ||||||||||||  |||||
                       ACTCACTGTCCTC  TGGTC
                          __            CAG    CIII
GAM204  GUK1         AGGGACAGGGGA-CAGCCC      2955 TGTGAGTG      C
                         ACAGGGGAC AGTC
                         ||||||||| ||||
                         TGTCCCCTG TCGG

                       _____    _
GAM204  HTR4         GTGAGTGAC-GGGAACATGTC      2962 TG     A    CA   C
                       TGAGTGAC GGGGAC  GTC
                       |||||||| |||||| |||
                       ACTCACTG CCCTTG  CAG
                          __      _    TA   T
GAM204  KRT4         AGTGACA-GGGCCCAGGCC      2956 TGTGAGTG    GA    T
                         ACAGGG  CCAG C
                         |||||| |||| |
                         TGTCCC  GGTC G
                       _____      G_   C
GAM204  NDST1        GTGAC-GACAGGGGA-CAGTC     2961 TG  G       C   C
                         TGA TGACAGGGGAC AGTC
                         ||| ||||||||||| ||||
                         ACT GCTGTCCCCTG TCAG
                          __  _       _   C
GAM204  PIGR         TGTCACTGAGGAGGGGACCAG    2966 TG____   T  CA       TCCT
                       TGAG GA  GGGGACCAG
                       |||| ||  |||||||||
                       ACTC CT  CCCCTGGTC
                     ACAGTG   _  __        IIIT
GAM204  SEPN1        GAGTGACAGGG---CAGCCC    2957 TGTGAG      GAC
                       TGACAGGG  CAGTC
                       |||||||| |||||
                       ACTGTCCC  GTCGG

                       _____    ___
GAM204  SH3BP2         GTGAGTGTGATGGGGGGACCAGT  2959 TG   ACA___      CCTI
                         TGAGTG   GGGGACCAGT
                         ||||||   ||||||||||
                         ACTCAC   CCCCTGGTCA
                          __   ACTACC      CIII
GAM204  ZNF43        TGGGTG-CAG-GGACCAGT     2965 TGTGA  A   G   C
                         GTG CAGGG ACCAGT
                         ||| ||||| ||||||
                         CAC GTCCC TGGTCA
                     C____  _  _     C
GAM205  BCL2L2       GTTCTGGCGAGCACAACTACGTTGC 2970 T    _  CCC  _  AGI
                       CTGGCG GC  ATT CGT
                       ||||||| ||  ||| |||
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                        GACCGC CG  TGA GCA
                        _       T TGT  T  AII
GAM205 BCL2L2           GTTCTGGCGAGCACAACTACGTTGC 2970 TG     _ CCC _ A II
                        TTCTGGCG GC  ATT CGT GC
                        IIIIIIII II  III III II
                        AAGACCGC CG  TGA GCA CG
                        __        T TGT  T  A GI
GAM205 EEF1A1           TGTTCTGGCGGCAAACCC--TCGT 2972        ___ AT  AGC
                        TGTTCTGGCGGC CCC TCGT
                        IIIIIIIIIII III IIII
                        ACAAGACCGCCG GGG AGCA
                        TTT __    III
GAM205 EEF1A1           TGTTCTGGCGGCAAACCC--TCGT 2972        ___ ATTCGI
                        TTCTGGCGGC  CCC
                        IIIIIIIIII III
                        AAGACCGCCG  GGG
                        TTT AGIIIG
GAM205 GPR56           TCTGCCCTGGGCCCCATTCG   2971 _____ CG       III
                        TCTGG GCCCCATTC
                        IIIII IIIIIIIII
                        GGACC CGGGGTAAG
                        AGACG  __       CII
GAM205 GPR56           TCTGCCCTGGGCCCCATTCG   2971 T   CG      AG
                        GTTCTGG GCCCCATTCGT
                        IIIIIII IIIIIIIIIII
                        CGGGACC CGGGGTAAGCG
                        _   __        GG
GAM205 RAB38           CTGGCGGCCGGCCAGACGT     2969       __ TT III
                        CTGGCGGCC CCA CG
                        IIIIIIIII III II
                        GACCGCCGG GGT GC
                        CC  CT AII
GAM205 RAB38           CTGGCGGCCGGCCAGACGT     2969 TGTTCT _ CCATT  A
                        GGC GGCC   CGT G
                        III IIII   III I
                        CCG CCGG   GCA C
                        G_____ G  TCT__  _
GAM206 ADCY7           TGTCTCTAAACAGACTCCAT    2996 GCA TT     GGA
                        TG  CT ACAGACTCCAT
                        II  II IIIIIIIIIII
                        AC  GA TGTCTGAGGTA
                        AGA TT       III
GAM206 ADCY7           TGTCTCTAAACAGACTCCAT    2996 GGCA TT      I
                        CT ACAGACTCCA
                        II IIIIIIIIII
                        GA TGTCTGAGGT
                        CAGA TT      I
GAM206 AS3             CACTTTCACAAGACTCCAT     2977 _ _     III
                        CACTT TACA GACTCCA
                        IIIII IIII IIIIIII
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                        GTGAA GTGT CTGAGGT
                          A    T    AII
GAM206 AS3              CACTTTCACAAGACTCCAT      2977 TGGCAC    _       A
                        TTTACA GACTCCATGG
                        IIIIII IIIIIIIIII
                        AAGTGT CTGAGGTATC
                          A_____    T     A
GAM206 B3GALT5          GCCCTTCTAT-GACTCCATG     2986 A  ACA       II
                        GC CTTT  GACTCCAT
                        II IIII  IIIIIIII
                        CG GAAG  CTGAGGTA
                          G   ATA    CI
GAM206 B3GALT5          GCCCTTCTAT-GACTCCATG     2986 TGGCA  ACA        A
                        CTTT  GACTCCATGG
                        IIII  IIIIIIIIII
                        GAAG  CTGAGGTACT
                          G____  ATA       A
GAM206 CDR2             TGGCACTTTGGCAGAACCCTCC   2993    A_  _  IIIG
                        TGGCACTTT CAGA CTC
                        IIIIIIIII IIII III
                        ACCGTGAAA GTCT GGG
                          CC   T   AGGI
GAM206 CDR2             TGGCACTTTGGCAGAACCCTCC   2993    A_  ___   ATGGAG
                        TGGCACTTT CAGA  CTCC
                        IIIIIIIII IIII  IIII
                        ACCGTGAAA GTCT  GAGG
                          CC   TGG  IIIGAG
GAM206 COL4A1           GGCACTTTACGGTTTTCAT      2989       AGACTCCAII
                        GGCACTTTAC
                        IIIIIIIIII
                        CCGTGAAATG
                          CCAAAAGTAI
GAM206 CRACC            TGTCAGGTGCATCTGCTTCT     3001     GAC    T AGG
                        TGTCAGGTG  CATCT CT
                        IIIIIIIII  IIIII II
                        ACAGTCCAC  GTAGA GA
                          ___   C AGA
GAM206 CRACC            TGTCAGGTGCATCTGCTTCT     3001     GAC    TCI
                        GTCAGGTG  CATCT
                        IIIIIIII  IIIII
                        CAGTCCAC  GTAGA
                          ___  CGA
GAM206 CSHL1            GTCAGGTGGCTGCCGTCTTCCAG  2991 TC    A__ A    I
                        AGGTGG  CC TCTTCTA
                        IIIIII  II IIIIIIII
                        TCCACC  GG AGAAGGT
                          __   GAC  C    I
GAM206 CSHL1            GTCAGGTGGCTGCCGTCTTCCAG  2991 TG    A__ A    GGI
                        TCAGGTGG  CC TCTTCTAG
                        IIIIIIII  II IIIIIIII
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                        AGTCCACC  GG AGAAGGTC
                         __    GAC  C    GII
GAM206 CSPG4            GCACTGTTTATCCAGGCTCCATGGA  2985 CACTTTA  A      I
                          CAG CTCCATGG
                          III IIIIIIII
                          GTC GAGGTACC
                       CAAATAG  C      I
GAM206 CSPG4            GCACTGTTTATCCAGGCTCCATGGA  2985 TGGCACTTTA  A       II
                          CAG CTCCATGGAG
                          III IIIIIIIIII
                          GTC GAGGTACCTT
                       TGACAAATAG  C      GI
GAM206 EIF2C1          CAGGTGGA-CATC-TCTGGG     2983      C   CTAI
                          CAGGTGGAC ATCTT
                          IIIIIIIII IIIII
                          GTCCACCTG TAGAG
                          _    ACCC
GAM206 EIF2C1          CAGGTGGA-CATC-TCTGGG     2983 TGTCAG   C   T A
                          GTGGAC ATCT CT G
                          IIIIII IIII II I
                          CACCTG TAGA GA C

                       _____   _  _ _
GAM206 EVC            CTTTGCACAACTCCATGGA      2984    A _      II
                          CTTT CA GACTCCATGG
                          IIII II IIIIIIIIII
                          GAAA GT TTGAGGTACC
                          C  G     TI
GAM206 EVC            CTTTGCACAACTCCATGGA      2984 TGGCACTT   A
                          TACAG CTCCATGGA
                          IIIII IIIIIIIII
                          GTGTT GAGGTACCT

                       _____  _
GAM206 HKE4           CACTTTACAGACTCTCTGG      2979        CA II
                          CACTTTACAGACTC TG
                          IIIIIIIIIIIII II
                          GTGAAATGTCTGAG AC
                          AG CI
GAM206 HKE4           CACTTTACAGACTCTCTGG      2979 TGGCAC     CA  A
                          TTTACAGACTC TGG
                          IIIIIIIIIII III
                          AAATGTCTGAG ACC
                          _____   AG  C
GAM206 MEPE          TGTCAGGTGG-CTCTCCTCTA    3002     ACCA    GG
                          TGTCAGGTGG  TCTTCTA
                          IIIIIIIIII  IIIIIII
                          ACAGTCCACC  AGGAGAT
                          GAG_    II
GAM206 MEPE          TGTCAGGTGG-CTCTCCTCTA    3002 _      ACCA   I
                          GTCAGGTGG  TCTTCT
                          IIIIIIIII  IIIIII
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                       CAGTCCACC   AGGAGA
                       A       GAG_    I
GAM206 MYO15A          CACTTAGCA-ACTCCATGGAG   2980 _   CTTTACAG
                       TGGCA     ACTCCATGGA
                       |||||     ||||||||||
                       ATCGT     TGAGGTACCT
                       A         _____
GAM206 MYO15A          CACTTAGCA-ACTCCATGGAG   2980 _   TACA       I
                       ACTT  GACTCCATGGA
                       ||||  ||||||||||
                       TGAA  TTGAGGTACCT
                       G    TCG_        I
GAM206 NOC4            TTACAAATTCCTCCATGGAG    3003    ___        III
                       TTACAGA  CTCCATGGA
                       |||||||  |||||||||
                       AATGTTT  GAGGTACCT
                          AAG       CII
GAM206 NRXN3           ACATTACAGACTCACTTGGAG   2975 CT      CA_  I
                       TTACAGACTC  TGGA
                       ||||||||||  ||||
                       AATGTCTGAG  ACCT
                       T_        TGA  I
GAM206 NRXN3           ACATTACAGACTCACTTGGAG   2975 TGGCACTT     CA_
                       TACAGACTC  TGGAG
                       |||||||||  |||||
                       ATGTCTGAG  ACCTC
                       _____           TGA
GAM206 PAP            GTCACATCCATCATCTTCTA    2992   G GGAC      I
                       TCA GT   CATCTTCT
                       ||| ||   ||||||||
                       AGT TA   GTAGAAGA
                        G  GGTA      I
GAM206 PHYH           CACTTTATTTGGACTCCATG    2978      CA__      III
                       CACTTTA  GACTCCAT
                       |||||||  ||||||||
                       GTGAAAT  CTGAGGTA
                          AAAC      CII
GAM206 PML           TGG-ACTTGAGAGGCCTCCATGGAG 2994   C   TAC A_      I
                       TGG ACTT  AG CTCCATGGAG
                       ||| ||||  || ||||||||||
                       ACC TGAA  TC GAGGTACCTC
                         _  CTC  CG        I
GAM206 PML           TGG-ACTTGAGAGGCCTCCATGGAG 2994  C   TAC A_       I
                       GG ACTT  AG CTCCATGGA
                       || ||||  || |||||||||
                       CC TGAA  TC GAGGTACCT
                        _  CTC  CG      I
GAM206 PPP1R3C         TGTACAGAGTGGACCATCTTATGAGG 2998 _ _        CT_ GII
                       TGT CAG GTGGACCATCTT  AGG
                       ||| ||| |||||||||||||  |||
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                        ACA GTC CACCTGGTAGAA  TCC
                         T  T        TAC  III
GAM206 PPP1R3C          TGTACAGAGTGGACCATCTTATGAGG 2998 T  _        CTAGI
                        CAG GTGGACCATCTT
                        III IIIIIIIIIII
                        GTC CACCTGGTAGAA
                         _  T      TACTI
GAM206 PTPRD            TGGCTCAGAAGAGACTCCATGGA  2997   ACTTTAC        GI
                        TGGC    AGACTCCATGGA
                        IIII    IIIIIIIIIII
                        ACCG    TCTGAGGTACCT
                         AGTCTTC          II
GAM206 PTPRD            TGGCTCAGAAGAGACTCCATGGA  2997   ACTTTAC        I
                        GGC    AGACTCCATGG
                        III    IIIIIIIIIII
                        CCG    TCTGAGGTACC
                         AGTCTTC         I
GAM206 SFRP1           CACTTTACAGCCTCACTGCAG    2982     A  CA  GAI
                       ACTTTACAG CTC  TG
                       IIIIIIIII III II
                       TGAAATGTC GAG  AC
                         G  TG GTI
GAM206 SFRP1           CACTTTACAGCCTCACTGCAG    2982 TGGCAC    A  CA  G
                        TTTACAG CTC  TG AG
                        IIIIIII III II II
                        AAATGTC GAG  AC TC
                        _____       G  TG  G
GAM206 STS            GCACTTTAC--ATTCCATAGGAG  2987 _      GAC    AI
                       CACTTTACA  TCCATGG
                       IIIIIIIII  IIIIIII
                       GTGAAATGT  AGGTATC
                        C     A__    CT
GAM206 STS            GCACTTTAC--ATTCCATAGGAG  2987 TGGC     GAC   _
                       ACTTTACA  TCCAT GGAG
                       IIIIIIII  IIIII IIII
                       TGAAATGT  AGGTA CCTC
                        ____      A__  T
GAM206 TBL2          TGTCAGGTGGAAATCCATTTGCT  2999         ___ CTTCTAGGGI
                     TGTCAGGTGGA  CCAT
                     IIIIIIIIIII  IIII
                     ACAGTCCACCT  GGTA
                      TTA  AACGAIIIGG
GAM206 TBL2          TGTCAGGTGGAAATCCATTTGCT  2999 GTC      ___  CTTCI
                      AGGTGGA  CCAT
                      IIIIIII  IIII
                      TCCACCT  GGTA
                      ___     TTA  AACGI
GAM206 USP9Y         CACTTTACA-ATTTCAGTGAG    2981 _      AC CA  AI
                      ACTTTACAG TC  TGG
                      IIIIIIIII II III
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                        TGAAATGTT AG ACT
                        G       AA  TC    II
GAM206  XRCC3           GTCAGTCTGTGGCCACCATCTTC  2990     ___  __        IIIG
                        GTCAG  GTGG  ACCATCTT
                        IIIII  IIII  IIIIIIII
                        CAGTC  CACC  TGGTAGAA
                          AGA   GG       GIII
GAM206  XRCC3           GTCAGTCTGTGGCCACCATCTTC  2990 T__  AG   __        TAGGGI
                        GTC  GTGG  ACCATCTTC
                        III  IIII  IIIIIIIII
                        CAG  CACC  TGGTAGAAG
                        AGT  A_   GG       CIIIGG
GAM206  ZNF2            AGGTGGACCTGTCTTCAAG      2976       A_   TAII
                        AGGTGGACC  TCTTC
                        IIIIIIIII  IIIII
                        TCCACCTGG  AGAAG
                          AC    TTCI
GAM206  ZNF2            AGGTGGACCTGTCTTCAAG      2976 TGTCAGGT   A_   T
                        GGACC  TCTTC  AGG
                        IIIII  IIIII  III
                        CCTGG  AGAAG  TCT
                        _____    AC   T
GAM206  ZNF255          TGG-ACTATGCAGACTCCA      2995   C  TTA      TGG
                        TGG  ACT  CAGACTCCA
                        III  III  IIIIIIIII
                        ACC  TGA  GTCTGAGGT
                        _   TAC       III
GAM206  ZNF255          TGG-ACTATGCAGACTCCA      2995   C  TTA      I
                        TGG  ACT  CAGACTCC
                        III  III  IIIIIIII
                        ACC  TGA  GTCTGAGG
                        _   TAC       T
GAM206  ZNF264          GGAATTTTACAAACATTCCATGGAG 2988 GCAC        __      I
                        TTTACAGAC  TCCATGGA
                        IIIIIIIII  IIIIIIII
                        AAATGTTTG  AGGTACCT
                        TA__      TA     I
GAM206  ZNF264          GGAATTTTACAAACATTCCATGGAG 2988 TGGCAC        __       II
                        TTTACAGAC  TCCATGGAG
                        IIIIIIIII  IIIIIIIII
                        AAATGTTTG  AGGTACCTC
                        CTTA__      TA      TI
GAM206  ZNF266          TGT-AGATGG-CCATCTTCT      3000  C   A      AG
                        TGT  AGGTGG  CCATCTTCT
                        III  IIIIII  IIIIIIIII
                        ACA  TCTACC  GGTAGAAGA
                        _    _       II
GAM206  ZNF266          TGT-AGATGG-CCATCTTCT      3000 _  C   A    I
                        GT  AGGTGG  CCATCTTC
                        II  IIIIII  IIIIIIII
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                        CA TCTACC GGTAGAAG
                        A  _    _     I
GAM207 AQP6             GGAGGAAGGTACCGGGAGAGA    3012 G     _ TA    I
                        AGGAAGG AC  GGAGGG
                        ||||||| ||  ||||||
                        TCCTTCC TG  CCTCTC
                        _       A GC    I
GAM207 AQP6             GGAGGAAGGTACCGGGAGAGA    3012 TTAGGGAG    _ TA
                        GAAGG AC  GGAGGGA
                        ||||| ||  |||||||
                        CTTCC TG  CCTCTCT
                        _____     A GC
GAM207 BIG1         AGGAGAGGAAGGAAGAGAAGAGA    3006        CT    I
                        GGGAGGAAGGA AGGAGGG
                        |||||||||| |||||||
                        CTCTCCTTCCT TCTTCTC
                             TC     I
GAM207 BIG1         AGGAGAGGAAGGAAGAGAAGAGA    3006 TTA       CT     I
                        GGGAGGAAGGA AGGAGGGA
                        |||||||||| ||||||||
                        CTCTCCTTCCT TCTTCTCT
                        ___       TC     C
GAM207 CALM1          AGGGAGGAA-GAGCA-GAGGGA    3008 _       ACTA    I
                        GGGAGGAAGG  GGAGGG
                        ||||||||||  ||||||
                        CCCTCCTTCT  TCTCCC
                        T       CG__    I
GAM207 CALM1          AGGGAGGAA-GAGCA-GAGGGA    3008 TTAG      ACTA
                        GGAGGAAGG  GGAGGG
                        |||||||||  ||||||
                        CCTCCTTCT  TCTCCC
                        ____       CG__
GAM207 JAM2         GGGAGGAAG----AGGAGGGA    3017 _     GACT
                        GGAGGAAG  AGGAGGG
                        ||||||||  |||||||
                        CCTCCTTC  TCCTCCC
                        C       ____
GAM207 LTBR         GGGAGGAAGG-C-AGGAGG    3013        AC    I
                        GGGAGGAAGG TAGGAG
                        |||||||||| ||||||
                        CCCTCCTTCC GTCCTC
                        __       C
GAM207 LTBR         GGGAGGAAGG-C-AGGAGG    3013 TTAGGG    AC
                        AGGAAGG TAGGAGG
                        ||||||| |||||||
                        TCCTTCC GTCCTCC
                        _____   __
GAM207 NCF2         TTAGGTAG-AA--ACTAGGAGG    3020    GA AG      G
                        TTAGG GGA GACTAGGAGG
                        ||||| ||| ||||||||||
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                        AATCC  TCT  TTGATCCTCC
                          A_  __       I
GAM207 NCF2          TTAGGTAG-AA--ACTAGGAGG   3020 _  GA  AG
                        TAGG  GGA  GACTAGGAG
                        |||| ||| |||||||||
                        ATCC  TCT  TTGATCCTC
                          A  A_  __
GAM207 NDST2          GGGAGGAAG-----GGAGGGA   3016 _     ACTAG
                        GGAGGAAGG   GAGG
                        ||||||||| ||||
                        CCTCCTTCC  CTCC
                          C      _____
GAM207 NDST2          GGGAGGAAG-----GGAGGGA   3016 TTAGGG    ACTA
                        AGGAAGG  GGAG
                        ||||||| ||||
                        TCCTTCC  CCTC
                        _____   CTC_
GAM207 NHLH1         GGGAGGAAGGGGGAGGAAGG    3015    ACTA   I
                        GGAGGAAGG  GGAGG
                        ||||||||| |||||
                        CCTCCTTCC  CCTCC
                            C___   T
GAM207 NHLH1         GGGAGGAAGGGGGAGGAAGG    3015 TTAGGG    ACT
                        AGGAAGG  AGGAGGG
                        ||||||| |||||||
                        TCCTTCC  TCCTTCC
                        _____    CCC
GAM207 PAFAH1B1     AGGGAGGAAGGA--GGGAGGGA   3010 _      CTA   I
                        GGGAGGAAGGA  GGAGGG
                        ||||||||||| ||||||
                        CCCTCCTTCCT  CCTCCC
                          T     C__  I
GAM207 PAFAH1B1     AGGGAGGAAGGA--GGGAGGGA   3010 TTAG      CTA
                        GGAGGAAGGA  GGAGGG
                        |||||||||| ||||||
                        CCTCCTTCCT  CCTCCC
                        ____     C__
GAM207 PMX1         AGGGAGGAA-GA--GGGAGGGA   3007 _      ACTA
                        GGGAGGAAGG  GGAGGG
                        ||||||||| ||||||
                        CCCTCCTTCT  CCTCCC
                          T      C___
GAM207 PMX1         AGGGAGGAA-GA--GGGAGGGA   3007 TTAG     ACTA
                        GGAGGAAGG  GGAGGG
                        ||||||||| ||||||
                        CCTCCTTCT  CCTCCC
                        ____      C___
GAM207 RAP1GA1       TTAGGGTAGAGTGAAGGAGTATAGGAGGGA3019   ___ _    C__    III
                        TTAGGG  AG GAAGGA  TAGGAGGGA  T
                        |||||| || ||||||  |||||||| |
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                    AATCCC  TC CTTCCT  ATCCTCCCT  A
                    ATC  A    CAT         III
GAM207 RAP1GA1          TTAGGGTAGAGTGAAGGAGTATAGGAGGGA3019 TAG   _    C__      I
                    GGAG GAAGGA  TAGGAGGG
                    |||| ||||||  |||||||||
                    TCTC CTTCCT  ATCCTCCC
                    ___    A    CAT      I
GAM207 TRPC5        AGGGAGGAAGGA-AGGGATGGA  3011 _       CTA  _ GI
                    GGGAGGAAGGA  GGA GG
                    |||||||||||  ||| ||
                    CCCTCCTTCCT  CCT CC
                    T      TC_  A II
GAM207 TRPC5        AGGGAGGAAGGA-AGGGATGGA  3011 TTAG      CTA  G
                    GGAGGAAGGA  GGA GGA
                    ||||||||||  ||| |||
                    CCTCCTTCCT  CCT CCT
                    ____        TC_  A
GAM207 TSLP       GGGAGGAAGGTCAGGGAGG    3014        ACTA  II
                    GGGAGGAAGG  GGAG
                    ||||||||||  ||||
                    CCCTCCTTCC  CCTC
                       AGTC  CI
GAM207 TSLP       GGGAGGAAGGTCAGGGAGG    3014 TTAGGG   ACTA
                    AGGAAGG  GGAGGG
                    |||||||  ||||||
                    TCCTTCC  CCTCCT
                    _____       AGTC
GAM207 ULBP2     TAGGGAGGAGAGACT-TGATGGA  3018 _      AG  A GA GI
                    AGGGAGGA  GACT G  GG
                    ||||||||  |||| |  ||
                    TCCCTCCT  CTGA C  CC
                       A    CT  A TA II
GAM207 ULBP2     TAGGGAGGAGAGACT-TGATGGA  3018 TT     AG   A GA
                    AGGGAGGA  GACT G  GGGA
                    ||||||||  |||| |  ||||
                    TCCCTCCT  CTGA C  CCTT
                    __      CT   A TA
GAM207 WNT10B       GGGAGGAAG-----GGAGGGA  3016 _      ACTAG
                    GGAGGAAGG   GAGG
                    |||||||||   ||||
                    CCTCCTTCC   CTCC
                    C          _____
GAM207 WNT10B       GGGAGGAAG-----GGAGGGA  3016 TTAGGG    ACTA
                    AGGAAGG   GGAG
                    |||||||   ||||
                    TCCTTCC   CCTC
                    _____       CTC_
GAM207 WNT10B     AGGGAGGAAG-----GGAGGGA  3009 _       ACTAG
                    GGGAGGAAGG   GAGG
                    ||||||||||   ||||
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                              CCCTCCTTCC   CTCC
                          T          _____
GAM207  WNT10B        AGGGAGGAAG-----GGAGGGA   3009 TTAG       ACTAG
                          GGAGGAAGG   GAGG
                          |||||||||   ||||
                          CCTCCTTCC   CTCC
                          _____       _____
GAM208  BACE         GTAGAATGATCTTGGGATG    3024  A      CC  II
                          GTA AATGATCTT GAT
                          ||| ||||||||| |||
                          CAT TTACTAGAA CTA
                           C       CC  CI
GAM208  CAPN11       TCAGTAAAAGTGGGC-TCCG    3027      _  AT   CII
                          TCAGTAAAA TG  CTTC
                          ||||||||| ||  ||||
                          AGTCATTTT AC  GAGG
                             C  CC    CII
GAM208  CAPN11       TCAGTAAAAGTGGGC-TCCG    3027 TGTC    _  ATC   AT
                          AGTAAAA TG  TTCCG
                          ||||||| ||  |||||
                          TCATTTT AC  GAGGC
                          _____       C CC_  GT
GAM208  CAV3         GTCACTTAAACATGATCTTCC    3025   G_  _      III
                          GTCA TAAA ATGATCTTC
                          |||| |||| |||||||||
                          CAGT ATTT TACTAGAAG
                           GA  G      GII
GAM208  CAV3         GTCACTTAAACATGATCTTCC    3025 TG  G_  _      ATG
                          TCA TAAA ATGATCTTCCG
                          ||| |||| |||||||||||
                          AGT ATTT TACTAGAAGGT
                          __  GA  G       III
GAM208  FOXO1A       TCAAAAAAATGATCATCACGGTG   3028 AGT     T _ AI
                          AAAATGATC TC CG
                          ||||||||| || ||
                          TTTTACTAG AG GC
                          TT_      T T CI
GAM208  FOXO1A       TCAAAAAAATGATCATCACGGTG   3028 TGTCAGT     T _ ATGI
                          AAAATGATC TC CG
                          ||||||||| || ||
                          TTTTACTAG AG GC
                          TTT____      T T CACC
GAM208  GPR85        AGTAATAAATGATCTTCC-ATG    3023 AGTA       AI
                          AAATGATCTTCCG
                          |||||||||||||
                          TTTACTAGAAGGT
                          TTA_       AC
GAM208  GPR85        AGTAATAAATGATCTTCC-ATG    3023 TGTCAGTA       ATG
                          AAATGATCTTCCG
                          |||||||||||||
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                          TTTACTAGAAGGT
                   TA_____           ACG
GAM208 NRG1        TGTCAGT-AAATAATCTTC   3029      A      CGA
                   TGTCAGTAAA TGATCTTC
                   ||||||||| |||||||
                   ACAGTCATTT ATTAGAAG
                       _        |||
GAM208 NRG1        TGTCAGT-AAATAATCTTC   3029      A     I
                   TGTCAGTAAA TGATCTT
                   ||||||||| ||||||
                   ACAGTCATTT ATTAGAA
                       _       G
GAM208 TCTE1L      GTCACTATTATGATCTTCC      3026 TG  G  AA       AT
                   TCA TA ATGATCTTCCG
                   ||| || |||||||||||
                   AGT AT TACTAGAAGGT
                     __  G  AA       ||
GAM208 TCTE1L      GTCACTATTATGATCTTCC      3026   G  AA      ||
                   GTCA TA ATGATCTTC
                   |||| || |||||||||
                   CAGT AT TACTAGAAG
                     G AA      G|
GAM209 ARHGEF12      AAGAACATTCAAAAA--TTGTGA 3035 TA       TA
                     AGAACATTC GAAGGTTGTGA
                     ||||||||| |||||||||||
                     TCTTGTAAG TTTTTAACACT

                     __       __
GAM209 EGLN3       TAAGAACA-TCTGGAA-ATTGT   3041       T  A  G  G
                   TAAGAACAT CT GAAG TTGT
                   ||||||||| || |||| ||||
                   ATTCTTGTA GA CTTT AACA
                       _  C  _  |
GAM209 FOXE3       AAAAACATGAGAGAAGGTTGATGA 3033 TA    TCT      _  I
                   AGAACAT AGAAGGTTG TGA
                   ||||||| ||||||||| |||
                   TTTTGTA TCTTCCAAC ACT
                     __      CTC     T  T
GAM209 GOCAP1      GAACATTCTAGTTTAAGATT      3038 TAAGAA      ___     G
                   CATTCTAG AAGGTTGT
                   |||||||| ||||||||
                   GTAAGATC TTCTAATA
                     _____     AAA     G
GAM209 GRAF        GAACATTCTAAGAAGCTGGT      3037 TAAGAA     GA    TG
                   CATTCTA AGGTTG
                   ||||||| ||||||
                   GTAAGAT TTCGAC
                     _____      TC   CA
GAM209 HNRPDL      AAGAACATTGTTCAAAGGTGTG   3034 TA      CTA_    T  A
                   AGAACATT GAAGGT GTG
                   |||||||| |||||| |||
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                              TCTTGTAA   TTTCCA CAC
                                 __   CAAG    _  C
GAM209 MDM4       TAAGAACATTCTCTGACAGGTTG   3039        AGA__     TGAI
                     TAAGAACATTCT   AGGTTG
                     ||||||||||   ||||||
                     ATTCTTGTAAGA   TCCAAC
                              GACTG   IIIA
GAM209 PBX3      AAGAACATTC-AAAATGTT    3032 TA     T  G  GT
                     AGAACATTC AGAA GTT
                     ||||||||| |||| |||
                     TCTTGTAAG TTTT CAA
                              __    _  A  AI
GAM209 SH2D1A      AGAACACTAGGCAAGAAGGTTG   3036 TAAG    CT___       GA
                     AACATT   AGAAGGTTGT
                     ||||||   ||||||||||
                     TTGTGA   TCTTCCAACG
                      ____    TCCGT     AI
GAM209 THO2      TAAGAACAT--TAGATGCCTGT   3042     TC  AGG   G
                     TAAGAACAT TAGA  TTGT
                     ||||||||| |||| ||||
                     ATTCTTGTA ATCT  GACA
                              __  ACG   I
GAM209 TRIM9     TAAGAACATTCTAGCAGGT     3040       A  TGTG
                     TAAGAACATTCTAG AGGT
                     |||||||||||||| ||||
                     ATTCTTGTAAGATC TCCA
                              G   IIIA
GAM210 B4GALT5      AGGTCGGGTTATTTTGTTCTT    3046       TATATGCACTI
                     GGTCGGGTT
                     |||||||||
                     CCAGCCCAA
                              TAAAACAAGAI
GAM210 B4GALT5      AGGTCGGGTTATTTTGTTCTT    3046 TGAG     TATA CA  A
                     GTCGGGTT  TG CTT
                     ||||||||  || |||
                     CAGCCCAA  AC GAA
                      ____    TAAA AA  A
GAM210 SAR1      TGAAGTAGGACATATATGCACT   3048    C  TT      TA
                     TGAGGT GGG  TATATGCACT
                     |||||| |||  |||||||||||
                     ACTTCA CCT  ATATACGTGA
                       T  GT       II
GAM210 SAR1      TGAAGTAGGACATATATGCACT   3048    C  TT     I
                     GAGGT GGG  TATATGCAC
                     ||||| |||  |||||||||
                     CTTCA CCT  ATATACGTG
                       T  GT     I
GAM210 WEE1     AGATCGG-TTTATATACAC     3045     G     I
                     AGGTCGG TTTATATGCA
                     ||||||| ||||||||||
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                   TCTAGCC AAATATATGT
                       _        G
GAM210 WEE1        AGATCGG-TTTATATACAC     3045 TGAG   G      T
                   GTCGG TTTATATGCAC
                   ||||| |||||||||||
                   TAGCC AAATATATGTG
                   ____    _        T
GAM210 ZNF184      TGAGTTAGGCTATTATATGCAATT 3047  GTC  __      CTTAI
                   TGAG  GGGT TTATATGCA
                   ||||  |||| |||||||||
                   ACTC  TCCG AATATACGT
                    AA_   AT      TAAII
GAM210 ZNF184      TGAGTTAGGCTATTATATGCAATT 3047 A CG  __      CTI
                   GGT GGT TTATATGCA
                   ||| ||| |||||||||
                   TCA CCG AATATACGT
                    _  AT AT      TII
GAM211 ADORA3      TGGCAGCCTCCTAACCTTAG    3063         __    AACAC
                   TGGCAGCCTTTT CCTTAG
                   |||||||||||| ||||||
                   ACCGTCGGAGGA GGAATC
                        TT    IIICC
GAM211 ARHGEF12    CCCTTTCCTTAGCAACCCC     3053 ___     TT  AGAACAC
                   TGGCAGCCTT CCTT
                   |||||||||| ||||
                   ATCGTTGGGG GGGG
                   GGA        GT  IIICCAC
GAM211 CARKL       TGGGAGACGTTTTTCTGGTAGAACACC3062  C _ C_  CT_    III
                   TGG AG C TTTTC  TAGAACACC
                   ||| || | |||||  |||||||||
                   ACC TC G AAAAG  ATCTTGTGG
                    C  T CA   ACC        III
GAM211 CYP1B1      CAACCTTTTCCT--GAACA     3052 TGGCAG      TA
                   CCTTTTCCT GAACA
                   ||||||||| |||||
                   GGAAAAGGA CTTGT
                   _____   __
GAM211 DCT         CAGACTTAATTTCCTTAGAA    3051 TGGCAGCCT      CAC
                   TTTCCTTAGAA
                   |||||||||||
                   AAAGGAATCTT
                   TGAATT___        CGC
GAM211 DMD         TGGCAG---TTTCCTTAGTAAC  3065    CCT    _ AC
                   TGGCAG TTTCCTTAG AAC
                   |||||| ||||||||| |||
                   ACCGTC AAAGGAATC TTG
                    ___            A II
GAM211 DMRT2       GCAGCCTTTCACTGAGAGACAC  3057 TGGC    TC T _ C
                   AGCCTTT CT AGA ACAC
                   ||||||| || ||| ||||
```

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                      TCGGAAA  GA TCT TGTG
                  ____      GT  C   C   C
GAM211 EDG8        GCTGCATTT--CTTAGAACAC   3058 TGGCA CT   C
                      GC  TTTC TTAGAACAC
                      || |||| |||||||||
                      CG  AAAG AATCTTGTG
                  A____     T_    _
GAM211 FUT3       TGGCAGCC-TCTCCTAGGAGACA  3067        T  TA _  CC
                      TGGCAGCCTTT CCT GA ACA
                      |||||||||| ||| || |||
                      ACCGTCGGAGA GGA  CT TGT
                          _  TC  C  ||
GAM211 GAB2       CCTTTTCC-TAGAATCCACC      3054 __  CAG _      AGAACAC
                      TGG  CC TTTTCCTT
                      |||  || |||||||||
                      ATC  GG GGAAGGGA
                      GG  TTA  T      |||CCAC
GAM211 GRF2       TGGCAGCCTGGGTAGCTTAGAA   3064        TTTC__     CACC
                      TGGCAGCCT    CTTAGAA
                      |||||||||    |||||||
                      ACCGTCGGA    GAATCTT
                          CCCATC     |||C
GAM211 INPP1      GCAGCCTTTCCCTCGAGAA      3056 TGGC        _  CAC
                      AGCCTTTTCCTT AGAA
                      |||||||||||| ||||
                      TCGGAAAGGGAG TCTT
                  ____           C  TGI
GAM211 MASP1      TGG-AGCCTTTTCCCTATACCAC   3068  C       GAA  C
                      TGG AGCCTTTTCCTTA  CAC
                      ||| |||||||||||| |||
                      ACC TCGGAAAAGGGAT  GTG
                      _           ATG  I
GAM211 MEF2C      GGCAGCCTTTTACAATGAGAAACAC 3060 TG      CCTT__  _  CII
                      GCAGCCTTTT    AGAA CAC
                      ||||||||||    |||| |||
                      CGTCGGAAAA    TCTT GTG
                      __          TGTTAC  T  TII
GAM211 MYCL2      TGTCAGCCTTTTCTTTGGA       3066  G      C  A ACAC
                      TG CAGCCTTTC TT GA
                      || ||||||||| || ||
                      AC GTCGGAAAAG AA CT
                      A          A C IIIC
GAM211 NBS1       GGCAGTCTT--CCTTAGAA       3061 TG  CC        CA
                      GCAG TTTTCCTTAGAA
                      |||| |||||||||||
                      CGTC AGAAGGAATCTT
                      __   __         TI
GAM211 SRGAP2     GCACCTCTTTTCCTTTGCACA    3055 TGGCAGC      AGA  CC
                      CTTTTCCTT ACA
                      ||||||||| |||
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                         GAAAAGGAA  TGT
                    TGGA___      ACG  CC
GAM211 ZNF8         GGAAGCATCATTTCCTTAGAA  3059 T_  GCCT      CACC
                       GGCA  TTTCCTTAGAA
                       ||||  ||||||||||
                       TCGT  AAAGGAATCTT
                    CT  AGT_       TIII
GAM212 MGAT5        GTCAGCCAGCTATGTGGCA    3073 T__  C ATT      TCGG
                       GTC GC  TATGTGGCA
                       ||| ||  |||||||||
                       CGG CG  ATACACCGT
                    AGT  T  ___       CIII
GAM212 PCDHGA8        GTCCAGCAGTTAGTTTGTGGCATC 3072 TG  _  T  ___      GGTI
                       TCC GCA TTA  TGTGGCATC
                       ||| ||| |||  |||||||||
                       AGG CGT AAT  ACACCGTAG
                    __  T  C  CAA      AIII
GAM212 SUFU         TGTGGGCACTCCTGTGGCATC   3074  CC    A      GGT
                       TGT  GCATTT TGTGGCATC
                       |||  |||||| |||||||||
                       ACA  CGTGAG ACACCGTAG
                       CC    G       III
GAM212 SUV39H2        CCCCTTTTCAGAGGCATCGGT   3071 TGTCCGCA  TGT
                        TTTA  GGCATCGGT
                        ||||  |||||||||
                        AAGT  CCGTAGCCA
                    GAA_____      CT_
GAM213 FBXL2        TGGCATGGTCCTAGCTGCATTGAGAC 3080        ___  C  _  TAII
                       TGGCATGGTT  GCT TATTG GAC
                       ||||||||||  ||| ||||| |||
                       ACCGTACCAG  CGA GTAAC CTG
                        GAT  C   T  IIIA
GAM213 GSTM5        GGCATGGTTCAGGCTTTACTGG     3079 TG     ___  C   ACTA
                       GCATGGTT  GCT TATTGG
                       ||||||||  ||| ||||||
                       CGTACCAA  CGA ATGACC
                       __      GTC  A   CIII
GAM213 LANGERIN      GCTTGGTTGCTC---TGGAGTA    3077 TGGCA       ATT  CT
                       TGGTTGCTCT  GGA
                       ||||||||||  |||
                       ACCAACGAGA  CCT
                    A____      ___  CA
GAM213 LENG4        GGCTATGGTTGCTAAGCTAT      3078 TG _     ___   TGGACT
                       GC ATGGTTGCT  CTAT
                       || ||||||||||  ||||
                       CG TACCAACGA  GATA
                       __  A     TTC  CIIIAT
GAM214 ADCY4        TGAGCTGCTCAATGACCTGGAAGA   3096       AAAT__  _  TGAI
                       TGAGCTGCT    CCTG AAGA
                       |||||||||    |||| ||||
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                         ACTCGACGA    GGAC TTCT
                          GTTACT   C   IIIA
GAM214 AP1G1         AGATGTTAAAAGTGCCTGAAGATG  3083 TGAGCTGCTAAAT        AI
                         CCTGAAGATG
                         ||||||||||
                         GGACTTCTAC
                        TACAATTTTCAC_       CA
GAM214 AQP8          TGAGCTGCTGGGAAACCTG   3095      AAAT__   AAGATG
                       TGAGCTGCT    CCTG
                       |||||||||    ||||
                       ACTCGACGA    GGAC
                         CCCTTT   IIIAGT
GAM214 ASTN          CTGTTATA-CCTGAAGATG     3088 TGAGCTGCTAAAT
                          CCTGAAGAT
                          |||||||||
                          GGACTTCTA
                       ATAT_____
GAM214 BLAME          TGAGCTGCT-TTTCTTGAAGTTG  3099     AAA C   A A
                       TGAGCTGCT  TC TGAAG TG
                       ||||||||| || ||||| ||
                       ACTCGACGA  AG ACTTC AC
                         AA_  A   A I
GAM214 CAPN7          CTGCTTACTGTCCTGAAGAT    3087 TGA   CTAAA       G
                          GCTG   TCCTGAAGAT
                          ||||   ||||||||||
                        TGAC   AGGACTTCTA
                       AA_   _____       A
GAM214 CTSL          GCTGGTAGA--CTGAAGATGA    3094 TGAGCTGCTAAATC
                          CTGAAGATG
                          |||||||||
                          GACTTCTAC
                       CCATCT_____
GAM214 HLA-DRA       GCTGGAAAACGCTGAAGATGA    3092 TGAGCTGCT   C
                          AAAT CTGAAGATGA
                          |||| ||||||||||
                          TTTG GACTTCTACT
                       CCT_____ C
GAM214 HLA-DRA       GCTGGAAAATGCTGAAGATGA    3093 TGAGCTGCT   C
                          AAAT CTGAAGATGA
                          |||| ||||||||||
                          TTTA GACTTCTACT
                       CCT_____ C
GAM214 MAP1A         TGAGCTGCTAA-----GAAGATGA 3100        ATCCT
                        TGAGCTGCTAA   GAAGATG
                        ||||||||||   |||||||
                        ACTCGACGATT   CTTCTAC
                           _____
GAM214 MKKS          AGCTGCTTCTTTACCTGAAGAT   3084 TGAG   AAAT__      GA
                         CTGCT   CCTGAAGAT
                         |||||   ||||||||||
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                       GACGA    GGACTTCTA
                    ____    AGAAAT       AC
GAM214  MLLT2        GCTTCTAAAAATTACTGAAGATGA  3090 TGAGCTG    TC___        I
                       CTAAA    CTGAAGATGA
                       |||||    ||||||||||
                       GATTT    GACTTCTACT
                     A_____     TTAAT        T
GAM214  PPARBP        TGAGCT--TTCATCCTGAAG  3098    GCTAA        AT
                       TGAGCT    ATCCTGAAG
                       ||||||    |||||||||
                       ACTCGA    TAGGACTTC
                          AAG__       II
GAM214  SMARCC1          TGAGAAGAAAAATCCTGAA   3097   CTGCT       GATG
                          TGAG    AAATCCTGAA
                          ||||    ||||||||||
                          ACTC    TTTAGGACTT
                          TTCTT       IIIA
GAM214  TBL2          GCTGCTAAAGTCCATGCAAGAT  3091 TGAGCT    _  _  _      A
                          GCTAAA TCC TG AAGATG
                          |||||| ||| || ||||||
                          CGATTT AGG AC TTCTAT
                          _____     C  T  G      A
GAM214  TDRD1         CTGCCAATATGCCTGAAGATG   3086 TGAGCTGCTAAAT       A
                             CCTGAAGATG
                             ||||||||||
                             GGACTTCTAC
                        GTTATAC_____          A
GAM214  TSN           CTTCTAAATCCTCAA-ATG   3089 TGAGCTGC     GA
                           TAAATCCT AGAT
                           |||||||| ||||
                           ATTTAGGA TTTA
                           _____       G_
GAM214  TYRP1         AGCT-CACAATCCTGAAGGATG   3085 TGAGCTGCTA      _  A
                            AATCCTGAAG ATG
                            |||||||||| |||
                            TTAGGACTTC TAC
                        GAGTG_____       C  A
GAM215  FCER1A        ACCAGTTTCACTCAG--TTTA   3104      CA   GATTI
                        ACCAGTTTC TCAG
                        ||||||||| ||||
                        TGGTCAAAG AGTC
                          TG  AAATI
GAM215  FCER1A        ACCAGTTTCACTCAG--TTTA   3104 TA     CA   GATTTAT
                         CCAGTTTC TCAG
                         |||||||| ||||
                         GGTCAAAG AGTC
                         __      TG  AAATTII
GAM215  FCGR2A        GTTTGC-TCAGGATTTTTC   3112  CCA       ATI
                         GTTT  TCAGGATTT
                         ||||  |||||||||
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                              CAAA  AGTCCTAAA
                              CG_      AAG
GAM215 IFRD1        ACCAGTTTCAAT-AGTATT      3103       C C GATI
                              ACCAGTTTC AT AG
                              ||||||||| || ||
                              TGGTCAAAG TA TC
                              T _ ATAA
GAM215 IFRD1        ACCAGTTTCAAT-AGTATT      3103 TA     C C  GATTTA
                              CCAGTTTC AT AG
                              |||||||| || ||
                              GGTCAAAG TA TC
                              __     T _ ATAACI
GAM215 LIFR       TAGCAGTTAAAATCAGGATTCAT   3116 AC    TCC         I
                              CAGTT  ATCAGGATTTA
                              |||||  ||||||||||
                              GTCAA  TAGTCCTAAGT
                              TC   TTT         I
GAM215 LIFR       TAGCAGTTAAAATCAGGATTCAT   3116 TAC    TCC        CI
                              CAGTT  ATCAGGATTTAT
                              |||||  |||||||||||
                              GTCAA  TAGTCCTAAGTA
                              ATC   TTT          II
GAM215 PSMA2        TAACAGTTT--ATTAGGATTTAT   3115 AC_    CC C       I
                              CAGTTT  AT AGGATTTA
                              ||||||  || ||||||||
                              GTCAAA  TA TCCTAAAT
                              ATT    __  A      I
GAM215 PSMA2        TAACAGTTT--ATTAGGATTTAT   3115 TAC    CC C       C
                              CAGTTT  AT AGGATTTAT
                              ||||||  || |||||||||
                              GTCAAA  TA TCCTAAATA
                              ATT    __  A      I
GAM215 PSME3       CCAGTTTCCCCATCACGAT       3108        __  G III
                              CCAGTTTCC ATCA GA
                              ||||||||| |||| ||
                              GGTCAAAGG TAGT CT
                              GG  G AII
GAM215 PSME3       CCAGTTTCCCCATCACGAT       3108 TACCAG TT    G  TTAT
                              T CCATCA GAT
                              | |||||| |||
                              A GGTAGT CTA
                              TCAA__GG    G  TCII
GAM215 RARG       AGTTTCCATCA--CTTTAT       3107        GGATTTAI
                              AGTTTCCATCA
                              |||||||||||
                              TCAAAGGTAGT
                              GAAATAII
GAM215 RCN1       TACCACTTTCACTTAATCAGGATTT 3113    G  C____       ATCII
                              TACCA TTTC   ATCAGGATTT
                              ||||| ||||    |||||||||
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                          ATGGT AAAG    TAGTCCTAAA
                            G   TGAAT         IIICT
GAM215  RCN1              TACCACTTTCACTTAATCAGGATTT  3113 AC__  G  TCC       I
                            CA TT  ATCAGGATT
                            II II  IIIIIIIII
                            GT AA  TAGTCCTAA
                          GAAA  G  T__         I
GAM215  SCA1              CCAGTTTCCACTGTCCGGCTTGAT  3109 TACC      CA___  ATTTATCI
                            AGTTTCCAT   GG
                            IIIIIIIII   II
                            TCAAAGGTG   CC
                          ____         ACAGG  GAACTAAA
GAM215  SLBP          AGTTTCCATAAAGATATTA       3106      C   TTII
                            AGTTTCCAT AGGAT
                            IIIIIIIII IIIII
                            TCAAAGGTA TTCTA
                            T    TAAT
GAM215  SPON1            AGTCTCCAAAATCAGGATTT      3105      ___      III
                            AGTTTCCA TCAGGATT
                            IIIIIIII IIIIIIII
                            TCAGAGGT AGTCCTAA
                            TTT     AII
GAM215  SPON1            AGTCTCCAAAATCAGGATTT      3105 TA  TTTCC     AT
                            CCAG   ATCAGGATTT
                            IIII   IIIIIIIIII
                            GGTT   TAGTCCTAAA
                          A_  T____       AT
GAM215  SRGAP2         TACCAGTTTTGATCAGTTGGATT  3114      CC   GATTTATCI
                            TACCAGTTT ATCAG
                            IIIIIIIII IIIII
                            ATGGTCAAA TAGTC
                            AC    AACCTAAII
GAM215  TCEB1L           CCAGTTTCCAACTCATGAT      3110       __  G  III
                            CCAGTTTCCA TCA GA
                            IIIIIIIIII III II
                            GGTCAAAGGT AGT CT
                            TG  A AII
GAM215  TCEB1L           CCAGTTTCCAACTCATGAT      3110 TACC      __  G  TTAT
                            AGTTTCCA TCA GAT
                            IIIIIIII III III
                            TCAAAGGT AGT CTA
                          ____       TG  A  TTII
GAM215  WNT8B           CCAGTTTCC-TCAGTTTTT       3111      A  GATTI
                            CCAGTTTCC TCAG
                            IIIIIIIII IIII
                            GGTCAAAGG AGTC
                          _  AAAAA
GAM215  WNT8B           CCAGTTTCC-TCAGTTTTT       3111 TACC     A  GA  A
                            AGTTTCC TCAG TTT
                            IIIIIII IIII III
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                         TCAAAGG AGTC  AAA
                         ____       _  AA  G
GAM215 ZNF124            TTTACATTTACAGGATTTAT    3117 TACCAGTTTCCAT
                              CAGGATTTAT
                              ||||||||||
                              GTCCTAAATA
                         AAAT_____
GAM215 ZNF124            TTTACATTTACAGGATTTAT    3117 TTTCCAT___      III
                              CAGGATTTA
                              |||||||||
                              GTCCTAAAT
                         AAATGTAAAT      AII
GAM216 ABCC5            AACTCCC-CGGCTCGGAGGA     3121 AAG   A      AI
                            TCCC CGGCTCGGA
                            |||| |||||||||
                            AGGG GCCGAGCCT
                         TG_   _       CC
GAM216 ABCC5            AACTCCC-CGGCTCGGAGGA     3121 TCCAAG   A      A
                            TCCC CGGCTCGGA GA
                            |||| |||||||| ||
                            AGGG GCCGAGCCT CT
                         _____   _       C
GAM216 ATOX1           CCAAGTCCCAGGTCTGTCTGGAAG  3128 CAA     C _ C___   I
                              GTCCCA GG CT   GGAA
                              |||||| || ||   ||||
                              CAGGGT CC GA   CCTT
                         ___     _ A CAGA    I
GAM216 ATOX1           CCAAGTCCCAGGTCTGTCTGGAAG  3128 TC      C _ C___   AGI
                             CAAGTCCCA GG CT   GGAAG
                             ||||||||| || ||   |||||
                             GTTCAGGGT CC GA   CCTTC
                         __      _ A CAGA    GII
GAM216 CHST7           CAAGTCCCA-GACTCTG-AGAG   3125        C   G AGI
                            CAAGTCCCA GGCTC GA
                            ||||||||| ||||| ||
                            GTTCAGGGT CTGAG CT
                         _ A CTC
GAM216 CHST7           CAAGTCCCA-GACTCTG-AGAG   3125 TCCA    C   G A
                             AGTCCCA GGCTC GA GA
                             ||||||| ||||| || ||
                             TCAGGGT CTGAG CT CT
                         ____     _ A _
GAM216 CNGB3          TCCAAGTCCCTTGAGC-CAGATGAG 3130        AC_ T  A  I
                            TCCAAGTCCC  GGC CGGA GAG
                            ||||||||||  ||| |||| |||
                            AGGTTCAGGG  TCG GTCT CTC
                         AAC  _ A  I
GAM216 CNGB3          TCCAAGTCCCTTGAGC-CAGATGAG 3130        AC_ T  A  I
                            CCAAGTCCC  GGC CGGA GA
                            |||||||||  ||| |||| ||
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                        GGTTCAGGG  TCG GTCT CT
                          AAC  _   A  I
GAM216 ESRRA            TCCAAGTCCCACTCTGCTTTGAAGAG 3129        G__  CG    II
                       TCCAAGTCCCAC  GCT  GAAGAG
                       ||||||||||  |||  ||||||
                       AGGTTCAGGGTG  CGA  CTTCTC
                           AGA  AA    II
GAM216 ESRRA            TCCAAGTCCCACTCTGCTTTGAAGAG 3129 CC       G__  CG   I
                        AAGTCCCAC  GCT  GAAGA
                        ||||||||  |||  |||||
                        TTCAGGGTG  CGA  CTTCT
                        __       AGA  AA    I
GAM216 IGHMBP2         CAAGTCCCA-GACATTGGAGGAG  3123       C  TC_  A  I
                       AAGTCCCA GGC  GGA GA
                       |||||||| |||  ||| ||
                       TTCAGGGT CTG  CCT CT
                        _  TAA  C  I
GAM216 IGHMBP2         CAAGTCCCA-GACATTGGAGGAG  3123 TCCA    C  TC_  A
                        AGTCCCA GGC  GGA GAG
                        ||||||| |||  ||| |||
                        TCAGGGT CTG  CCT CTC
                        ____      _  TAA  C
GAM216 IRS1          CCAAGTCCCAACGTTGCACGG    3126         _ __  T  III
                     CCAAGTCCCA CG  GC CG
                     |||||||||| ||  || ||
                     GGTTCAGGGT GC  CG GC
                       T  AA  T  CII
GAM216 IRS1          CCAAGTCCCAACGTTGCACGG    3126 TC      _ __  T  AAGAG
                      CAAGTCCCA CG  GC CGG
                      ||||||||| ||  || |||
                      GTTCAGGGT GC  CG GCC
                       __       T  AA  T  CIIIG
GAM216 MAT1A         CAATTGCCCACGGCTCAACAAGAG  3122 AA T        _  I
                      G CCCACGGCTCGG AAGA
                      | |||||||||||| ||||
                      C GGGTGCCGAGTT TTCT
                      AA _        G  I
GAM216 MAT1A         CAATTGCCCACGGCTCAACAAGAG  3122 TCCAA T        _  I
                      G CCCACGGCTCGG AAGAG
                      | |||||||||||| |||||
                      C GGGTGCCGAGTT TTCTC
                      TAA__ _        G  G
GAM216 PAEP          AAGTCCCACTGCTCTGGAG     3120       G  _  AII
                      AAGTCCCAC GCTC GGA
                      ||||||||| |||| |||
                      TTCAGGGTG CGAG CCT
                       A  A  CII
GAM216 PAEP          AAGTCCCACTGCTCTGGAG     3120 TCCAAG    G  _  AGA
                       TCCCAC GCTC GGA
                       |||||| |||| |||
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                              AGGGTG CGAG CCT
                   _____      A    A   CCA
GAM216 RGL          CCAAGTCCCAGCCAGC-CGGA    3127        __   T  II
                    CCAAGTCCCA CGGC CGG
                    |||||||||| |||| |||
                    GGTTCAGGGT GTCG GCC
                         CG   _  TI
GAM216 RGL          CCAAGTCCCAGCCAGC-CGGA    3127 TC      __   T  AGA
                     CAAGTCCCA CGGC CGGA
                     ||||||||| |||| ||||
                     GTTCAGGGT GTCG GCCT
                      __       CG   _  GII
GAM216 SOST          CAAGTCCCACG--T-GGAAGA   3124 _       GCTC
                     AAGTCCCACG   GGAAG
                     ||||||||||   |||||
                     TTCAGGGTGC   CCTTC
                       G       A___
GAM216 SOST          CAAGTCCCACG--T-GGAAGA   3124 TCCA     GCTC
                      AGTCCCACG   GGAAG
                      |||||||||   |||||
                      TCAGGGTGC   CCTTC
                       ____       A___
GAM216 WHSC1L1        TCCTCGGCGCTCGGCTCGGAA  3131   AAGTCCCA      GAG
                      TCC     CGGCTCGGAA
                      |||     ||||||||||
                      AGG     GCCGAGCCTT
                       AGCCGCGA         |||
GAM216 WHSC1L1        TCCTCGGCGCTCGGCTCGGAA  3131 CCAAGTCCCA        I
                            CGGCTCGGA
                            |||||||||
                            GCCGAGCCT
                       GGAGCCGCGA       I
GAM217 ACCN2          CCCTGAGCTGGACGCTAACC   3153 AC  G      C   TC
                      CC GGGCTGGACGC AGCC
                      || |||||||||| ||||
                      GG CTCGACCTGCG TTGG
                       __  A      A  TI
GAM217 ADRA2A         CCCGGGGCTGGGGCG-CGGACTCT 3146 AC      A_  CAGC  I
                      CCGGGGCTGG CGC   CTCT
                      |||||||||| |||   ||||
                      GGCCCCGACC GCG   GAGA
                        __      CC  CCT_  C
GAM217 ATRN           CCCGGGGCTGAGACGGC-GCC   3147 AC       _   CCA  C
                      CCGGGGCTG GACG  GCCT
                      ||||||||| |||| ||||
                      GGCCCCGAC CTGC  CGGG
                        __       T  CG_  I
GAM217 BTEB1          TGGCCG-GTCCGGGCCTCCTGGCTC 3170    T  AC _     I
                      TGGCTG GTCC GC TCCTGGCTC
                      |||||| |||| || |||||||||
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                    ACCGGC CAGG  CG AGGACCGAG
                       _    CC  G       I
GAM217 CCND1        CGGGGCCGGCCCCCGCCAGCCT   3162 ACCCGG    A___        CT
                       GGCTGG  CGCCAGCCT
                       ||||||  |||||||||
                       CCGGCC  GCGGTCGGA
                        _____    GGGG     CA
GAM217 CENTD2       ACCCGGGGCTGCCACGCC-CCCTCT 3140      G_   AG  I
                       ACCCGGGGCTG ACGCC CCTCT
                       |||||||||| ||||| |||||
                       TGGGCCCGAC TGCGG GGAGA
                          GG   G_   I
GAM217 CRYBA2       ACCCGGGGGCTGGAC-CCGGCCT  3135      _   G A  CT
                       ACCCGGGG CTGGAC CC GCCT
                       |||||||| |||||| || ||||
                       TGGGCCCC GACCTG GG CGGA
                          C    _ C  II
GAM217 DRP2         CCGGGGCTGG--G-CTGCCTCT   3160 ACCC      AC  CA
                       GGGGCTGG GC GCCTC
                       |||||||| || |||||
                       CCCCGACC CG CGGAG
                        ____      __ A_
GAM217 DUSP4        CCCGGGTTTGGACGCCAGC    3151 AC   GC      CTC
                       CCGGG TGGACGCCAGC
                       ||||| |||||||||||
                       GGCCC ACCTGCGGTCG
                        __   AA     CII
GAM217 EMX2         CTGGGCTCCCAGCTCCTGGC   3163 T  GTG  C     T
                       GGCT  TCCA GCTCCTGGC
                       ||||  |||| |||||||||
                       CCGA  GGGT CGAGGACCG
                        _  ___  _       C
GAM217 EXTL1        CCCGGGGCTCGCAAGCCAGTCCT  3145 AC     GGAC_  _  CTI
                       CCGGGGCT   GCCAG CCT
                       ||||||||    ||||| |||
                       GGCCCCGA    CGGTC GGA
                        __    GCGTT   A CII
GAM217 EXTL1        GGCCGTGTCCCCCTGCCCTCCTGGCT 3168 TG     ACG____      CII
                       GCTGTGTCC    CTCCTGGCT
                       |||||||||    |||||||||
                       CGGCACAGG    GAGGACCGA
                        __        GGGACGG     CII
GAM217 FE65L2       ACCCCGGCTGCTCCCCGCCAGCCTCT 3136 A_   G_  GGA       II
                       CCCGG GCT  CGCCAGCCTCT
                       ||||| |||  ||||||||||
                       GGGCC CGA  GCGGTCGGAGA
                        TG   GA  GGG        II
GAM217 FGFR2        CCCGGGGCTCGCGGCCGGCC   3152 AC     GGAC A  C
                       CCGGGGCT  GCC GCCT
                       ||||||||   ||| ||||
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                             GGCCCCGA   CGG CGGG
                                GCGC   C   I
GAM217 GAK           ACCCGGGGCTCGGAGCCCCACCCT 3138      _ C A_  CTI
                     ACCCGGGGCT GGA GCC  GCCT
                     |||||||||| ||| ||| ||||
                     TGGGCCCCGA CCT CGG TGGG
                            G  _  GG  AII
GAM217 GRB10         ACCCGGGGCTGCAGGGACGCC   3137       ____    AGCCTCT
                     ACCCGGGGCT  GGACGCC
                     ||||||||||   |||||||
                     TGGGCCCCGA  CCTGCGG
                            CGTC     IIITCTC
GAM217 HPS3        CCGGGTCACGTGAACGCCAGCC   3155 ACCC  __ _       TCT
                     GGG  GC TGGACGCCAGCC
                     ||| || |||||||||||
                     CCC  TG ACTTGCGGTCGG
                     ____  AG  C       CCI
GAM217 IKBKB        ACCCGGGGCTATGACACCCCCT  3139        _  AG   I
                    ACCCGGGGCTG GACGCC  CCTCT
                    ||||||||||| |||||| |||||
                    TGGGCCCCGAT CTGTGG GGGGA
                            A    __   I
GAM217 KIP2        CCCGGGGCTGGACCACAGC     3150 AC       GC  CTC
                     CCGGGGCTGGAC CAGC
                     |||||||||||| ||||
                     GGCCCCGACCTG GTCG
                     __           GT  CII
GAM217 KRT16       ACCCGGCACAGGCCATTGACGCCAGCCTC3134     ____   G__        TIII
                    ACCCGG  GGCT GACGCCAGCCTC   G
                    ||||||  |||| |||||||||||   |
                    TGGGCC  CCGG CTGCGGTCGGAG  C
                      GTGT  TAA        IIIT
GAM217 LZTS1       CCGGGGCTGG--GACAGCC      3159 ACCC      ACGC
                     GGGGCTGG  CAGCCT
                     ||||||||   ||||||
                     CCCCGACC  GTCGGG
                     ____       CT__
GAM217 MAP3K8      CTGAGTC-AGACTCCTGGCT     3165 TGGCTGT  CAC
                      GTC  GCTCCTGGCT
                      |||  ||||||||||
                      CAG  TGAGGACCGA
                    T_____  TC_
GAM217 MATN1       CCAGGGGCTGGA-GCCCGC      3149 ACCC     C A CT
                      GGGGCTGGA GCC GC
                      ||||||||| ||| ||
                      CCCCGACCT CGG CG
                     GT__       _ G CI
GAM217 NDUFV3      TGGCTGGG-CCACGCTCCT      3171    T T      GGC
                    TGGCTG G CCACGCTCCT
                    |||||| | |||||||||||
```

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                              ACCGAC C GGTGCGAGGA
                                 C _        III
GAM217 NFRKB           GGCTGTGTCACCACACTCCT   3167 TG    __        GGCT
                         GCTGTGT CCACGCTCCT
                         ||||||| |||||||||
                         CGACACA GGTGTGAGGA
                               __   GT     GIII
GAM217 PABPC1          CCGGGGCTGGGGGCCGGAGCC   3158 ACCC     AC __   TCT
                          GGGGCTGG GCC AGCC
                          |||||||| ||| ||||
                          CCCCGACC CGG TCGG
                          ____       CC  CC  CCI
GAM217 PCSK1           GGCTCTAGACCAC--TCCTGGCTC  3166 TG  G TCCA
                         GCT TG  CGCTCCTGGCTC
                         ||| ||  |||||||||||
                         CGA AT  GTGAGGACCGAG
                         __  G CTG_
GAM217 POU2F2          CCCGGGGCTGCACCGGCTGCC   3148 AC     G __ CA  CT
                         CCGGGGCTG AC GC GCCT
                         ||||||||| || || ||||
                         GGCCCCGAC TG CG CGGG
                         __        G GC A_  II
GAM217 POU3F1          CCCGGGGCTCGGGCGACGCAGCCT  3144 AC     _ A __   CTI
                         CCGGGGCT GG CG C CAGCCT
                         |||||||| || || | ||||||
                         GGCCCCGA CC GC G GTCGGA
                         __     G C T C    TII
GAM217 PPP3CB          CCCGGGGCTCG--GCTAGGCTCT  3154 AC     GGAC C C
                         CCGGGGCT  GC AG CTCT
                         ||||||||  || || ||||
                         GGCCCCGA  CG TC GAGA
                         __       GC__ A C
GAM217 PRKACA          ACCCGGGGCCCCACCCCAGGCCT  3141      GG G _ CTI
                         ACCCGGGGCT AC CCAG CCT
                         |||||||||| || |||| |||
                         TGGGCCCCGG TG GGTC GGA
                           GG G  C  III
GAM217 PXN             GGGGTGGAGCCCCCAGCCTCT   3169 ACCC    GGACG
                            GGGGCT  CCAGCCTCT
                            ||||||  |||||||||
                            CCTCGG   GGTCGGAGA
                            ____      G____
GAM217 SET7            CGGGGCTGGCTCGCACTGCCTC  3161 ACCCGG   A_ CA_
                           GGCTGG CGC  GCCTCT
                           |||||| |||  ||||||
                           CCGACC GCG  CGGAGG
                           _____    GA  TGA
GAM217 SHOX            CCGGGGCTGG-CGAGCAGCC   3156 ACCC    A C_ TC
                          GGGGCTGG CG CAGCC
                          |||||||| || |||||
```

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                        CCCCGACC GC  GTCGG
                        ____      _ TC   CC
GAM217 SHOX             CCCGGGCTGGACGCACGGCCGCT  3157 ACCCG       CA_  T I
                        GGGCTGGACGC  GCC CT
                        ||||||||||   ||| ||
                        CCCGACCTGCG  CGG GA
                        G____         TGC  C G
GAM217 SORL1           CCCGGGGCTCCAGGCCGCCCGC   3143 AC      ___  A  A CTCT
                        CCGGGGCT  GG CGCC GC
                        |||||||| || |||| ||
                        GGCCCCGA  CC GCGG CG
                        __       GGT G  G CIII
GAM217 STC1            CTCTTTCC-CTCTCCTGGCT    3164 TGGCTGTG  ACG
                        TCC  CTCCTGGCT
                        ||| |||||||||
                        AGG  GAGGACCGA
                        AA_____   GA_
GAM217 WHSC1           ACACGGGCCTC-AC-CCAGCCTCT 3142 ACCCG   GG G
                        GGGCT  AC CCAGCCTCT
                        |||||  || |||||||||
                        CCCGG  TG GGTCGGAGA
                        TGTG_    AG _
GAM218 ADAM19          GGCAAGGAC---ATGGGGAA     3194      C AT  I
                        GGCAAGGAC TG  GGAG
                        ||||||||| ||  ||||
                        CCGTTCCTG AC  CCTT
                        T C_  I
GAM218 ADAM19          GGCAAGGAC---ATGGGGAA     3194 TG    CTG  A G
                        GCAAGGAC  ATGG GAA
                        ||||||||  |||| |||
                        CGTTCCTG  TACC CTT
                        __    ___    C  G
GAM218 AOC3            GGAAAGGACCTGGAT-GAGAGGG  3190 GC      _ _  AAI
                        AAGGACCTG ATG GAG
                        ||||||||| ||| |||
                        TTCCTGGAC TAC CTC
                        T_    C  T CII
GAM218 AOC3            GGAAAGGACCTGGAT-GAGAGGG  3190 TGGC     ATG  A T
                        AAGGACCTG  GAGA GG
                        ||||||||| |||| ||
                        TTCCTGGAC  CTCT CC
                        CT__      CTA  C T
GAM218 ARPC2          GGCAAGGA-CGGAGGGAGA     3192      CT T  I
                        GGCAAGGAC GA GGAG
                        ||||||||| || ||||
                        CCGTTCCTG CT CCTC
                        C_  C  T
GAM218 ARPC2          GGCAAGGA-CGGAGGGAGA     3192 TG    CT T  AG
                        GCAAGGAC GA GGAGA
                        ||||||||| || |||||
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                          CGTTCCTG CT CCTCT
                       __      C_ C   CI
GAM218 BSN            TGGCAAAGGACCTGCCTGGAAAA  3199    _    A_     GGTI
                       TGGCAA GGACCTG TGGAGAA
                       |||||| ||||||| |||||||
                       ACCGTT CCTGGAC ACCTTTT
                          T      GG     IIIT
GAM218 BSN            TGGCAAAGGACCTGCCTGGAAAA  3199 G C      A_    I
                          G AAGGACCTG TGGAGA
                          | |||||||||| ||||||
                          G TTCCTGGAC ACCTTT
                       _T       GG     I
GAM218 CAPON            GCAAGGGCCT---GGAGAAGG    3185    A  AT  AI
                          GCAAGG CCTG GGAG
                          |||||| |||| ||||
                          CGTTCC GGAC CTTC
                             C   CT   CI
GAM218 CAPON            GCAAGGGCCT---GGAGAAGG    3185 TGGC   A  GAT
                          AAGG CCT  GGAGAAG
                          |||| |||  |||||||
                          TTCC GGA  CCTCTTC
                       ____      C  ___
GAM218 CNTN2           AAGGACCTGGGGCGAGAGAAGG   3175       AT___     III
                          AAGGACCTG   GGAGAAG
                          |||||||||   |||||||
                          TTCCTGGAC   TCTCTTC
                             CCCGC     CII
GAM218 CSF3            GCAAGGACCCAGATGGGGAA     3181      _    A II
                          GCAAGGACCT GATGG GA
                          |||||||||| ||||| ||
                          CGTTCCTGGG CTACC CT
                             T    C  TI
GAM218 CSF3            GCAAGGACCCAGATGGGGAA     3181 TGGC     _   A GG
                          AAGGACCT GATGG GAA
                          |||||||| ||||| |||
                          TTCCTGGG CTACC CTT
                       ____       T   C GT
GAM218 DCX            CAAGGTGAACTGATGGAGAA      3179    AC__       III
                          CAAGG  CTGATGGAGA
                          |||||  |||||||||||
                          GTTCC  GACTACCTCT
                          ACTT       TII
GAM218 DCX            CAAGGTGAACTGATGGAGAA      3179 TGGCAA   C
                           GGAC TGATGGAGAAGG
                           |||| |||||||||||||
                           CTTG ACTACCTCTTTT
                       CCA___   _
GAM218 EIF2AK3         GGCAAGGACGTGCTAGGGA      3193     C AT_ AGII
                          GGCAAGGAC TG  GG
                          ||||||||| ||  ||
```

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                        CCGTTCCTG AC  CC
                          C GAT CTII
GAM218 EIF2AK3        GGCAAGGACGTGCTAGGGA    3193 TG    C AT_ A AGG
                        GCAAGGAC TG  GG GA
                        |||||||| ||  || ||
                        CGTTCCTG AC  CC CT
                        __    C GAT _ GII
GAM218 ESRRG          GGAAAGAAGATGATGGAGAAAGT  3198 GC   CC         I
                        AAGGA TGATGGAGAAGG
                        ||||| |||||||||||
                        TTCTT ACTACCTCTTC
                        CT   CT         I
GAM218 ESRRG          GGAAAGAAGATGATGGAGAAAGT  3198 TGGC   CC        I
                        AAGGA TGATGGAGAAGGT
                        ||||| ||||||||||||
                        TTCTT ACTACCTCTTCA
                        CT__   CT        T
GAM218 FXR2           GCAAG--CGAGATGGAGAAGG    3184   _ CCT     I
                        GCAAG GA  GATGGAGAA
                        ||||| ||  |||||||||
                        CGTTC CT  CTACCTCTT
                          G ___      C
GAM218 GLUL           TGGGAGAGGGC--GATGGAGAAGG  3200 __ CA  ACC       I
                        GG AGG  TGATGGAGAAG
                        || |||  |||||||||||
                        CC TCC  GCTACCTCTTC
                        AC TC  C__        I
GAM218 GLUL           TGGGAGAGGGC--GATGGAGAAGG  3200 T_ CA  ACC        T
                        GG AGG  TGATGGAGAAGG
                        || |||  ||||||||||||
                        CC TCC  GCTACCTCTTCC
                        AC TC  C__         I
GAM218 GNRH1          TGGCAAGGACAGTGAAGGA       3201        C_ T II
                        TGGCAAGGAC TGA GG
                        |||||||||| ||| ||
                        ACCGTTCCTG ACT CC
                          TC  T  TI
GAM218 GNRH1          TGGCAAGGACAGTGAAGGA       3201        CTGAT A
                        TGGCAAGGAC   GG GAAGG
                        ||||||||||   || |||||
                        ACCGTTCCTG   TC CTTCC
                          _____  A
GAM218 GPR4          AAGGTCACCAGTAAGGAGAAGGT   3174 AGG  TGAT_    I
                          ACC   GGAGAAGG
                          |||   ||||||||
                          TGG   CCTCTTCC
                        AG_  TCATT     I
GAM218 GPR4          AAGGTCACCAGTAAGGAGAAGGT   3174 TGGCAAGG  TGAT_    I
                          ACC   GGAGAAGGT
                          |||   |||||||||
```

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                      TGG    CCTCTTCCA
                   AG_____   TCATT       A
GAM218  HMGCR           TGGCA-GGAG-TGAGGGAGAAGGT  3203    A  CC  T
                       TGGCA GGA  TGA GGAGAAGGT
                       ||||| ||| ||| |||||||||
                       ACCGT CCT  ACT CCTCTTCCA
                         _  C_  C
GAM218  HMGCR           TGGCA-GGAG-TGAGGGAGAAGGT  3203 _  A  CC  T    I
                        GGCA GGA  TGA GGAGAAGG
                        |||| ||| ||| ||||||||
                        CCGT CCT  ACT CCTCTTCC
                        A  _  C_  C     I
GAM218  HOXC13         GGCTAGTGCCCTGATGGA-AAGGT  3188  A  GA_        A  I
                        GC AG  CCTGATGGAGA GG
                        || ||  |||||||||||| ||
                        CG TC  GGACTACCTTT CC
                         A ACG          _ I
GAM218  HOXC13         GGCTAGTGCCCTGATGGA-AAGGT  3188 TG A  GA_        A  I
                         GC AG  CCTGATGGAGA GGT
                         || ||  |||||||||| |||
                         CG TC  GGACTACCTTT CCA
                         __ A ACG         _ C
GAM218  IGF2         GGGATGGAACCTGATGGA-AACGT  3189 CAA           AI
                          GGACCTGATGGAGA
                          |||||||||||||||
                          CTTGGACTACCTTT
                        TAC          GI
GAM218  IGF2         GGGATGGAACCTGATGGA-AACGT  3189 T  CAA          AGGTI
                          GG  GGACCTGATGGAGA
                          ||  |||||||||||||||
                          CC  CTTGGACTACCTTT
                          _ TAC         GCAGI
GAM218  IL1F5        GCCAGGACCTGA-GGAGGAG    3182 GCA       T  AI
                         AGGACCTGA GGAG
                         ||||||||| ||||
                         TCCTGGACT CCTC
                        GG_       _  CT
GAM218  IL1F5        GCCAGGACCTGA-GGAGGAG    3182 TGGCA      T  A  G
                         AGGACCTGA GGAG AG
                         ||||||||| |||| ||
                         TCCTGGACT CCTC TC
                        G____     _  C G
GAM218  ITGA2B       GGCAA---CTTGTTGGAGAAGG  3196   AGG C A    I
                        GGCA  AC TG TGGAGAA
                        ||||  || || |||||||
                        CCGT  TG AC ACCTCTT
                          ___  A A    C
GAM218  ITGA2B       GGCAA---CTTGTTGGAGAAGG  3196 TGGCAAG  C  A
                         GAC TG TGGAGAAGG
                         ||| || |||||||||
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                              TTG AC ACCTCTTCC
                         CG_____     A A
GAM218 LHX3          AAGGATCTGATGGAGGAGG    3176 TGGCAAGGAC      A
                         CTGATGGAG AGG
                         |||||||| |||
                         GACTACCTC TCC
                         TA_____        C
GAM218 LHX3          AAGGATCTGATGGAGGAGG    3176   C      AAGII
                         AAGGA CTGATGGAG
                         ||||| |||||||||
                         TTCCT GACTACCTC
                          A       CTCCI
GAM218 LRP1         GGCAGGGAGGGGATGGAGAA    3195  A  CCT        I
                         GCA GGA  GATGGAGA
                         ||| |||  ||||||||
                         CGT CCT  CTACCTCT
                          C  CCC       I
GAM218 LRP1         GGCAGGGAGGGGATGGAGAA    3195 TG  A  CCT        G
                          GCA GGA  GATGGAGAAG
                          ||| |||  ||||||||||
                          CGT CCT  CTACCTCTTT
                          __  C  CCC        I
GAM218 NEK2         CAGGGACCTGGATGGAGAAG    3180  A    _       II
                          CA GGACCTG ATGGAGAA
                          || ||||||| ||||||||
                          GT CCTGGAC TACCTCTT
                           C      C      CI
GAM218 NEK2         CAGGGACCTGGATGGAGAAG    3180 TGGCAA     _      G
                          GGACCTG ATGGAGAAG
                          ||||||| |||||||||
                          CCTGGAC TACCTCTTC
                          _____         C     G
GAM218 NXF5        GGACACTGGGATGGAGAAGG    3186   _ __         III
                          GGAC CT GATGGAGAAG
                          |||| || ||||||||||
                          CCTG GA CTACCTCTTC
                           T CC        CII
GAM218 RECQL5       GCAAATATCTGGTGGAGAAGG    3183    GAC  A      I
                          CAAG  CTG TGGAGAAG
                          ||||  ||| |||||||||
                          GTTT  GAC ACCTCTTC
                          ATA  C      I
GAM218 RECQL5       GCAAATATCTGGTGGAGAAGG    3183 TGGCAAGGAC  A      T
                          CTG TGGAGAAGG
                          ||| |||||||||
                          GAC ACCTCTTCC
                         TTTATA____   C      C
GAM218 RNGTT        AAGGACCTGGTGGTGTATGT    3177      A AGAAGGI
                          AGGACCTG TGG
                          |||||||| |||
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                          TCCTGGAC ACC
                           C  ACATACI
GAM218 RNGTT           AAGGACCTGGTGGTGTATGT    3177 TGGCAAGG   A  AGAAGG
                           ACCTG TGG
                           ||||| |||
                           TGGAC ACC
                   _____     C  ACATAC
GAM218 RXRA            GGGAAAGAC-T-ATGGAGAAGG  3197 _ C    CTG      I
                          GG AAGGAC  ATGGAGAA
                          || |||||| |||||||||
                          CC TTTCTG  TACCTCTT
                          C _   A__     C
GAM218 RXRA            GGGAAAGAC-T-ATGGAGAAGG   3197 T C    CTG
                          GG AAGGAC  ATGGAGAAGG
                          || |||||| |||||||||||
                          CC TTTCTG  TACCTCTTCC
                          _  _      A__
GAM218 SCAP2           GGAAAGGACCTGCGCTGAAAAGGT 3191 GC      ATG_    I
                          AAGGACCTG  GAGAAGG
                          |||||||||  |||||||
                          TTCCTGGAC  CTTTTCC
                          T_        GCGA    I
GAM218 SCAP2           GGAAAGGACCTGCGCTGAAAAGGT 3191 TGGC      ATG_     I
                           AAGGACCTG  GAGAAGGT
                           |||||||||  ||||||||
                           TTCCTGGAC  CTTTTCCA
                          CT__       GCGA     C
GAM218 THRA          GGCAGAGG-CCTG--GGAGAAGGT  3187 _  _  A  AT      I
                          GCA AGG CCTG  GGAGAAGG
                          ||| ||| ||||  ||||||||
                          CGT TCC GGAC  CCTCTTCC
                          C  C  _   __       I
GAM218 THRA          GGCAGAGG-CCTG--GGAGAAGGT  3187 TG _  A  AT
                          GCA AGG CCTG  GGAGAAGGT
                          ||| ||| ||||  |||||||||
                          CGT TCC GGAC  CCTCTTCCA
                          __   C  _   __
GAM218 ZNF192         TGGCAAGAAACAGATGGAGAA    3202      CCT     GGT
                          TGGCAAGGA  GATGGAGAA
                          ||||||||| ||||||||||
                          ACCGTTCTT  CTACCTCTT
                           TGT       III
GAM218 ZNF192         TGGCAAGAAACAGATGGAGAA    3202      CCT    I
                          GGCAAGGA  GATGGAGA
                          |||||||| ||||||||
                          CCGTTCTT  CTACCTCT
                           TGT     I
GAM218 ZNFN2A1        AGGAAGCCCTGCTGGAGAAGG    3178    ___   A     III
                          AGGA  CCTG TGGAGAAG
                          ||||  |||| |||||||||
```

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                              TCCT  GGAC ACCTCTTC
                              TCG   G     CII
GAM218  ZNFN2A1       AGGAAGCCCTGCTGGAGAAGG   3178 TGGCAAGGA   A
                              CCTG TGGAGAAGGT
                              IIII IIIIIIIIII
                              GGAC ACCTCTTCCG
                              CG_____  G
GAM219  DUT           ATCAGTCCCATATCTGCAATG   3208     T  CG  TI
                              TCAGTCCC TATC  GTA
                              IIIIIIIII IIII  III
                              AGTCAGGG ATAG  CGT
                               T   A_  TA
GAM219  DUT           ATCAGTCCCATATCTGCAATG   3208 TA     T  CG  TGTG
                              TCAGTCCC TATC  GTA
                              IIIIIIIII IIII  III
                              AGTCAGGG ATAG  CGT
                              __     T  A_  TACT
GAM219  FACL4         ATCAAGTCCCTTATCAAGTA    3206  _      C  II
                              ATCA GTCCCTTATC GGT
                              IIII IIIIIIIIII III
                              TAGT CAGGGAATAG TCA
                               T     T  TI
GAM219  FACL4         ATCAAGTCCCTTATCAAGTA    3206 TA  _      C  TGT
                              TCA GTCCCTTATC GGTA
                              III IIIIIIIIII IIII
                              AGT CAGGGAATAG TCAT
                              __  T     T  TII
GAM219  GABPA         ATCAGTCCC-ACTCCGGAAT    3207 _     TTA   TAI
                              TCAGTCCC  TCCGG
                              IIIIIIII  IIIII
                              AGTCAGGG  AGGCC
                               T    TG_  TTI
GAM219  GABPA         ATCAGTCCC-ACTCCGGAAT    3207 TA     TTA   T GT
                              TCAGTCCC  TCCGG AT
                              IIIIIIII  IIIII II
                              AGTCAGGG  AGGCC TA
                              __    TG_  T GI
GAM219  PPP1R12B      GTCCCTTATTCAGGAATAGTG   3209     C  TATGTIII
                              GTCCCTTAT CGG
                              IIIIIIIII III
                              CAGGGAATA GTC
                              A  CTTATCAC
GAM220  C4orf1        TAACATTAGAAAAATTAAACCAAAT 3239    C    __      GII
                              TAACAT AGAGAA  TAAACCAAAT
                              IIIIII IIIII  IIIIIIIIII
                              ATTGTA TCTTT  ATTTGGTTTA
                               A   TA    III
GAM220  C4orf1        TAACATTAGAAAAATTAAACCAAAT 3239 AA  C    __       I
                              CAT AGAGAA  TAAACCAAA
                              III IIIIII  IIIIIIIII
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```
                              GTA TCTTTT  ATTTGGTTT
                               __     A      TA         I
GAM220 CHAC          AACTACTGAGAATAAAC--AATG   3221 AACATCA         CI
                              GAGAATAAAC
                              ||||||||||
                              CTCTTATTTG
                          ATGA___          TT
GAM220 CHAC          AACTACTGAGAATAAAC--AATG   3221 TAACATCA        CA
                              GAGAATAAAC  AATG
                              ||||||||||  ||||
                              CTCTTATTTG  TTAC
                       TGATGA__            __
GAM220 COG3          TAACATCAGCGGCAAAACCAA    3243        AGAAT    ATG
                            TAACATCAG    AAACCAA
                            |||||||||    |||||||
                            ATTGTAGTC    TTTGGTT
                             GCCGT          III
GAM220 COG3          TAACATCAGCGGCAAAACCAA    3243        AGAAT   I
                             AACATCAG    AAACCA
                             ||||||||    ||||||
                             TTGTAGTC    TTTGGT
                             GCCGT      I
GAM220 DUOX2         CAACAGAAGAATAAACAAACTG    3230 T    _     C    I
                            CAGA GAATAAAC AAAT
                            |||| |||||||| ||||
                            GTCT CTTATTTG TTTG
                          T   T     _     I
GAM220 DUOX2         CAACAGAAGAATAAACAAACTG    3230 TAACAT   _     C   G
                            CAGA GAATAAAC AAAT
                            |||| |||||||| ||||
                            GTCT CTTATTTG TTTG
                          _____   T    _   A
GAM220 EFNB2         ACAGCACCGCATAAACCAAA      3227 ___  AGAGA      I
                            CATC   ATAAACCAA
                            ||||   |||||||||
                            GTGG   TATTTGGTT
                        GTC   CG___      I
GAM220 EFNB2         ACAGCACCGCATAAACCAAA      3227 TAA  AGAGA       T
                            CATC   ATAAACCAAA
                            ||||   ||||||||||
                            GTGG   TATTTGGTTT
                         TC_  CG___        C
GAM220 FACL4         CATCA-AGAATAAACACAAA      3231     G    _  II
                            CATCA AGAATAAAC CAA
                            ||||| ||||||||| |||
                            GTAGT TCTTATTTG GTT
                             _        T  TI
GAM220 FACL4         CATCA-AGAATAAACACAAA      3231 TAACATCA       _  T
                            GAGAATAAAC CAAA
                            |||||||||| ||||
```

```
                          TTCTTATTTG GTTT
                       G_____        T   T
GAM220  FIGF           AACTTCACACAGAAAACCAAAT   3220 A___   T  G   TA     I
                          CA CA AGAA  AACCAAA
                          || || |||| |||||||
                          GT GT TCTT  TTGGTTT
                       TGAA _ G   __       I
GAM220  FIGF           AACTTCACACAGAAAACCAAAT   3220 TA___   T   ATAA
                          ACA CAGAGA   ACCAAATG
                          ||| ||||||   |||||||||
                          TGT GTCTTT   TGGTTTAT
                       TGAAG   _   ____
GAM220  FXYD7          CAGAGGAAAAAACCAAATG       3229   _ T       II
                          CAGAG AA AAACCAAAT
                          ||||| || ||||||||||
                          GTCTC TT TTTGGTTTA
                          C  T      CI
GAM220  GALNT3         AACATTGACAGACAAGTAAACCAAA 3212 ACAT    G  _      I
                          CAGA AA TAAACCAA
                          |||| || |||||||||
                          GTCT TT ATTTGGTT
                       ACT_   G C     I
GAM220  GALNT3         AACATTGACAGACAAGTAAACCAAA 3212 TA    ____    G _      GII
                          ACAT   CAGA AA TAAACCAAAT
                          ||||    |||| || ||||||||||
                          TGTA   GTCT TT ATTTGGTTTG
                       __  AACT  G C       III
GAM220  GEMIN5         ACATGAAAGAATAAAACCAAAT    3225 CATC        _   I
                          AGAGAATAAA CCAAA
                          |||||||||| |||||
                          TTTCTTATTT GGTTT
                       TAC_       T  I
GAM220  GEMIN5         ACATGAAAGAATAAAACCAAAT    3225 TAACATC      _   G
                          AGAGAATAAA CCAAAT
                          |||||||||| ||||||
                          TTTCTTATTT GGTTTA
                       TAC____       T   A
GAM220  HIRA           AACATTTAAAAATTAAAACCAAATG 3215 ACATCA     __      I
                          GAGAAT AAACCAAAT
                          |||||| ||||||||||
                          TTTTTA TTTGGTTTA
                       TAAA__     AT     I
GAM220  HIRA           AACATTTAAAAATTAAAACCAAATG 3215 TA   CA     __        II
                          ACAT GAGAAT AAACCAAATG
                          |||| |||||| ||||||||||
                          TGTA TTTTTA TTTGGTTTAC
                       __   AA   AT     TI
GAM220  HOXA3          TAAATTCAGAGAAT--GCCAAAT   3245 AACA_       AAA    I
                          TCAGAGAAT  CCAAA
                          ||||||||| |||||
```

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                              AGTCTCTTA GGTTT
                         ATTTA        C__     I
GAM220  HOXA3      TAAATTCAGAGAAT--GCCAAAT  3245 TAACA      AAA     G
                           TCAGAGAAT  CCAAAT
                           ||||||||| ||||||
                           AGTCTCTTA GGTTTA
                         ATTTA        C__     I
GAM220  HPSE       TAAC-TCAG-GAATGGAAAACCAAAT 3240   A   A   ___        GI
                         TAAC TCAG GAAT   AAACCAAAT
                         |||| |||| ||||   |||||||||
                         ATTG AGTC CTTA   TTTGGTTTA
                          _    _   CCT       II
GAM220  HPSE       TAAC-TCAG-GAATGGAAAACCAAAT 3240 AACA   A   ___        I
                              TCAG GAAT   AAACCAAA
                              |||| ||||   ||||||||
                              AGTC CTTA   TTTGGTTT
                          TG__    _   CCT        I
GAM220  INPP4A     AAGAACACAAAATAAACCAA        3219 ACAT  G        I
                             CA AGAATAAACCA
                             || ||||||||||||
                             GT TTTTATTTGGT
                          TCTT  G           I
GAM220  INPP4A     AAGAACACAAAATAAACCAA        3219 TAACAT  G        AT
                             CA AGAATAAACCAA
                             || |||||||||||||
                             GT TTTTATTTGGTT
                          TCTT__  G          AI
GAM220  MTMR8      TATCATCTGAGAATAAATGTAAATG 3241 A   A       CCAAATI
                             CATC GAGAATAAA
                             |||| |||||||||
                             GTAG CTCTTATTT
                          A    A       ACATTTI
GAM220  MTMR8      TATCATCTGAGAATAAATGTAAATG 3241 TAA   A      CC_    II
                             CATC GAGAATAAA  AAATG
                             |||| ||||||||| |||||
                             GTAG CTCTTATTT  TTTAC
                          ATA   A       ACA    II
GAM220  MYO15A     AACATCAGACCCTGAGTAAACCAAA 3213 ACAT    ____  A     I
                             CAGA   GA TAAACCAA
                             ||||   || ||||||||
                             GTCT   CT ATTTGGTT
                             ____    GGGA C      I
GAM220  MYO15A     AACATCAGACCCTGAGTAAACCAAA 3213 TA        ____  A     TGII
                             ACATCAGA   GA TAAACCAAA
                             ||||||||   || |||||||||
                             TGTAGTCT   CT ATTTGGTTT
                             __       GGGA C      CIII
GAM220  NOTCH2     TAACAATAAA-AATAAACCAAA     3244    TCA         TG
                             TAACA GAGAATAAACCAAA
                             ||||| ||||||||||||
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                              ATTGT  TTTTTATTTGGTTT
                                TA_           II
GAM220  NOTCH2       TAACAATAAA-AATAAACCAAA  3244 _  TCA        I
                         AACA  GAGAATAAACCAA
                         IIII  IIIIIIIIIII
                         TTGT  TTTTTATTTGGTT
                          A  TA_         I
GAM220  NOTCH2       ACATGGAGAGAATAAAGCAGAGAATG 3222 TAACATC      C  AATGII
                            AGAGAATAAA CA
                            IIIIIIIIII II
                            TCTCTTATTT GT
                         TACC___       C CTCTTA
GAM220  NOTCH2       ACATGGAGAGAATAAAGCAGAGAATG 3222 TC       C  AATI
                            AGAGAATAAA CA
                            IIIIIIIIII II
                            TCTCTTATTT GT
                         C_        C CTCT
GAM220  OPHN1        TAAC-TCACC-AATAAACCA     3242   A  GAG      AA
                         TAAC TCA  AATAAACCA
                         IIII III  IIIIIIIII
                         ATTG AGT  TTATTTGGT
                          _  GG_        II
GAM220  OSCAR        AACATCAGA----AAACCA      3218          AAACC
                         AACATCAGAGAAT
                         IIIIIIIIIIII
                         TTGTAGTCTTTTG
                            GTIII
GAM220  OSCAR        AACATCAGA----AAACCA      3218 TA       ATAA  A
                         ACATCAGAGA  ACCA
                         IIIIIIIIII  IIII
                         TGTAGTCTTT  TGGT
                          __     ___   C
GAM220  PCDHB16      TAACAATCAGAGAAAAATACC    3234   _     TAA_ AAATG
                        TAACA TCAGAGAA   ACC
                        IIIII IIIIIIII   III
                        ATTGT AGTCTCTT   TGG
                          T     TTTA  IIIGT
GAM220  PCDHB16      TAACAATCAGAGAAAAATACC    3234   _     TAAACIII
                        TAACA TCAGAGAA
                        IIIII IIIIIIII
                        ATTGT AGTCTCTT
                         T     TTTATGGI
GAM220  PHKA1        TAACAGATCTAGAGAATAAAAACACATG3233     __ _       CCAAATGIII
                         TAACA  TC AGAGAATAAA
                         IIIII  II IIIIIIIIII
                         ATTGT  AG TCTCTTATTT
                          CT A        TTGTGTACII
GAM220  PHKA1        TAACAGATCTAGAGAATAAAAACACATG3233 _      CCAAAI
                         ATC AGAGAATAAA
                         III IIIIIIIII
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                              TAG TCTCTTATTT
                               A        TTGTII
GAM220 PIGK           ACATTAAAGAATAAACCAAA      3228   C           I
                              CAT AGAGAATAAACCAA
                              ||| |||||||||||||
                              GTA TTTCTTATTTGGTT
                               A           I
GAM220 PIGK           ACATTAAAGAATAAACCAAA      3228 TAACATC           T
                                  AGAGAATAAACCAAA
                                  |||||||||||||
                                  TTTCTTATTTGGTTT
                              TAA____            C
GAM220 PKP2          AAAATCAGAGAAAAACAACCAA    3216 AC        TA__  I
                              ATCAGAGAA   AACCA
                              |||||||||   |||||
                              TAGTCTCTT   TTGGT
                               __        TTTG  I
GAM220 PKP2          AAAATCAGAGAAAAACAACCAA    3216 TAAC      TA__   ATG
                              ATCAGAGAA   AACCAA
                              |||||||||   ||||||
                              TAGTCTCTT   TTGGTT
                              TT__       TTTG  CII
GAM220 PPARGC1        ACATCAGAGAATGTAGCAA       3226          AAACCAII
                              ACATCAGAGAAT
                              ||||||||||||
                              TGTAGTCTCTTA
                                  CATCGTTI
GAM220 PPARGC1        ACATCAGAGAATGTAGCAA       3226 TAAC       AAACCAAAT
                              ATCAGAGAAT
                              ||||||||||
                              TAGTCTCTTA
                              ____       CATCGTTAA
GAM220 PX19          ACATCAGAGAACAAAACCAAA      3224 C          _  I
                              ATCAGAGAATAAA CCAA
                              ||||||||||||| ||||
                              TAGTCTCTTGTTT GGTT
                              _          T  I
GAM220 PX19          ACATCAGAGAACAAAACCAAA      3224 TAAC        _   TG
                              ATCAGAGAATAAA CCAAA
                              ||||||||||||| |||||
                              TAGTCTCTTGTTT GGTTT
                              ____       T   TC
GAM220 RBBP5          TCAGAGAATTTCAAACACCAAATG  3246      AA_____    IIIC
                              TCAGAGAAT    ACCAAAT
                              |||||||||    |||||||
                              AGTCTCTTA    TGGTTTA
                                  AAGTTTG     CIII
GAM220 RDX          TAAAATAAGAATTAACAAACCAAAT 3237 AACATC   __        I
                              AGAG AATAAACCAAA
                              |||| |||||||||||
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                          TCTT TTGTTTGGTTT
                    TTAT__    AA          I
GAM220 RDX    TAAAATAAGAATTAACAAACCAAAT 3237 TAACATC   __        GII
                    AGAG  AATAAACCAAAT
                    IIII  IIIIIIIIIIII
                    TCTT  TTGTTTGGTTTA
                 ATTTTAT   AA          III
GAM220 SOX11    TAAATTCTGAAGTAAAAACCAAATG 3236 TAACA A  AAT_        II
                  TC GAG    AAACCAAATG
                  II III    IIIIIIIIII
                  AG CTT    TTTGGTTTAC
                 ATTTA A  CATT          II
GAM220 SPG4    AACATCAGAAGACAAACAAACAAATG 3217 ACA    GA    ___      I
                  TCAGA  ATAAAC   CAAAT
                  IIIII  IIIIII   IIIII
                  AGTCT  TGTTTG   GTTTA
                  ___     TC    TTT    I
GAM220 SPG4    AACATCAGAAGACAAACAAACAAATG 3217 TA      GA    ___      II
                 ACATCAGA ATAAAC  CAAATG
                 IIIIIIIII IIIIII  IIIIII
                 TGTAGTCT TGTTTG  GTTTAC
                  __       TC   TTT    AI
GAM220 SPP1    CATGAGAGAATAA--CAAAT     3232   C       ACCAAI
                    CAT AGAGAATAA
                    III IIIIIIIII
                    GTA TCTCTTATT
                     C      GTTTAI
GAM220 SPP1    CATGAGAGAATAA--CAAAT     3232 TAACATC     AC
                    AGAGAATAA  CAAA
                    IIIIIIIII  IIII
                    TCTCTTATT  GTTT
                  C_____       __
GAM220 STX7    AACATCAGACTTAAATAGACCATATG 3214 A    ___   A  AATI
                  TCAGA  GAATA ACCA
                  IIIII  IIIII IIII
                  AGTCT   TTTAT TGGT
                  _  GAA    C  AIII
GAM220 STX7    AACATCAGACTTAAATAGACCATATG 3214 TA      ___    A  A II
                 ACATCAGA  GAATA ACCA ATG
                 IIIIIIIII  IIIII IIII III
                 TGTAGTCT  TTTAT TGGT TAC
                  __       GAA   C  A  AI
GAM220 TBX5    TAA-ATAA-AGACATAAACCAA     3238 AACATC   _      I
                    AGAGA ATAAACCA
                    IIIII IIIIIIII
                    TTTCT TATTTGGT
                 ATTTA_   G      I
GAM220 TBX5    TAA-ATAA-AGACATAAACCAA     3238 TAACATC   _      AT
                    AGAGA ATAAACCAA
                    IIIII IIIIIIIII
```

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                      TTTCT TATTTGGTT
                 ATTTA__    G       II
GAM220  TEM7R         ACATCAGAGAACATTTGAACCAAA  3223 CATC      ____      I
                 AGAGAATA    AACCAA
                 ||||||||    ||||||
                 TCTCTTGT    TTGGTT
                 ____        AAAC    I
GAM220  TEM7R         ACATCAGAGAACATTTGAACCAAA  3223 TAAC      ____      TGI
                 ATCAGAGAATA    AACCAAA
                 |||||||||||    |||||||
                 TAGTCTCTTGT    TTGGTTT
                 ____           AAAC    CCI
GAM220  TRAM          TAA-ATATGATGAATAAACCAAATG  3235 AACATCA _          I
                 GA GAATAAACCAAAT
                 || |||||||||||||
                 CT CTTATTTGGTTTA
                 TTTATA_ A          I
GAM220  TRAM          TAA-ATATGATGAATAAACCAAATG  3235 TAACATCA _         I
                 GA GAATAAACCAAATG
                 || ||||||||||||||
                 CT CTTATTTGGTTTAC
                 ATTTATA_ A          I
GAM220  ZNF255        TAAC-TCAG-GAATGGAAAACCAAAT 3240   A   A   ___      GI
                 TAAC TCAG GAAT   AAACCAAAT
                 |||| |||| ||||   |||||||||
                 ATTG AGTC CTTA   TTTGGTTTA
                 _    _    CCT        II
GAM220  ZNF255        TAAC-TCAG-GAATGGAAAACCAAAT 3240 AACA   A   ___      I
                 TCAG GAAT   AAACCAAA
                 |||| ||||   ||||||||
                 AGTC CTTA   TTTGGTTT
                 TG__    _   CCT      I
GAM221  AKAP1         TGCTTCCGGTGAAAACTGG      3260 ACTTTGCT    AC   A
                 TCCGGT  AAAC  GG
                 ||||||  ||||  ||
                 AGGCCA  TTTG  CC
                 _____     CT   A
GAM221  CD5           TTTTCT-CAGG-ACAAACAGG      3263 ACTTTGC   C   T
                 TTC GG ACAAACAGG
                 ||| || |||||||||
                 GAG CC TGTTTGTCC
                 AA_____    T  _
GAM221  EIF4EBP2      ACTTTGCTTTCTTGAAGTACAA     3251        _C___     ACAGGC
                 ACTTTGCTT C   GGTACAA
                 ||||||||| |   |||||||
                 TGAAACGAA G   TCATGTT
                 A AACT      IIICGG
GAM221  EN2           ACTTTGCTTCCTGCTA-AAA-AGGC 3252         G AC  C  I
                 ACTTTGCTTCC GT  AAA AGGC
                 |||||||||||| || ||| ||||
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                              TGAAACGAAGG CG  TTT TCCG
                                 A A_  T   I
GAM221 ESRRBL1         ACTTTGCTTCTGATTGAAA     3254       C  ACAAACAGG

                              ACTTTGCTTC GGT
                              ||||||||| |||
                              TGAAACGAAG CTA
                                 A  ACTTTIIIC
GAM221 FUT4           ACTTTGCTTCCATTCACAGGACAGG 3253       G_  A_  CII

                              ACTTTGCTTCCG TACA ACAGG
                              |||||||||| |||| |||||
                              TGAAACGAAGGT GTGT TGTCC
                                   AA  CC   III
GAM221 INSR          ACTTTTGTTCC---ACAAACAGG  3257    GC   GGT

                              ACTTT TTCC  ACAAACAGG
                              ||||| |||| |||||||||
                              TGAAA AAGG  TGTTTGTCC
                                AC    ___
GAM221 KIF3B        TTTG-TTCTTATTCAAACAGGC   3265 ACTT C  CG A

                              TG TTC GT CAAACAGGC
                              || ||| || |||||||||
                              AC AAG TA GTTTGTCCG
                              ____ _  AA A
GAM221 MCL1          ACTTTGCTTC--TTTCAGACAG   3255     CGGTA A  G

                              ACTTTGCTTC   CA ACAG
                              ||||||||||   || ||||
                              TGAAACGAAG   GT TGTC
                                AAA__ C  I
GAM221 NCOA4         ACTTTGCTTTACTAGTTCAAA   3250     CC__  A  CAGGC

                              ACTTTGCTT   GGT CAAA
                              |||||||||   ||| ||||
                              TGAAACGAA   TCA GTTT
                                ATGA  A   IIICG
GAM221 PIGA         TTTGCATTTTAGTACAAACA      3261 ACTT  TTCC_

                              TGC   GGTACAAACAGG
                              |||   ||||||||||||
                              ACG   TCATGTTTGTTT
                              ____   TAAAA
GAM221 PRKG1        CTTTGCTTCAGG-ACCACCA      3258 AC      C T AAA GG

                              TTTGCTTC GG AC  CA
                              |||||||| || ||  ||
                              AAACGAAG CC TG  GT
                              __    T _ GTG AI
GAM221 RAPSN        TTTTTTTCCAGGTACAAACAG     3262 ACTTGC  _       GC

                              TTCC GGTACAAACAG
                              |||| |||||||||||
                              AAGG CCATGTTTGTC
                                AAA____  T     AA
GAM221 SP3          ACTATTGATT--GGTACAAAC    3249 ACTTTGCTTCC       AGG

                              GGTACAAAC
                              |||||||||
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                          CCATGTTTG
                        TGATAACTAA_         III
GAM221  STK38       TTTTCTGGAGG-ACAAACAGG    3264 ACTTTGCTTCC  T
                        GG ACAAACAGG
                        II IIIIIIIII
                        CC TGTTTGTCC
                       AAGACCT____ _
GAM221  ZIC1        CTTGCCATTCAGTACAAACAG    3259 ACT   TC_        GC
                        TTGCT  CGGTACAAACAG
                        IIIII  IIIIIIIIIIII
                        AACGG  GTCATGTTTGTC
                       ___    TAA       AI
GAM221  ZNF289      ACTTTGTTTCAA-TACAAACAG   3256     C  C       GC
                        ACTTTG TTC GGTACAAACAG
                        IIIIII III IIIIIIIIIII
                        TGAAAC AAG TTATGTTTGTC
                            A  _        II
GAM222  ADCY2       TGACCAGGAATAATGCTCT      3277 T  C_       II
                        TG CCAG ATAATGCTC
                        II IIII IIIIIIIII
                        AC GGTC TATTACGAG
                         T  CT      AI
GAM222  ADCY2       TGACCAGGAATAATGCTCT      3277 CAGTGTGTCCAGC
                            ATAATGCTCT
                            IIIIIIIIII
                            TATTACGAGA
                       TCCT_____
GAM222  BIN3        AGTGTGTCCTCCACA--GCTCT   3268 _      AG   AT   I
                        GTGTGTCC CATA GCTC
                        IIIIIIII IIII IIII
                        CACACAGG GTGT CGAG
                         T    AG  __  I
GAM222  BIN3        AGTGTGTCCTCCACA--GCTCT   3268 CA     AG   AT
                        GTGTGTCC CATA GCTCT
                        IIIIIIII IIII IIIII
                        CACACAGG GTGT CGAGA
                         __     AG  __
GAM222  BLMH        CAGTGATACTGTCCAGCAGCATGC 3269 ____      TA   TCTCI
                        CAGTG  TGTCCAGCA ATGC
                        IIIII  IIIIIIIII IIII
                        GTCAC  ACAGGTCGT TACG
                         TATG      CG  IIICT
GAM222  BLMH        CAGTGATACTGTCCAGCAGCATGC 3269 AGTG      TAATGI
                          TGTCCAGCA
                          IIIIIIIII
                          ACAGGTCGT
                        TATG      CGTACI
GAM222  GGT2        CAGTGTGTCCCTCCCAAT-CTC   3274         AGCA  G  TC
                        CAGTGTGTCC  TAAT CTC
                        IIIIIIIIII    IIII III
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                    GTCACACAGG  GTTA GAG
                        GAGG  _   II
GAM222 GGT2         CAGTGTGTCCCTCCCAAT-CTC  3274 _      AGCA  GCTI
                        AGTGTGTCC  TAAT
                        |||||||||  ||||
                        TCACACAGG  GTTA
                        G    GAGG  GAII
GAM222 HLCS         CACTTTGTACC-CA-AATGCTCTC  3275 AG___  GT  GCAT    I
                        TGT CCA  AATGCTCT
                        ||| |||  ||||||||
                        ACA GGT  TTACGAGA
                        GTGAA TG ____    I
GAM222 HLCS         CACTTTGTACC-CA-AATGCTCTC  3275 CAG__  GT  GCAT
                        TGT CCA  AATGCTCTC
                        ||| |||  |||||||||
                        ACA GGT  TTACGAGAG
                        GTGAA TG ____
GAM222 KLK3         GTGTCCAGCA-CATGTCACTCTC  3276 TG     A__   I
                        TCCAGCATA  TGCTCT
                        ||||||||||  ||||||
                        AGGTCGTGT  GTGAGA
                        __       ACA    I
GAM222 MYLK         CAGTGTGT-CAG-AAGATGTTC   3273     C CATA  C T
                        CAGTGTGTC AG   ATG TC
                        ||||||||| ||   ||| ||
                        GTCACACAG TC   TAC AG
                         _ TTC_  A I
GAM222 MYLK         CAGTGTGT-CAG-AAGATGTTC   3273     C CATA  CI
                        CAGTGTGTC AG   ATG
                        ||||||||| ||   |||
                        GTCACACAG TC   TAC
                         _ TTC_  AA
GAM222 OCRL         TGTCAAACATGAATGCTCTC   3278  C  _     II
                        TGTC AGCAT AATGCTCT
                        |||| ||||| ||||||||
                        ACAG TTGTA TTACGAGA
                         T    C    GI
GAM222 RBM8A        CAGTGTGT-CACCA-AAGGC   3271      C G  TAAT  TC
                        CAGTGTGTC A CA   GC
                        ||||||||| | ||   ||
                        GTCACACAG T GT   CG
                         _ G TTC_ II
GAM222 RBM8A        CAGTGTGT-CACCA-AAGGC   3271      C G  TAATI
                        CAGTGTGTC A CA
                        ||||||||| | ||
                        GTCACACAG T GT
                         _ G TTCCG
GAM222 SNX2         CACTGTGGAATCCAGCATAA   3270  G  ___      TGCTCT
                        CA TGTG  TCCAGCATAA
                        || ||||  ||||||||||
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                        GT ACAC  AGGTCGTATT
                         G  CTT      IIICTC
GAM222 SNX2             CACTGTGGAATCCAGCATAA   3270 G  ___      III
                        CA TGTG  TCCAGCATA
                        II IIII  IIIIIIIII
                        GT ACAC  AGGTCGTAT
                         G  CTT      TII
GAM222 ZNF36           CACTATGTCCAGCACTGTGCT   3272 G       AA  CTC
                        CA TGTGTCCAGCAT TGCT
                        II IIIIIIIIIII IIII
                        GT ATACAGGTCGTG ACGA
                         G      AC  III
GAM222 ZNF36           CACTATGTCCAGCACTGTGCT   3272 AG       AA  I
                         TGTGTCCAGCAT TGC
                         IIIIIIIIIII III
                         ATACAGGTCGTG ACG
                        TG      AC  I
GAM223 APPBP2          CCACTCATGCTATAGATACCT   3283 CC    ATC AT G CT
                        CACTCATG  TA TA CT
                        IIIIIIII II II II
                        GTGAGTAC  AT AT GA
                        __      GAT CT G TI
GAM223 APPL            CCCACTCATAACTTCTATTTAGC  3285       __ A   TCTI
                        CCCACTCATGA TCTA TTAGC
                        IIIIIIIIII IIII IIIII
                        GGGTGAGTATT AGAT AATCG
                          GA  A   IIIT
GAM223 DISC1           ACTC-TGAGGTTAATTAGCTCT   3281 CCCACTCA  TC_
                         TGA  TAATTAGCTCT
                         III  IIIIIIIIIII
                         ACT  ATTAATCGAGA
                        G_____  CCA
GAM223 EFG1            ACACAT--TC-AATTAGCTC    3282 CCCACTCATGATC
                         TAATTAGCT
                         IIIIIIIII
                         GTTAATCGA
                        GTAA_____
GAM223 MICB            CCCA-TGATAATCTAATTA    3286   CTC       GCT
                        CCCA  ATGATCTAATTA
                        IIII  IIIIIIIIIIII
                        GGGT  TATTAGATTAAT
                        AC_         III
GAM223 NRCAM           CCCATTCACTGCAT-TAATTAGCT  3284  C GATC_     CTI
                        CCCA TCAT   TAATTAGCT
                        IIII IIII   IIIIIIIII
                        GGGT AGTG   ATTAATCGA
                         A  ACGTA       III
GAM224 BCL9            TGATCTGTTTTTCTTCTGACT    3299 AA  A       GTG
                        TGA TGTTTT CTTCTGACT
                        III IIIIII IIIIIIIII
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                          ACT  ACAAAA GAAGACTGA
                          AG      A      III
GAM224  BCL9         TGATCTGTTTTTCTTCTGACT    3299 AA    A      I
                          GA  TGTTTT CTTCTGAC
                          II  IIIIII IIIIIIII
                          CT  ACAAAA GAAGACTG
                          AG      A      I
GAM224  CGTHBA           AAATGTTTTATTTCTAGAAAACTGTG 3289 TGAA     C   ____      II
                          ATGTTTTA TTCT   GACTGTG
                          IIIIIIIII IIII   IIIIIII
                          TACAAAAT AAGA   TTGACAC
                          ____      A TCTT      GG
GAM224  CHN2         GAAATGTTTTA-TCCTTAGCTGTG  3294      C  GA_  I
                          AAATGTTTTA TTCT  CTGT
                          IIIIIIIIII IIII   IIII
                          TTTACAAAAT AGGA   GACA
                          _   ATC  I
GAM224  CHN2         GAAATGTTTTA-TCCTTAGCTGTG  3294 TG    C  GA_  I
                          AAATGTTTTA TTCT  CTGTG
                          IIIIIIIIII IIII   IIIII
                          TTTACAAAAT AGGA   GACAC
                          __      _ ATC   A
GAM224  CPB2         GAAATCTTTAATGTACTTCTGAC  3293   G  ____      IIIG
                          GAAAT TTT   TACTTCTGA
                          IIIII III   IIIIIIIII
                          CTTTA AAA   ATGAAGACT
                          G  TTAC      GIII
GAM224  CPB2         GAAATCTTTAATGTACTTCTGAC  3293 TGA_____    TTT     GTGI
                          AATGT ACTTCTGACT
                          IIIII IIIIIIIIII
                          TTACA TGAAGACTGG
                          TTTAGAAA    ___      IIIG
GAM224  DAZL        TGAAATGTTTGTA-TTCAGAC    3295      TAC  T  TGT
                          TGAAATGTTT  TTC GAC
                          IIIIIIIIII  III III
                          ACTTTACAAA  AAG CTG
                          CAT  T  III
GAM224  FBP2         GAAACCTTGCTTACTTCTGA    3292   G __      III
                          GAAAT TT TTACTTCTG
                          IIIII II IIIIIIIII
                          CTTTG AA AATGAAGAC
                          G  CG      TII
GAM224  FBP2         GAAACCTTGCTTACTTCTGA    3292 TGAAA_  T      CTGT
                          TGTTT ACTTCTGA
                          IIIII IIIIIIII
                          ACGAA TGAAGACT
                          TTTGGA    _      CIII
GAM224  GPR85        TGAAATGTTTTAAAGTCTTCAAACT 3296          ____  T  GTGII
                          TGAAATGTTTTA   CTTC GACT
                          IIIIIIIIIIII   IIII IIII
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                    ACTTTACAAAAT   GAAG TTGA
                        TTCA   T   IIIGT
GAM224 HAO2         TGAGATCTTTTACTTCAGA      3298  A  G      T CTGT
                    TGA AT TTTTACTTC GA
                    III II IIIIIIIII II
                    ACT TA AAAATGAAG CT
                        C  G      T IIIG
GAM224 HAO2         TGAGATCTTTTACTTCAGA      3298  A  G      TGII
                    TGA AT TTTTACTTC
                    III II IIIIIIIII
                    ACT TA AAAATGAAG
                        C  G     TCTI
GAM224 HOXB3        TGTTCTGAAACTTCTGACTG     3304     ___      III
                    TGTTTT ACTTCTGACT
                    IIIIII IIIIIIIIII
                    ACAAGA TGAAGACTGA
                      CTT      CII
GAM224 HOXB3        TGTTCTGAAACTTCTGACTG     3304 TGAAATGTTTT
                        ACTTCTGACTGT
                        IIIIIIIIIIII
                        TGAAGACTGACG
                    ACTT_____
GAM224 HSPA8        TGAAATGTTTGTCTTTT--CTGT  3302        TAC__  ACTI
                    TGAAATGTTT   TTCTG
                    IIIIIIIIII   IIIII
                    ACTTTACAAA   AAGAC
                      CAGAA    AIII
GAM224 HSPA8        TGAAATGTTTGTCTTTT--CTGT  3302       TACT GA_  G
                    TGAAATGTTT  TCT CTGT
                    IIIIIIIIII  III IIII
                    ACTTTACAAA  AGA GACA
                      C___  AAA   I
GAM224 JUN         TGAAATGTTTGACTTCTCAGTG    3301        T   GACT
                    TGAAATGTTT ACTTCT  GTG
                    IIIIIIIIII IIIIII  III
                    ACTTTACAAA TGAAGA  CAC
                      C   GT__
GAM224 JUN         TGAAATGTTTGACTTCTCAGTG    3301        T   GACTI
                    GAAATGTTT ACTTCT
                    IIIIIIIII IIIIII
                    CTTTACAAA TGAAGA
                       C   GTCAI
GAM224 LANCL1      TGAAATGTT---CTTCTCCCTG    3300       TTA  GA T
                    TGAAATGTT CTTCT CTG
                    IIIIIIIII IIIII III
                    ACTTTACAA GAAGA GAC
                       ___   GG   I
GAM224 LANCL1      TGAAATGTT---CTTCTCCCTG    3300        A   GAI
                    TGAAATGTTTT CTTCT
                    IIIIIIIIIII IIIII
```

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                              ACTTTACAAGA GAGGG
                               A    ACl
GAM224  NDUFA9        TGAAATGTTTTAATAGTGGAACTGTG 3297        CTTCT__    ll
                     TGAAATGTTTTA      GACTGTG
                     llllllllllll      llllll
                     ACTTTACAAAT    TTGACAC
                               TATCACC    ll
GAM224  NDUFA9        TGAAATGTTTTAATAGTGGAACTGTG 3297 GA       CTTCT__   l
                         AATGTTTTA      GACTGT
                         lllllllll      llllll
                         TTACAAAAT    TTGACA
                     __       TATCACC    l
GAM224  TGFA          TGTCTTACTTCTGCAATGTG    3305        AC_ ll
                     TGTTTACTTCTG  TGT
                     llllllllllll  lll
                     ACAGAATGAAGAC  ACA
                               GTT  Cl
GAM224  UGT2A1        AAATGTTTTTC-TCTG-CTG    3291      A T  ACl
                     AAATGTTTT CT CTG
                     lllllllll ll lll
                     TTTACAAAA GA GAC
                               A _  GAC
GAM224  UGT2A1        AAATGTTTTTC-TCTG-CTG    3291 TGAA    A T  A
                       ATGTTTT CT CTG CTG
                       lllllll ll lll lll
                       TACAAAA GA GAC GAC
                     ____      A _  _
GAM224  UVRAG         AAATGCTGACCTTCTGACTG    3290      TTA    l
                       AATGTT  CTTCTGACT
                       llllll  llllllllll
                       TTACGA  GAAGACTGA
                               CTG      l
GAM224  UVRAG         AAATGCTGACCTTCTGACTG    3290 TGAA  TTA      T
                       ATGTT  CTTCTGACTG
                       lllll  llllllllll
                       TACGA  GAAGACTGAC
                     ____   CTG       T
GAM224  ZNF200        TGAAATGTTTT-CTTC--CCTGTG 3303       A    GA
                     TGAAATGTTTT CTTCT CTGTG
                     lllllllllll lllll lllll
                     ACTTTACAAAA GAAGG GACAC

                               _    __
GAM224  ZNF200        TGAAATGTTTT-CTTC--CCTGTG 3303 _     A    GA
                       GAAATGTTTT CTTCT CTGT
                       llllllllll lllll llll
                       CTTTACAAAA GAAGG GACA
                     A       _    __
GAM225  BUB1B         TGAGACTTGATTGCCTAGC    3314    ATT_      TGATG
                     TGAGAC  TTGCCTAGC
                     llllll  llllllllll
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                          ACTCTG   AACGGATCG
                          AACT        IIIAG
GAM225  HOXB5        AGACATTTTGC--A-CTGAGGA   3312 TGAG      CTA    T
                         ACATTTTGC  GCTGA G
                         ||||||||| ||||| |
                         TGTAAAACG  TGACT C
                         ____      ___   C
GAM225  LNK          ACCTTTTGCCTA--TAATGA    3309 TGAGACAT      GC_
                         TTTGCCTA  TGAT
                         |||||||| ||||
                         AAACGGAT  ACTA
                         _____      ATT
GAM225  SET          ACACTTTTGCCTA-TTGATG    3308 TGAGACA      GC
                         TTTTGCCTA  TGATG
                         ||||||||| |||||
                         AAAACGGAT  ACTAC
                         _____      A_
GAM225  TRPS1        AGACATTTTG-AGAGCTGAT    3310 TGAG     CCT     G
                         ACATTTTG  AGCTGAT
                         ||||||||  |||||||
                         TGTAAAAC  TCGACTA
                         ____      TC_    G
GAM225  TRPS1        AGACATTTT--CT-GCTGGTGA   3311 TGAG    GC A  A
                         ACATTTT  CT GCTG TG
                         |||||||  || |||| ||
                         TGTAAAA  GA CGAC AC
                         ____      __  _    C
GAM225  XYLB         TGAGAATCACTTTTC--AGCTGATGA 3313    __     GCC       I
                         TGAGA CATTTT  TAGCTGATGA
                         ||||| ||||||  ||||||||||
                         ACTCT GTGAAA  GTCGACTACT
                         TA    A__    I
GAM226  ALDH8A1      TCCTGAACTCAAGTGATCCACCCA 3332     C          I
                         TCTTGA CTCAAGTGATCCACCCA
                         |||||| |||||||||||||||||
                         AGGACT GAGTTCACTAGGTGGGT
                         T         I
GAM226  ANKH         TCCTGACCTTAAGTGATCCACCC  3326       C      AI
                         TCTTGACCT AAGTGATCCACCC
                         ||||||||| |||||||||||||
                         AGGACTGGA TTCACTAGGTGGG
                         A         II
GAM226  BCAS1        TCCTGACCTCAGGTGATCCACC   3320       A     CA
                         TCTTGACCTCA GTGATCCACC
                         ||||||||||| ||||||||||
                         AGGACTGGAGT CACTAGGTGG
                         C           II
GAM226  C5R1         TCTTGACCTCAGGTGATCCACCCA 3338       A      I
                         TCTTGACCTCA GTGATCCACCCA
                         ||||||||||| |||||||||||
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                        AGAACTGGAGT CACTAGGTGGGT
                             C         I
GAM226 CD68      TCCTGACCTCCAGTGATCCACC   3321       A      CA
                 TCTTGACCTC AGTGATCCACC
                 IIIIIIIIII IIIIIIIIII
                 AGGACTGGAG TCACTAGGTGG
                      G        II
GAM226 CHST5     TCCTGACCTCAGGTGATCCACCC   3325        A      AI
                 TCTTGACCTCA GTGATCCACCC
                 IIIIIIIIIII IIIIIIIIII
                 AGGACTGGAGT CACTAGGTGGG
                      C        II
GAM226 CPT2      TCCTGACCTCAAGTGATCCACCC   3323                AI
                 TCTTGACCTCAAGTGATCCACCC
                 IIIIIIIIIIIIIIIIIIIIIII
                 AGGACTGGAGTTCACTAGGTGGG
                            II
GAM226 DMC1      TCCTGACCTCAAGTGATCCACC   3319                 CA
                 TCTTGACCTCAAGTGATCCACC
                 IIIIIIIIIIIIIIIIIIIII
                 AGGACTGGAGTTCACTAGGTGG
                            II
GAM226 DNASE2    TCCTGAGTTCAAGTGATCCTCCC   3327    CC       A AI
                 TCTTGA TCAAGTGATCC CCC
                 IIIIII IIIIIIIIIII III
                 AGGACT AGTTCACTAGG GGG
                      CA       A II
GAM226 DNASE2    TCCTGACCTCAAGTGATCTGCCCA   3334               CA  I
                 TCTTGACCTCAAGTGATC CCCA
                 IIIIIIIIIIIIIIIIII IIII
                 AGGACTGGAGTTCACTAG GGGT
                      AC  I
GAM226 HIP1      TCCTGACCTCAGGTGATCCACCC   3325       A       AI
                 TCTTGACCTCA GTGATCCACCC
                 IIIIIIIIIII IIIIIIIIII
                 AGGACTGGAGT CACTAGGTGGG
                      C        II
GAM226 HTR2A     TCTTGGCCTCAAGTGATCCTCCCA   3340    A       A  I
                 TCTTG CCTCAAGTGATCC CCCA
                 IIIII IIIIIIIIIIII IIII
                 AGAAC GGAGTTCACTAGG GGGT
                      C         A  I
GAM226 IL10      TCCTGACCTCAAGTGATCCACCC   3323                 AI
                 TCTTGACCTCAAGTGATCCACCC
                 IIIIIIIIIIIIIIIIIIIIIII
                 AGGACTGGAGTTCACTAGGTGGG
                            II
GAM226 IL4R      TCCTGATCTCAAGTGATCTGCCC   3328    C       CA AI
                 TCTTGA CTCAAGTGATC CCC
                 IIIIII IIIIIIIIIII III
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                          AGGACT GAGTTCACTAG  GGG
                               A        AC  II
GAM226  ITGAL           TCCTGACCTCAGGTGATCCACCC   3325       A       AI
                        TCTTGACCTCA GTGATCCACCC
                        ||||||||||| |||||||||||
                        AGGACTGGAGT CACTAGGTGGG
                               C        II
GAM226  LAMP2           TCCTGGCCTCAAGTGATCCACCCA  3336    A            I
                        TCTTG CCTCAAGTGATCCACCCA
                        ||||| |||||||||||||||||
                        AGGAC GGAGTTCACTAGGTGGGT
                             C          I
GAM226  LRRC2           TCCTGGGCTCAAGTGATTTTCCCA  3337   AC       CCA  I
                        TCTTG CTCAAGTGAT  CCCA
                        ||||| |||||||||  ||||
                        AGGAC GAGTTCACTA  GGGT
                             CC       AAA  I
GAM226  LRRC2           GACCTCAGGTGATCCACCCA    3317 TCTTGACC  A
                          TCA GTGATCCACCC
                          ||| |||||||||||
                          AGT CACTAGGTGGG
                        _____     C
GAM226  NPHP1           TCCTGACCTCAGGTGATCCACCCA  3335       A        I
                        TCTTGACCTCA GTGATCCACCCA
                        ||||||||||| ||||||||||||
                        AGGACTGGAGT CACTAGGTGGGT
                               C        I
GAM226  NPHS1           TCCTGACCTCAGGTGATCCACCC   3325       A       AI
                        TCTTGACCTCA GTGATCCACCC
                        ||||||||||| |||||||||||
                        AGGACTGGAGT CACTAGGTGGG
                               C        II
GAM226  OPA3            TCCTGACCTCAAGTGATCCGCCC   3324            A AI
                        TCTTGACCTCAAGTGATCC CCC
                        |||||||||||||||||| |||
                        AGGACTGGAGTTCACTAGG GGG
                               C  II
GAM226  OPTN            TGACCCCAAGTGATCCACCCA    3342 TCTTGA
                          CCTCAAGTGATCCACCCA
                          ||||||||||||||||||
                          GGGGTTCACTAGGTGGGT
                        _____
GAM226  PA2G4           TCGTGACCTCAGGTGATCCACCC   3330 T    A       AI
                        TC TGACCTCA GTGATCCACCC
                        || |||||||| |||||||||||
                        AG ACTGGAGT CACTAGGTGGG
                             C  C       II
GAM226  PCDH11X         TCCTGACCTC--GTGATCCACCC   3322        AA      A
                        TCTTGACCTC GTGATCCACCC
                        |||||||||| |||||||||||
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                          AGGACTGGAG CACTAGGTGGG
                              __          I
GAM226  PCDH11X        TCCTGACCTCAGGTGATCCACCCA  3335      A        I
                       TCTTGACCTCA GTGATCCACCCA
                       |||||||||| ||||||||||||
                       AGGACTGGAGT CACTAGGTGGGT
                           C           I
GAM226  PCDH11Y        TCCTGACCTC--GTGATCCACCC   3322      AA       A
                       TCTTGACCTC GTGATCCACCC
                       ||||||||| |||||||||||
                       AGGACTGGAG CACTAGGTGGG
                           __          I
GAM226  PCDH11Y        TCCTGACCTCAGGTGATCCACCC   3325      A        AI
                       TCTTGACCTCA GTGATCCACCC
                       |||||||||| ||||||||||
                       AGGACTGGAGT CACTAGGTGGG
                           C            II
GAM226  PRY        TCTTGACCTC-ACTGCATCC      3318      AG _  ACCC
                   TCTTGACCTCA TG ATCC
                   |||||||||| || ||||
                   AGAACTGGAGT AC TAGG
                       G_  G   IIIA
GAM226  PSD        TCTTGACCT--TGTGATCCGCCC   3331      CAA    A A
                   TCTTGACCT  GTGATCC CCC
                   ||||||||| |||||||  |||
                   AGAACTGGA  CACTAGG GGG
                       A__        C  I
GAM226  SUDD        TCCTGACCTCAAGTGATCCACCC  3323                AI
                    TCTTGACCTCAAGTGATCCACCC
                    |||||||||||||||||||||||
                    AGGACTGGAGTTCACTAGGTGGG
                              II
GAM226  SWAP70        TCCTGACCTCAGGTGATCCACCC   3325      A        AI
                      TCTTGACCTCA GTGATCCACCC
                      |||||||||| ||||||||||
                      AGGACTGGAGT CACTAGGTGGG
                           C           II
GAM226  TIRAP        TCTTGACCTCATG-GA-GCAGCCA  3339      AGT  TC  C
                     TCTTGACCTCA  GA CA CCA
                     |||||||||||  ||  || |||
                     AGAACTGGAGT  CT GT GGT
                        AC_  C_  C
GAM226  TNFRSF10A        TGACCTCAAGTGATCCACCC   3341      A        CA
                        TCTTGACCTCA GTGATCCACC
                        |||||||||| ||||||||||
                        AGGACTGGAGT CACTAGGTGG
                             G           II
GAM226  XT3        TCCTGACCTCAAGTGATCCACCCA   3333                I
                   TCTTGACCTCAAGTGATCCACCCA
                   ||||||||||||||||||||||||
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                        AGGACTGGAGTTCACTAGGTGGGT
                                    I
GAM226  ZNF264          TCCTGGCCTCAGGTGATCCACCC  3329    A    A      AI
                        TCTTG CCTCA GTGATCCACCC
                        ||||| ||||| ||||||||||||
                        AGGAC GGAGT CACTAGGTGGG
                            C    C      II
GAM227  BRCA1           GGAGTTTCACCACGTTGGTCAGG  3345          C   I
                        GGGTTTCACCATGTTGG CAG
                        ||||||||||||||| |||
                        CTCAAAGTGGTGCAACC GTC
                                A   I
GAM227  BRCA1           GGAGTTTCACCACGTTGGTCAGG  3345 TG      C   I
                          GGGTTTCACCATGTTGG CAGG
                          ||||||||||||||| ||||
                          CTCAAAGTGGTGCAACC GTCC
                              __       A   G
GAM227  MAN2C1         GGCTTTCACCCCCATGTTGGCCA  3348 GGT_  A      I
                        TTC CCATGTTGGCC
                        ||| |||||||||||
                        GGG GGTACAACCGG
                       AAGT  _      I
GAM227  MAN2C1         GGCTTTCACCCCCATGTTGGCCA  3348 TGGGG    ___       I
                        TTTCACC  ATGTTGGCCAGG
                        |||||||  |||||||||||||
                        AAAGTGG  TACAACCGGTTT
                       G____     GGG        I
GAM227  PSD         TGGGGTTTCACTACGTTGGCCAGG  3349        C       I
                      TGGGGTTTCAC ATGTTGGCCAGG
                      ||||||||||| ||||||||||||
                      ACCCCAAAGTG TGCAACCGGTCC
                              A       I
GAM227  PSD         TGGGGTTTCACTACGTTGGCCAGG  3349        C       I
                        GGGGTTTCAC ATGTTGGCCAG
                        |||||||||| ||||||||||||
                        CCCCAAAGTG TGCAACCGGTC
                              A       I
GAM227  SLC22A1LS      GGGGTTT---CATGCT-GCCAGG  3346      CCA    G
                        GGGGTTTCA TGTTG CCA
                        ||||||||| ||||| |||
                        CCCCAAAGT ACGAC GGT
                           __    _
GAM227  SLC22A1LS      GGGGTTT---CATGCT-GCCAGG  3346 TG    CCA    G
                        GGGTTTCA TGTTG CCAG
                        |||||||| ||||| ||||
                        CCCAAAGT ACGAC GGTC
                           __    _
GAM227  TRIM9          GGTGTTTTTCCATGTTGGTCAGG  3347 GG   CA      C  I
                        GTTT  CCATGTTGG CAG
                        ||||  |||||||||| |||
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                         CAAA  GGTACAACC GTC
                         CA   AA       A  I
GAM227  TRIM9            GGTGTTTTTCCATGTTGGTCAGG  3347 TGGG   CA       C  I
                            GTTT  CCATGTTGG CAGG
                            |||| ||||||||| ||||
                            CAAA  GGTACAACC GTCC
                         CA__    AA      A  G
GAM228  ACAT2            CTTCTCCTGCCGCCGTCTGC   3356 _     ___  _ ___   CGTCT
                            TGCCGCC  TGCTC GTG  GC   G
                            |||||| |||||| ||| ||   |
                            ACGGCGG  ACGGG CGC  CG   C
                         G    CAG   A  III TCTGC
GAM228  AP2M1            GCCCCCTGCTCGTCTGCCCGCTGC  3362 TG  G      __G  T  I
                            CC CCTGCTCGT G CCG CTGC
                            || ||||||||| | ||| ||||
                            GG GGACGAGCA C GGC GACG
                         __  G     GA G  _  G
GAM228  CALM1            GCCGCCTG--CGCCGCCGCCTG   3365 TG      TC  G
                            CCGCCTGC GT GCCGTCTG
                            |||||||| || |||||||||
                            GGCGGACG CG CGGCGGAC
                         __     __ G
GAM228  CDC34            GCCGCCTGCCTCCT--CC-TCTGC  3360 TG       CGTGG  G
                            CCGCCTGCT   CC TCTGC
                            |||||||||    || |||||
                            GGCGGACGG   GG AGACG
                         __      AGGA_  _
GAM228  DPP4             GCCTGCTCGTGTTGGTATGC   3369 TGCCGCCT    GCC  C
                            GCTCGTG  GT TG
                            ||||||| || ||
                            CGAGCAC  CA AC
                         _____       AAC  T
GAM228  DVL3             GCGGCCTGCTCGGGCGGCCG   3361 TGCC     __    TCTG
                            GCCTGCTC GTGGCCG
                            |||||||| |||||||
                            CGGACGAG CGCCGGC
                         GC__      CC    CIII
GAM228  EDN3             GCCGACGCCTCGTGGCCCTC   3363 _ C  TGC     G  TG
                            TG CGCC  TCGTGGCC TC
                            || |||| ||||||||| ||
                            GC GCGG  AGCACCGG AG
                         G  T   ___    G  TI
GAM228  EIF2B1           GCCGCCTG--CGAGCCAGTCTG   3364 TG      TCGT  _
                            CCGCCTGC  GGCC GTCTG
                            |||||||| |||| |||||
                            GGCGGACG  TCGG CAGAC
                         __        C___  T
GAM228  ESR2             GCCGCCTGCTCTTCGCC--CTGC  3367 TG      GTG  GT
                            CCGCCTGCTC  GCC  CTGC
                            ||||||||||  |||  ||||
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                    GGCGGACGAG  CGG  GACG
                     __          AAG  __
GAM228 GNA15        TGCCGCCTGCCCCAGGTGG    3371        ___    CCGTCTG
                    TGCCGCCTGCTC  GTGG
                    |||||||||||  ||||
                    ACGGCGGACGGG  CACC
                         GTC   |||CGTC
GAM228 GRB14        GCCGCCTGCGCTCGGGGCC    3358 TG    __  T  GTCTG
                    CCGCCTGC  TCG GGCC
                    ||||||||  ||| ||||
                    GGCGGACG  AGC CCGG
                         __    CG  C   G|||C
GAM228 HS2ST1       CCGCCTGCT--TGCCCGCCT    3352 TGCC    CG  G
                     GCCTGCT  TG CCGTCT
                     |||||||  || ||||||
                     CGGACGA  AC GGCGGA
                        ____      __ G
GAM228 ICA1         TGGCTCCTTCACTTGGCCGTCT    3374 T_  CG  GCTCG      GC
                     GC  CCT    TGGCCGTCT
                     ||  |||     |||||||||
                     CG  GGA    ACCGGCAGA
                    AC  A_  AGTGA        ||
GAM228 MAGOH        GCCGCACTGC-CG---CCGTCTGC  3357 TG   _    CGTG
                     CCGC CTGCT   GCCGTCTG
                     |||| |||||   ||||||||
                     GGCG GACGG   CGGCAGAC
                        __   T   ____
GAM228 MDFI         TGCGCGCCTGCTCCGGGCGCCCCTGC 3370  _     G  C   GC||
                    TGC CGCCTGCTC TGG CGTCT
                    ||| |||||||||| ||| |||||
                    ACG GCGGACGAG GCC GCGGG
                        C    _  C   GACG
GAM228 PDGFB        CCGCCTGCTCGCCGC--TCTG    3353 TGCC      G CG
                    GCCTGCTCGT GC  TCTG
                    |||||||||| ||  ||||
                    CGGACGAGCG CG  AGAC
                        ____       G  __
GAM228 RGS6         GCCGCCTGCCTGTGG-GGTCCGC   3366 TG    TC   CC
                    CCGCCTGC  GTGG  GTCTGC
                    ||||||||  ||||  ||||||
                    GGCGGACG  CACC  CAGGCG
                        __       GA  C_
GAM228 RNF12        CGCCTGCTCGGAGACGT-TGC    3355 TGCCGC    TG C  C
                    CTGCTCG  G CGT  TG
                    |||||||  | |||  ||
                    GACGAGC  C GCA  AC
                        _____      CT T  _
GAM228 SLC9A5       TGCCGCCTGCCCAGCCGCCCTC    3372         GT     GC
                    TGCCGCCTGCTC  GGCCGTCT
                    |||||||||||  |||||||||
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                        ACGGCGGACGGG  TCGGCGGG
                          __              AG
GAM228  TIMP3       GCCGCCTGCCTGCTGCCCGCTCTGC  3359 TG      TC _ G _     II
                        CCGCCTGC  G TG CCG TCTGC
                        IIIIIIII I II III IIIII
                        GGCGGACG  C AC GGC AGACG
                            __        GA G  G   G   CI
GAM228  TRPS1         TGCCTC-TGCCCTTGGCCGTCT    3373   GC     G      GC
                        TGCC  CTGCTC TGGCCGTCT
                        IIII  IIIIII IIIIIIIII
                        ACGG  GACGGG ACCGGCAGA
                            A_      A      II
GAM228  WNT6          CGCCTTTTCGGGGCCGTCTG     3354 TGCCGC GC  T
                          CT  TCG GGCCGTCTG
                          II  III IIIIIIIII
                          GA  AGC CCGGCAGAC
                        _____     AA  C
GAM228  WNT7A        GCGTCCCCGGGGCCGTCTG      3368 TGCCGCCTG   T
                          CTCG GGCCGTCTG
                          IIII IIIIIIIII
                          GGGC CCGGCAGAC
                      G_____      C
GAM229  ABR         ATGCGGTGGTGAGGCTGGGGCTGG  3380 TA      C _ _   _ AAI
                        TGCGGTGG G GG TGGGG TGG
                        IIIIIIIII I II IIIII III
                        ACGCCACC C CC ACCCC ACC
                          __        A T  G   G  CII
GAM229  ADD2        TATGGGTTTGGGGGGTGGGGTG    3394    C __ C      GAA
                        TATG GGT  GG GGGTGGGGTG
                        IIII III  II IIIIIIIIII
                        ATAC CCA  CC CCCACCCCAC
                          _   AA  C        III
GAM229  ALOX12B       TGAGGTGGCGAGGTGGGGTG    3401 TATGC     _     A
                          GGTGGCG GGTGGGGTGG
                          IIIIIII IIIIIIIIII
                          CCACCGC CCACCCCACT
                        T____      T      G
GAM229  ANXA11       TATACGG-GTCAGGAGGGGTGGAA  3395     TGG   T      I
                        TATGCGG  CGGG GGGGTGGAA
                        IIIIIII  IIII IIIIIIIII
                        ATATGCC  GTCC CCCCACCTT
                          CA_    T      I
GAM229  ARF3        TATGTCAGGGGTGGGTGGGGTG    3393   _ T C       GAA
                        TATG CGG GG GGGTGGGGTG
                        IIII III II IIIIIIIIII
                        ATAC GTC CC CCCACCCCAC
                          A  C A       III
GAM229  CD7        CGGTGGCGGCGTGGGCTGG       3381 TAT   GC  G  TG A
                        GCGGTG GGGT GGG  G
                        IIIIII IIII III  I
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                       CGCCGC  CCCG CCC  C
                       C__    A_   A  GT I
GAM229  COPE           ATGCAGGTGGATGCCGGGTGGGGAGG 3377 TA  _   ____        T  AAII
                       TGC GGTGG   CGGGTGGGG GG
                       ||| |||||   |||||||||| ||
                       ACG CCACC   GCCCACCCC CC
                       __  T   TACG      T CIII
GAM229  CTNNB1         TGCGGTGGCGGCTCGGCGGGGA  3403 TATG     G_  _ T  A
                       CGGTGGCGG  TGG GG GGA
                       ||||||||| ||| || |||
                       GCCACCGCC  GCC CC CCT
                       ____          GA  G _  G
GAM229  ENIGMA         GGTGGAGGGAGTGGGGTGG      3390 TATGCGGT  C       A
                       GG GGGTGGGGTGG
                       || |||||||||||
                       CC CTCACCCCACC
                       T_____  _        C
GAM229  ENO2           GCGGTGGC-GGTGGCGGTGG     3386 TAT     GTGG    A
                       GCGGTGGCGG  GGTGG
                       ||||||||||  |||||
                       CGCCACCGCC  CCGCC
                       CAC        A___    I
GAM229  EXTL1          ATG-GGTGGCGGGGTGGGGCGG   3379 TA C        _     AA
                       TG GGTGGCGGG TGGGGTGG
                       || ||||||||| ||||||||
                       AC CCACCGCCC ACCCCGCC
                       __ _      C    CI
GAM229  FASN           GCGGGGGTGGGGTGGGGTGG     3385 TATGC   CG     A
                       GGTGG GGTGGGGTGG
                       ||||| ||||||||||
                       CCACC CCACCCCACC
                       CC___    __       C
GAM229  FASN           TGGGGTGG--GGTGGGGTGG     3406 TATGC   CG
                       GGTGG GGTGGGGTGG
                       ||||| ||||||||||
                       CCACC CCACCCCACC
                       C____    __
GAM229  FLT1           TGAGGTGGCGG--GGGTTGGA    3407 TATGC      T GG
                       GGTGGCGGG GG TGGA
                       ||||||||| || ||||
                       CCACCGCCC CC ACCT
                       T____      _ A_
GAM229  GAL            TGCGGTGGCGGGTCTGGGCGG    3402 TATG      G_   AA
                       CGGTGGCGGGT GGGTGG
                       ||||||||||| ||||||
                       GCCACCGCCCA CCCGCC
                       ____          GA  GT
GAM229  GRM7           TGCGGTGGCGGCGGCGGCGCTGGA 3400 TATG       __  G _  AI
                       CGGTGGCGG GTGG G TGGA
                       ||||||||| |||| | ||||
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                        GCCACCGCC  CGCC C ACCT
                        ____      GC   G G   CC
GAM229  HSF4          TGGGGTGGAGTGGGGTGGGGTGG  3399 TATGC   C___        AAI
                         GGTGG  GGGTGGGGTGG
                         IIIII  IIIIIIIIIII
                         CCACC  CCCACCCCACC
                        C____    TCAC       CCI
GAM229  HSF4          TGGGGTGG--GGTGGGGTG      3404 TATGC   CG
                         GGTGG  GGTGGGGTGG
                         IIIII  IIIIIIIIII
                         CCACC  CCACCCCACT
                      C____     __
GAM229  INSR        TGCTGGGGGCGGGTGGGG-GGAA   3396 TA  C  T        T
                       TG GG GGCGGGTGGGG GGAA
                       II II IIIIIIIIIII IIII
                       AC CC CCGCCCACCCC CCTT
                      G_  _  _      _
GAM229  MADH4         GCGGTGGCGAGGGGAGTGG       3388 TATGCG    T    A
                        GTGGCGGG GGGGTGG
                        IIIIIIIII IIIIIII
                        CACCGCTC CCTCACC
                        _____     C    C
GAM229  MAF         TGCGGTGGCGGCGGTGGTGG       3405 TATG     G  _  A
                        CGGTGGCGG TGG GGTGG
                        IIIIIIIIII III IIIII
                        GCCACCGCC GCC CCACC
                        ____      _  A   G
GAM229  MLLT7        TGCTTTGGGGGCTGGGGTGGA     3408 TATGCGG  C  _      A
                        TGG GGG TGGGGTGGA
                        III III IIIIIIIII
                        ACC CCC ACCCCACCT
                      GAA____   _  G      C
GAM229  PKP1        GGTGGCGGGAGGCGGGTGG        3392 TATGC T     G  GA
                        GG GGCGGGTGG GTG
                        II IIIIIIIII III
                        CC CCGCCCACC CGC
                      GC___  T    G  GI
GAM229  PPT2        CGGTGGCGGGGGGAAGGGTG       3382 TATGC   C  T    A
                        GGTGG GGG GGGGTGG
                        IIIII III IIIIIII
                        CCGCC CCC TCCCACT
                        _____    C  T    C
GAM229  RANBP3       GGGGGCGGGTGGGCGGGTGGA     3391 TATGC    _    G  A
                        GGTGG CGGGTGGG TGGA
                        IIIII IIIIIIIII IIII
                        CCACC GCCCACCT ATCT
                      GC___    C    _  G
GAM229  RFX1        GCGGGGGCGGGTGGGGCGG        3387 TATGC T          A
                        GG GGCGGGTGGGGTGG
                        II IIIIIIIIIIIIII
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                        CC CCGCCCACCCCGCC
                        ____  _           C
GAM229  RNH      ATGCGGGGAGGGGTGGGTGGGGTGG  3378 TA    T____  C         AAII
                        TGCGG    GG GGGTGGGGTGG
                        IIIII    II IIIIIIIIII
                        ACGCC    CC CCCACCCCACC
                        __    CCTCC  A       CIII
GAM229  S100A1      TGGGGTGGGCAAGGGTGGGGT    3398 TATGC   _ __        GGAA
                        GGTGG C GGGTGGGGT
                        IIIII I IIIIIIIII
                        CCACC G CCCACCCCA
                        C____   C TT       ATII
GAM229  SLC12A7       TGGGGTGG--GGTGGGGTGG     3406 TATGC    CG
                        GGTGG GGTGGGGTGG
                        IIIII IIIIIIIIII
                        CCACC CCACCCCACC
                        C____     __
GAM229  SMURF1       TGCAGATGGCGGGTGGGG-GGA     3397 TATGC          T  A
                        GGTGGCGGGTGGGG GGA
                        IIIIIIIIIIIII III
                        CTACCGCCCACCCC CCT
                        GT___          _ G
GAM229  STAU       GCGGTGGCGGCGAGGAGGGGAA     3384 TATGC    _ T  T_  A
                        GGTGGCG GG GGGG  GGA
                        IIIIIII II IIII  III
                        CCGCCGC CC CCCC  CCT
                        CA___       T T  TT  I
GAM229  ZNF278       GCGGTGGCGCGGGCCGGGT     3383 TATGC   G   G   GGA
                        GGTG CGGGT GGGT
                        IIII IIIII IIII
                        CCGC GCCCG CCCA
                        CA___   _  G   GGG
GAM229  ZNF278       GCGGTGGCGGCGGCGGCGG     3389 TATGC       G  _  A
                        GGTGGCGG TGG GGTGG
                        IIIIIIII III IIIII
                        CCGCCGCC GCC CCGCC
                        CA___       _  G   I
GAM230  AF5Q31       CGGTGACAGGCTGCCAAGGGC     3411      C  __    III
                        CGGTGACAG CT CAAGGG
                        IIIIIIIII II IIIIII
                        GCCACTGTC GA GTTCCC
                        C CG    GII
GAM230  AF5Q31       CGGTGACAGGCTGCCAAGGGC     3411 GTCG    C  __    TTC
                        GTGACAG CT CAAGGGC
                        IIIIIII II IIIIIIII
                        CACTGTC GA GTTCCCG
                        ____       C CG    CTI
GAM230  ATP8B2       TGACAGCCTCCAGCAGGCT     3416        AA__  III
                        TGACAGCCTC  GGGC
                        IIIIIIIIII  IIII
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                              ACTGTCGGAG   TCCG
                                 GTCG   AII
GAM230 FACL4        TGGCAGAGCCAG-CCGAATC      3418        A   CTCI
                      TGGCAGAGCCAG CCGA
                      ||||||||||| ||||
                      ACCGTCTCGGTC GGCT
                          _   TAGI
GAM230 FACL4        TGGCAGAGCCAG-CCGAATC      3418 _       A   CTI
                        GGCAGAGCCAG CCGA
                        ||||||||||| ||||
                        CCGTCTCGGTC GGCT
                      A     _   TAI
GAM230 GNA11        TCGGTGCCTCAGTGCCTCAAGGG   3415      ACA____        IIIC
                        TCGGTG    GCCTCAAGG
                        ||||||    |||||||||
                        AGCCAC    CGGAGTTCC
                          GGAGTCA      CIII
GAM230 GNA11        TCGGTGCCTCAGTGCCTCAAGGG   3415 GT   ACA____        CTTCI
                        CGGTG    GCCTCAAGGG
                         |||||    ||||||||||
                         GCCAC    CGGAGTTCCC
                          __   GGAGTCA      CIIIC
GAM230 MAP3K5       CGGTG-CAGC-TCAAGGGC       3413    A   C      I
                        CGGTG CAGC TCAAGGG
                        ||||| |||| |||||||
                        GCCAC GTCG AGTTCCC
                          _   _     G
GAM230 MAP3K5       CGGTG-CAGC-TCAAGGGC       3413 GTCG A   C      T
                         GTG CAGC TCAAGGGC
                         ||| |||| ||||||||
                         CAC GTCG AGTTCCCG
                         ____  _   _     C
GAM230 MTMR6        CGGTGACAGCGACAGAGAGC      3412        CT _  II
                        CGGTGACAGC CA AGGG
                        |||||||||| || ||||
                        GCCACTGTCG GT TCTC
                          CT  C  GI
GAM230 MTMR6        CGGTGACAGCGACAGAGAGC      3412 GTCG    CT _  TT
                         GTGACAGC CA AGGGC
                         |||||||| || |||||
                         CACTGTCG GT TCTCG
                         ____      CT C  TT
GAM230 NPR2L        GTCAGAGACAGCCTCGAGGCCT    3414    T     A G TC
                        GTCGG GACAGCCTC AGG CT
                        ||||| ||||||||| ||| ||
                        CAGTC CTGTCGGAG TCC GA
                          T     C G II
GAM230 NPR2L        GTCAGAGACAGCCTCGAGGCCT    3414    T     A GCI
                        TCGG GACAGCCTC AGG
                        |||| ||||||||| |||
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                            AGTC CTGTCGGAG TCC
                             T     C  GGI
GAM230 TAZ          TGGCAGTCT-AAGGGCTTC     3417 A  C  C      I
                       TG CAG CT AAGGGCTT
                       || ||| || |||||||||
                       AC GTC GA TTCCCGAA
                        C  A  _      G
GAM231 CTF1         ACAGGGCCACGAGAAGGCAG     3423 TAACAG     C  TTGG
                          CACGAGAAG CAG
                          ||||||||| |||
                          GTGCTCTTC GTC
                       TCCCG_       C  CTII
GAM231 GATA6           TAAAGGCACGAGAATCACGTT     3430 TAACA      GCCA  GGG
                            GCACGAGAA  GTT
                            ||||||||| |||
                            CGTGCTCTT  CAA
                       ATTTC      AGTG III
GAM231 GRB10         ACAGCACGAAGACAACCAGGTG     3424 TAAC     _ _     T GG
                          AGCACGA GA AGCCAG TG
                          ||||||| || ||||||| ||
                          TCGTGCT CT TTGGTC AC
                       ____        T  G   C GG
GAM231 HNF4G         TAACAGCACCAATGAAGAAGCC--TTGG3428         _____      AG  GII
                        TAACAGCAC   GAGAAGCC TTGG
                        |||||||||   |||||||| ||||
                        ATTGTCGTG   TTCTTCGG AACC
                          GTTAC        __  III
GAM231 IL1R1         AACACCAGACTAGAAGCCAG     3421 TAA_  C G      TTGG
                          CAG AC AGAAGCCAG
                          ||| || |||||||||
                          GTC TG TCTTCGGTC
                       TGTG  _  A      TIII
GAM231 ITPKB         TAACAGCACTGGCCGCCAG     3429       GAGAA   TTGG
                        TAACAGCAC   GCCAG
                        |||||||||   |||||
                        ATTGTCGTG   CGGTC
                          ACCGG    IIIG
GAM231 MKKS         CAGCTACAAGAAGCCAGTT     3425 TAACAGC        GG
                          ACGAGAAGCCAGTT
                          ||||||||||||||
                          TGTTCTTCGGTCAA
                       GA_____        GA
GAM231 RAB36         AACAGCACGAGA---CGGGTGGG     3422 TA      AGCCAGT
                          ACAGCACGAGA     TGG
                          |||||||||||     |||
                          TGTCGTGCTCT     ACC
                         __       GCCC___
GAM231 SH3BP2         TAACGAGCCAAAGAAGCCAGCTG     3427  _ AC        GGI
                        TAAC AGC  GAGAAGCCAGTTG
                        |||| |||  |||||||||||||
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                          ATTG TCG  TTCTTCGGTCGAC
                           C   GT           III
GAM231 SLC22A1LS          CAGCCCCGGGAGAAGCCA--TGGG  3426 TAACAGCAC      GT
                              GAGAAGCCA TGGG
                              IIIIIIIII IIII
                              CTCTTCGGT ACCC
                          GGGGCC___       __
GAM232 ADCY8              GCGGATATCTG-AGGCTGAG   3435 TGGC TTC   G      T
                              GG  TCTG AGGCTGAG
                              II   IIII IIIIIIII
                              CC  AGAC TCCGACTC
                          ____    TAT  _    T
GAM232 ATP7B             GCAGTTCTCTGGAAAGGCCCAGTG  3434 TGGC       __  G   I
                              GGTTCTCTGGA GGCT AGTG
                              IIIIIIIIIII IIII IIII
                              TCAAGAGACCT CCGG TCAC
                          ____         TT  G  T
GAM232 CLECSF11         CGGCTACTCAGGAGGCTGAG    3433 TGGCGGTT  T     T
                              CTC GGAGGCTGAG
                              III IIIIIIIIII
                              GAG CCTCCGACTC
                          GAT_____  T      C
GAM232 DEFB1           TGGC--TCCTTTGGAGGCTGAG   3447 TGGC   C_       T
                              GGTTCT TGGAGGCTGAG
                              IIIIII IIIIIIIIIII
                              CCGAGG ACCTCCGACTC
                          A___    AA        I
GAM232 EBAG9           GGCGG--CTTTGGAGGCTGCGTG   3441 TG    CTC      A
                              GCGGTT TGGAGGCTG GTG
                              IIIIII IIIIIIIII III
                              CGCCGA ACCTCCGAC CAC
                          __    A__     G
GAM232 F2RL3          GGCTGGTTCCCTCTGGAGGCTG   3436 __ CGG       AGTG
                              TGG TTCTCTGGAGGCTG
                              III IIIIIIIIIIIII
                              ACC GGGAGACCTCCGAC
                          CG AA_        AIII
GAM232 GJB3          GGCGGCTCCTCTGGAGG--GAGT   3438 TG    _     CT
                              GCGGTTC TCTGGAGG GAGTG
                              IIIIIII IIIIIIII IIIII
                              CGCCGAG AGACCTCC CTCAT
                          __    G     __
GAM232 GPC1          GGGGCTTCTCTGGAGGCTG   3439 T GG        AGT
                              GGC TTCTCTGGAGGCTG
                              III IIIIIIIIIIIIII
                              CCG AAGAGACCTCCGAC
                          C __         CII
GAM232 HGF          TGGCGGATCCCTCTGGAGG   3443    __        CTGAGT
                              TGGCGG TTCTCTGGAGG
                              IIIIII IIIIIIIIIII
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                          ACCGCC  GGGAGACCTCC
                            TA       IIIGTG
GAM232  HSPA1L        GGTTCTCT-GAGGCCTAGT      3442 TGGCGGTT    G    G
                          CTCTG AGGCT AG
                          ||||| ||||| ||
                          GAGAC TCCGG TC
                          _____  _   A
GAM232  ITGA11         TGG-GTTTCTCTGGAGGATG     3445  CGG       C AGT
                          TGG  TTCTCTGGAGG TG
                          |||  ||||||||||| ||
                          ACC  AAGAGACCTCC AC
                          CA_       T III
GAM232  PTGIS          TGGGGGTGC-CTGGAGGCTGAG    3448  C T T       TG
                          TGG GGT C CTGGAGGCTGAG
                          ||| ||| | |||||||||||
                          ACC CCA G GACCTCCGACTC
                          C C_        II
GAM232  RET            TGGCTGTGCTCCCAGTGCAGGCTGAGTG3444  G__   __ G      III
                          TGGC  GTTCTC TG AGGCTGAGTG
                          ||||  |||||| || |||||||||
                          ACCG  CGAGGG AC TCCGACTCAC
                          ACA     TC G        III
GAM232  RNPEP         GGCAGGTTCTCTGTCTCGGGGCTCAGTG3437 TG  _     GA____  G  III
                          GC GGTTCTCTG    GGCT AGTG
                          || |||||||||    |||| ||||
                          CG CCAAGAGAC    CCGA TCAC
                          __ T     AGAGCC   G  CII
GAM232  SLA2          TGG-GGTGCCCAGGAGGCTGA     3446  C T T      GT
                          TGG GGT CTC GGAGGCTGA
                          ||| ||| ||| |||||||||
                          ACC CCA GGG CCTCCGACT
                          _  C  T      II
GAM232  XPNPEP1       GGTGGCTTTCTGGAGGCTG      3440 TGGC   C       AGT
                          GGTT TCTGGAGGCTG
                          |||| |||||||||||
                          CCGA AGACCTCCGAC
                          CA__   A       GII
GAM233  ATF5          GAAAGAAGG--TGGGAGCGG      3457 TG     ACC       C
                          AAAGAGG  TGGGAGCGG
                          |||||||  ||||||||||
                          TTTCTTC  ACCCTCGCC
                          __     C__       T
GAM233  ATP6V1G2      AAAGGGGCCGCCTGGGAGCAGCA   3451 TGAA A A__         AI
                          AG GG  CCTGGGAGCGGCA
                          || ||  |||||||||||||
                          TC CC  GGACCCTCGTCGT
                          ____   C GGC        CT
GAM233  CENPB         GAAAGAGGATTCTGAGAAAGAGGCAA 3454 TG     C_    C__   II
                          AAAGAGGA CTGGGAG GGCAA
                          |||||||| ||||||| |||||
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                        TTTCTCCT GACTCTT  CCGTT
                        __      AA   TCT   AI
GAM233  CHST2           GAAAGAGGACAAGAGA-AGGCAA  3459 TG      CT   C
                        AAAGAGGAC GGGAG GGCAA
                        |||||||| ||||| |||||
                        TTTCTCCTG CTCTT CCGTT
                        __       TT      _
GAM233  CNTN2           TGAGAAAGGACCTGGG-GCG   3463  A       A  GCA
                        TGA AGAGGACCTGGG GCG
                        ||| ||||||||||| |||
                        ACT TTTCCTGGACCC CGC
                           C        _  |||
GAM233  CYLN2           TGAATGAAGGACCTGGGGAGGGG  3460  A_      _  C  CAAI
                        TGAA GAGGACCTGGG AG GG
                        |||| ||||||||||| || ||
                        ACTT TTCCTGGACCC TC CC
                           AC       C _ CIII
GAM233  DDX26           GAAAGAGGAGATGGTAGAGG   3458 TG    CC  G C  CA
                        AAAGAGGA TGG AG GG
                        |||||||| ||| || ||
                        TTTCTCCT ACC TC CC
                        __       CT  A  T AI
GAM233  EMD             AAAGAGGACCATGGAG-GGC    3452 TGAA    TG   C  A
                        AGAGGACC GGAG GGC
                        |||||||| |||| |||
                        TCTCCTGG CCTC CCG
                        ____         TA _ G
GAM233  FZD4            TGAGACAGTGACCTGGGAGAGGAAA 3461 T__ A AG      C  CAAII
                        GA AG GACCTGGGAG GG
                        || || ||||||||| ||
                        CT TC CTGGACCCTC CC
                        ACT G A_       T TTTII
GAM233  HAGH            AGACGGGCCTGGGAGCGGC      3453 TGAAAGA A      A
                        GG CCTGGGAGCGGC
                        || |||||||||||
                        CC GGACCCTCGCCG
                        C_____ _       C
GAM233  MAFF            GAAATGGGACCTGGGCACAGAGGC 3456 TG  GA      ___ C  AAI
                        AAA GGACCTGGG AG GGC
                        ||| |||||||| || |||
                        TTT CCTGGACCC TC CCG
                        __  AC       GTG T CII
GAM233  MBNL            TGAAAGAGGCCCTTGCACCGG   3464     A  GGGAG  CAA
                        TGAAAGAGG CCT   CGG
                        ||||||||| |||    |||
                        ACTTTCTCC GGA    GCC
                          G  ACGTG  III
GAM233  MPHOSPH6        TGACA-ATGACCTGGGAGC   3462  AAGAG        GGC
                        TGA   GACCTGGGAGC
                        |||   |||||||||||
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                        ACT    CTGGACCCTCG
                        GTTA_        III
GAM233 PCDHGA1          GAAAGAGGAACTGTTGGAGTGG    3455 TG     C  __  C CAA
                        AAAGAGGA CTG  GGAG GG
                        |||||||| ||| |||| ||
                        TTTCTCCT GAC  CCTC CC
                          __     T  AA   A CII
GAM233 PCDHGA10         GAAAGAGGAACTGTTGGAGTGG    3455 TG     C  __  C CAA
                        AAAGAGGA CTG  GGAG GG
                        |||||||| ||| |||| ||
                        TTTCTCCT GAC  CCTC CC
                          __     T  AA   A CII
GAM233 PCDHGA11         GAAAGAGGAACTGTTGGAGTGG    3455 TG     C  __  C CAA
                        AAAGAGGA CTG  GGAG GG
                        |||||||| ||| |||| ||
                        TTTCTCCT GAC  CCTC CC
                          __     T  AA   A CII
GAM233 PCDHGA12         GAAAGAGGAACTGTTGGAGTGG    3455 TG     C  __  C CAA
                        AAAGAGGA CTG  GGAG GG
                        |||||||| ||| |||| ||
                        TTTCTCCT GAC  CCTC CC
                          __     T  AA   A CII
GAM233 PCDHGA2          GAAAGAGGAACTGTTGGAGTGG    3455 TG     C  __  C CAA
                        AAAGAGGA CTG  GGAG GG
                        |||||||| ||| |||| ||
                        TTTCTCCT GAC  CCTC CC
                          __     T  AA   A CII
GAM233 PCDHGA3          GAAAGAGGAACTGTTGGAGTGG    3455 TG     C  __  C CAA
                        AAAGAGGA CTG  GGAG GG
                        |||||||| ||| |||| ||
                        TTTCTCCT GAC  CCTC CC
                          __     T  AA   A CII
GAM233 PCDHGA4          GAAAGAGGAACTGTTGGAGTGG    3455 TG     C  __  C CAA
                        AAAGAGGA CTG  GGAG GG
                        |||||||| ||| |||| ||
                        TTTCTCCT GAC  CCTC CC
                          __     T  AA   A CII
GAM233 PCDHGA5          GAAAGAGGAACTGTTGGAGTGG    3455 TG     C  __  C CAA
                        AAAGAGGA CTG  GGAG GG
                        |||||||| ||| |||| ||
                        TTTCTCCT GAC  CCTC CC
                          __     T  AA   A CII
GAM233 PCDHGA6          GAAAGAGGAACTGTTGGAGTGG    3455 TG     C  __  C CAA
                        AAAGAGGA CTG  GGAG GG
                        |||||||| ||| |||| ||
                        TTTCTCCT GAC  CCTC CC
                          __     T  AA   A CII
GAM233 PCDHGA7          GAAAGAGGAACTGTTGGAGTGG    3455 TG     C  __  C CAA
                        AAAGAGGA CTG  GGAG GG
                        |||||||| ||| |||| ||
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                                    TTTCTCCT GAC  CCTC CC
                                  __       T  AA   A  CII
GAM233  PCDHGA8        GAAAGAGGAACTGTTGGAGTGG    3455 TG      C  __   C CAA
                       AAAGAGGA CTG  GGAG GG
                       |||||||| |||  |||| ||
                                    TTTCTCCT GAC  CCTC CC
                                  __       T  AA   A  CII
GAM233  PCDHGA9        GAAAGAGGAACTGTTGGAGTGG    3455 TG      C  __   C CAA
                       AAAGAGGA CTG  GGAG GG
                       |||||||| |||  |||| ||
                                    TTTCTCCT GAC  CCTC CC
                                  __       T  AA   A  CII
GAM233  PCDHGB1        GAAAGAGGAACTGTTGGAGTGG    3455 TG      C  __   C CAA
                       AAAGAGGA CTG  GGAG GG
                       |||||||| |||  |||| ||
                                    TTTCTCCT GAC  CCTC CC
                                  __       T  AA   A  CII
GAM233  PCDHGB2        GAAAGAGGAACTGTTGGAGTGG    3455 TG      C  __   C CAA
                       AAAGAGGA CTG  GGAG GG
                       |||||||| |||  |||| ||
                                    TTTCTCCT GAC  CCTC CC
                                  __       T  AA   A  CII
GAM233  PCDHGB3        GAAAGAGGAACTGTTGGAGTGG    3455 TG      C  __   C CAA
                       AAAGAGGA CTG  GGAG GG
                       |||||||| |||  |||| ||
                                    TTTCTCCT GAC  CCTC CC
                                  __       T  AA   A  CII
GAM233  PCDHGB4        GAAAGAGGAACTGTTGGAGTGG    3455 TG      C  __   C CAA
                       AAAGAGGA CTG  GGAG GG
                       |||||||| |||  |||| ||
                                    TTTCTCCT GAC  CCTC CC
                                  __       T  AA   A  CII
GAM233  PCDHGB5        GAAAGAGGAACTGTTGGAGTGG    3455 TG      C  __   C CAA
                       AAAGAGGA CTG  GGAG GG
                       |||||||| |||  |||| ||
                                    TTTCTCCT GAC  CCTC CC
                                  __       T  AA   A  CII
GAM233  PCDHGB6        GAAAGAGGAACTGTTGGAGTGG    3455 TG      C  __   C CAA
                       AAAGAGGA CTG  GGAG GG
                       |||||||| |||  |||| ||
                                    TTTCTCCT GAC  CCTC CC
                                  __       T  AA   A  CII
GAM233  PCDHGB7        GAAAGAGGAACTGTTGGAGTGG    3455 TG      C  __   C CAA
                       AAAGAGGA CTG  GGAG GG
                       |||||||| |||  |||| ||
                                    TTTCTCCT GAC  CCTC CC
                                  __       T  AA   A  CII
GAM233  PCDHGC3        GAAAGAGGAACTGTTGGAGTGG    3455 TG      C  __   C CAA
                       AAAGAGGA CTG  GGAG GG
                       |||||||| |||  |||| ||
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                          TTTCTCCT GAC  CCTC CC
                            __      T  AA   A CII
GAM233 PCDHGC4         GAAAGAGGAACTGTTGGAGTGG  3455 TG    C  __   C CAA
                      AAAGAGGA CTG  GGAG GG
                      |||||||| ||| |||| ||
                          TTTCTCCT GAC  CCTC CC
                            __      T  AA   A CII
GAM233 PCDHGC5         GAAAGAGGAACTGTTGGAGTGG  3455 TG    C  __   C CAA
                      AAAGAGGA CTG  GGAG GG
                      |||||||| ||| |||| ||
                          TTTCTCCT GAC  CCTC CC
                            __      T  AA   A CII
GAM234 DAB2           TCAA-ATA-AACATAACCTC    3467     ATA       I
                      TCAAG  AAACATAACT
                      |||||  ||||||||||
                      AGTTT  TTTGTATTGG
                        A__      A
GAM234 DAB2           TCAA-ATA-AACATAACCTC    3467 TTCA    A
                       AGATAAA CATAACTTCT
                       ||||||| ||||||||||
                       TTTATTT GTATTGGAGG
                      G___     _
GAM234 SLC26A3        TTCAAGATAAAGTTCTAAGTTCTA 3468      ACA_  C   CI
                      TTCAAGATAAA   TAA TTCTA
                      |||||||||||   ||| |||||
                      AAGTTCTATTT   ATT AAGAT
                         CAAG  C   II
GAM234 SLC26A3        TTCAAGATAAAGTTCTAAGTTCTA 3468 T      ACA_  C  I
                       CAAGATAAA   TAA TTCT
                       |||||||||   ||| ||||
                       GTTCTATTT   ATT AAGA
                       _        CAAG  C  I
GAM235 APOL1          TGGCCAACATGGTGAAACCCCATC 3489 A      A       I
                      TG CCAACATGG GAAACCCCATC
                      || ||||||||| |||||||||||
                      AC GGTTGTACC CTTTGGGGTAG
                         C       A      I
GAM235 BRIP1          TGGCCAACATGGTGAAACCCCATC 3489 A      A       I
                      TG CCAACATGG GAAACCCCATC
                      || ||||||||| |||||||||||
                      AC GGTTGTACC CTTTGGGGTAG
                         C       A      I
GAM235 CAMLG          TGACCAACATGGAGAAACCC     3473 A      A      I
                      TG CCAACATGG GAAACCCCATC
                      || ||||||||| |||||||||||
                      AC GGTTGTACC CTTTGGGGTAG
                         C       A      I
GAM235 CBFA2T2        TGACCAACAAGGAGAAACCCCGTC 3476       T      ATCI
                      TGACCAACA GGAGAAACCCC
                      ||||||||| |||||||||||
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                              ACTGGTTGT CCTCTTTGGGG
                                 T          CAGI
GAM235  CLECSF11        TGGCCAACATAGTGAAACCCCATC  3483  A      A       I
                        TG CCAACATGG GAAACCCCATC
                        || |||||||||| ||||||||||||
                        AC GGTTGTATC CTTTGGGGTAG
                             C         A      I
GAM235  CNGA1           TGGCCAACATGGTGAAATCCCATC  3492  A      A  C    I
                        TG CCAACATGG GAAA CCCATC
                        || |||||||||| |||| ||||||
                        AC GGTTGTACC CTTT GGGTAG
                             C         A  A    I
GAM235  CNN2            TGGCCAACATGGGGAAACCCCATC  3486  A      A       I
                        TG CCAACATGG GAAACCCCATC
                        || |||||||||| ||||||||||||
                        AC GGTTGTACC CTTTGGGGTAG
                             C         C      I
GAM235  CYP1A2          TGGCCAACATGGTGAAACCCCATC  3489  A      A       I
                        TG CCAACATGG GAAACCCCATC
                        || |||||||||| ||||||||||||
                        AC GGTTGTACC CTTTGGGGTAG
                             C         A      I
GAM235  CYP1A2          TGACCAACATGGTGAAACCC       3474         A  CAT
                        TGACCAACATGG GAAACCC
                        |||||||||||| |||||||
                        ACTGGTTGTACC CTTTGGG
                                 A    III
GAM235  DHFR            ACCAACATGTGAAAAGCCC        3471 TGAC   _  A  CAT
                        CAACATG GAGAA CCC
                        ||||||| ||||| |||
                        GTTGTAC CTTTT GGG
                          ____       A  C  CTI
GAM235  DHFR            TGACCAACATGGTGAAACCCCATC  3479         A      I
                        TGACCAACATGG GAAACCCCATC
                        |||||||||||| ||||||||||||
                        ACTGGTTGTACC CTTTGGGGTAG
                             A         I
GAM235  GM2A            TGGCCAACATGGTGAAACCCCATC  3489  A      A       I
                        TG CCAACATGG GAAACCCCATC
                        || |||||||||| ||||||||||||
                        AC GGTTGTACC CTTTGGGGTAG
                             C         A      I
GAM235  GRM7            TGGCCAACATGGTGAAACCCAATC  3488  A      A    C  I
                        TG CCAACATGG GAAACCC ATC
                        || |||||||||| ||||||| |||
                        AC GGTTGTACC CTTTGGG TAG
                             C         A   T  I
GAM235  HTR1E           TGGCCAACATGGTGAAATCCCGTC  3493  A      A  C ATCI
                        TG CCAACATGG GAAA CCC
                        || |||||||||| |||| |||
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                         AC GGTTGTACC CTTT GGG
                          C        A   A   CAGI
GAM235  HYAL4          TGGCCAACACGGTGAAACCCCATC  3482  A      A        I
                        TG CCAACATGG GAAACCCCATC
                        II IIIIIIIII IIIIIIIIIII
                        AC GGTTGTGCC CTTTGGGGTAG
                          C        A          I
GAM235  LTB4R          TGGCCAACATGGTGAAACCCCGTC  3490  A      A      ATCI
                        TG CCAACATGG GAAACCCC
                        II IIIIIIIII IIIIIIII
                        AC GGTTGTACC CTTTGGGG
                          C        A       CAGI
GAM235  MEF2A          TGGCCAACATGGTGAAACTCCATC  3491  A      A    C   I
                        TG CCAACATGG GAAAC CCATC
                        II IIIIIIIII IIIII IIIII
                        AC GGTTGTACC CTTTG GGTAG
                          C        A   A        I
GAM235  MLANA          TGACCAACATGGAGAAACCCCGTC  3477                ATCI
                        TGACCAACATGGAGAAACCCC
                        IIIIIIIIIIIIIIIIIIIII
                        ACTGGTTGTACCTCTTTGGGG
                                          CAGI
GAM235  MRPL49         TGGCCAACATGGTGAAACCCCATC  3489  A      A        I
                        TG CCAACATGG GAAACCCCATC
                        II IIIIIIIII IIIIIIIIIII
                        AC GGTTGTACC CTTTGGGGTAG
                          C        A          I
GAM235  NCOA6          TGGCCAACATGATGAAACCCCATC  3484  A      GA       I
                        TG CCAACATG GAAACCCCATC
                        II IIIIIIII IIIIIIIIIII
                        AC GGTTGTAC CTTTGGGGTAG
                          C        TA          I
GAM235  PPEF2          TGACCAACATGGAGAAACCC       3473  A      A       I
                        TG CCAACATGG GAAACCCCATC
                        II IIIIIIIII IIIIIIIIIII
                        AC GGTTGTACC CTTTGGGGTAG
                          C        A           I
GAM235  PPID           TGACCAATATGGTGAAACCCCATC  3481    C    A        I
                        TGACCAA ATGG GAAACCCCATC
                        IIIIIII IIII IIIIIIIIIII
                        ACTGGTT TACC CTTTGGGGTAG
                              A    A            I
GAM235  PTGIS          TGACCAACATGGGGAAACCCCGTC  3478         A      ATCI
                        TGACCAACATGG GAAACCCC
                        IIIIIIIIIIII IIIIIIII
                        ACTGGTTGTACC CTTTGGGG
                                 C       CAGI
GAM235  RHD            TGGCCAACATGGTGAAACCCCATC  3489  A      A        I
                        TG CCAACATGG GAAACCCCATC
                        II IIIIIIIII IIIIIIIIIII
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                        AC GGTTGTACC CTTTGGGGTAG
                           C       A           I
GAM235  RPH3AL        TGGCCAACATGGAGAAACCCCATC  3485  A                I
                      TG CCAACATGGAGAAACCCCATC
                      II IIIIIIIIIIIIIIIIIIII
                      AC GGTTGTACCTCTTTGGGGTAG
                         C             I
GAM235  SCML2         TGACCAACATGGAGAAACCCCATC  3470 TGACCAAC    A
                           ATGG GAAACCCCAT
                           IIII IIIIIIIIII
                           TACC CTTTGGGGTA
                           _____      A
GAM235  SH3GL3        TGGCCAACATGGTGAAA-CCCATC  3487  A       A     C  I
                      TG CCAACATGG GAAACCC ATC
                      II IIIIIIIII IIIIIII III
                      AC GGTTGTACC CTTTGGG TAG
                         C       A    _   I
GAM235  SIL           GACCAACATGGTGAAACCCCGTC  3472 TG       A     ATCI
                      ACCAACATGG GAAACCCC
                      IIIIIIIIII IIIIIIII
                      TGGTTGTACC CTTTGGGG
                      __         A    CAGA
GAM235  SMAC          TGACCAACATGGTGAAACCCCATC  3479        A      I
                      TGACCAACATGG GAAACCCCATC
                      IIIIIIIIIIII IIIIIIIIIII
                      ACTGGTTGTACC CTTTGGGGTAG
                              A       I
GAM235  SULT2B1       TGGCCAACATGGTGAAACCCC  3475  A     A    ATC
                      TG CCAACATGG GAAACCCC
                      II IIIIIIIII IIIIIIII
                      AC GGTTGTACC CTTTGGGG
                         C       A   III
GAM235  TNFRSF10B     TGACCAACATGGTGAAACCCCGTC  3480       A     ATCI
                      TGACCAACATGG GAAACCCC
                      IIIIIIIIIIII IIIIIIII
                      ACTGGTTGTACC CTTTGGGG
                            A    CAGI
GAM235  TPMT          TGACCAACATGGTGAAACCCCGTC  3480       A     ATCI
                      TGACCAACATGG GAAACCCC
                      IIIIIIIIIIII IIIIIIII
                      ACTGGTTGTACC CTTTGGGG
                            A    CAGI
GAM235  TRPM6         TGGCCAACATGGTGAAACCCCATC  3489 A      A      I
                      TG CCAACATGG GAAACCCCATC
                      II IIIIIIIII IIIIIIIIIII
                      AC GGTTGTACC CTTTGGGGTAG
                         C       A      I
GAM236  APP           CTA-TTCATGCACTAGTTT     3499 TCACTACTTC     CT
                         GCACTAGTTT
                         IIIIIIIIII
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                              CGTGATCAAA
                        AAGTA_____          CT
GAM236  CACNA1A         GGGATAGCAGCTCG--GGAC    3502 AG      _   AA   TC
                        GGATAGCA TTCG GGAC
                        |||||||| |||| ||||
                        CCTATCGT GAGC CCTG
                             __      C  __  TI
GAM236  CORO2B          GGAAGAACATTCGAAGGAGCTC   3503 AG  T        _   G
                        GGA AGCATTCGAAGGA CTCG
                        ||| ||||||||||||| ||||
                        CTT TTGTAAGCTTCCT GAGT
                             __  C     C  I
GAM236  CYP24           GGGACAGGCAGCAGAAGGACTCGG  3501 A___  A   TTC       I
                        GGG TAGCA  GAAGGACTCGG
                        ||| |||||  |||||||||||
                        TCC GTCGT  CTTCCTGAGCC
                        CCTG _  ___        G
GAM236  GPC3            AGCGAGAGCAGTCCCAGGACTCGG  3497 G T  T GA      I
                        AG GA AGCA TC AGGACTCGG
                        || || |||| || |||||||||
                        TC CT TCGT AG TCCTGAGCC
                          G C  C GG      I
GAM236  IL10RA          CACATACCCTGCACTAGTT       3498 TC _  TC      CT
                        AC TACT GCACTAGTTT
                        || |||| |||||||||||
                        TG ATGG CGTGATCAAG
                          __  T  GA        II
GAM236  PAX2            AGGGACAGG---CGAAGGACT      3496      CATT      C
                        AGGGATAG  CGAAGGACT
                        ||||||||  ||||||||||
                        TCCCTGTC  GCTTCCTGA
                              C___       I
GAM236  PRKG1           GGCATGCCAGT-GAAGGACTC     3504 AGGGATA ATTC
                        GC  GAAGGACTCG
                        ||  |||||||||||
                        CG  CTTCCTGAGT
                        CGTA___  GTCA
GAM236  WBSCR5          TCACTACTT--CTCTAGACTCTC   3505       GCA  T
                        TCACTACTTC  CTAG TTCTC
                        ||||||||||  |||| |||||
                        AGTGATGAAG  GATC GAGAG
                             A__  T
GAM236  ZNF146          CTACCTT-CACTAGTTTCTC      3500 TCACTA   GC
                        CTTC ACTAGTTTCT
                        |||| ||||||||||
                        GAAG TGATCAAAGA
                          G_____  __
GAM237  ABCA4           CAATATGGAGGCCAAAGCTG      3516       AGAT  I
                        AATATGGAGG  AGGT
                        ||||||||||  ||||
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                          TTATACCTCC  TTCG
                            GGT_    A
GAM237 ABCA4        CAATATGGAGGCCAAAGCTG   3516 ATCA       AGAT G  G
                        ATATGGAGG   AG TG
                        |||||||||  || ||
                        TATACCTCC   TC AC
                            ____     GGTT  G  G
GAM237 AFM         TCAATATGGAGTAAAATAG   3520         _    II
                        TCAATATGGAG GAGATA
                        |||||||||| ||||||
                        AGTTATACCTC TTTTAT
                             A    CI
GAM237 AFM         TCAATATGGAGTAAAATAG   3520 AT        _      TGG
                         CAATATGGAG GAGATAGG
                         |||||||||| ||||||||
                         GTTATACCTC TTTTATCT
                            __       A    III
GAM237 AP2B1      ATCAATATGGA----ATATGTG   3514          GAGATAG
                       ATCAATATGGAG    GTG
                       ||||||||||||    |||
                       TAGTTATACCTT    CAC
                           ATA____
GAM237 AP2B1      ATCAATATGGA----ATATGTG   3514          GAGATAI
                       ATCAATATGGAG
                       ||||||||||||
                       TAGTTATACCTT
                           ATACACI
GAM237 ARAF1      AATGATGGAGGAGACAGGGGG    3508 T         TGI
                       A ATGGAGGAGATAGG
                       | |||||||||||||
                       A TACCTCCTCTGTCC
                        C       CCI
GAM237 ARAF1      AATGATGGAGGAGACAGGGGG    3508 ATCAAT       T  A
                       ATGGAGGAGATAGG GG
                       |||||||||||||| ||
                       TACCTCCTCTGTCC CC
                      C_____       _ C
GAM237 CLCA2      TCAATATGGATGCAGAT-GGT   3519      GG_  A  I
                       CAATATGGA  AGAT GG
                       ||||||||| |||| ||
                       GTTATACCT  TCTA CC
                          ACG   _  I
GAM237 CLCA2      TCAATATGGATGCAGAT-GGT   3519 AT      GGAGA
                        CAATATGGA   TAGGTGG
                        ||||||||| |||||||
                        GTTATACCT  GTCTACC
                           __      AC___
GAM237 GCLM      ATATGGAGGCAAGATAAGT    3512      __      III
                       ATATGGAGG AGATAGG
                       ||||||||| |||||||
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                    TATACCTCC TCTATTC
                     GT     AII
GAM237 GFPT2        TATAGGAGGC-ATAGGTGGA    3518 TAT_    AG      II
                        GGAGG ATAGGTGG
                        ||||| ||||||||
                        CCTCC TATCCACC
                       ATAT  G_     TI
GAM237 IRAK4        AAAATGGTTGAGATAGGTG     3509 AAT   AG      II
                        ATGG GAGATAGGT
                        |||| |||||||||
                        TACC CTCTATCCA
                        TTT AA    CI
GAM237 IRAK4        AAAATGGTTGAGATAGGTG     3509 ATCAAT   AG      G
                         ATGG GAGATAGGTG
                         |||| ||||||||||
                         TACC CTCTATCCAC
                        _____  AA     A
GAM237 LZTFL1       AATATGGA-GAGACAGGTG     3510       G   I
                        AATATGGAG AGATAGGT
                        ||||||||| ||||||||
                        TTATACCTC TCTGTCCA
                          _       C
GAM237 LZTFL1       AATATGGA-GAGACAGGTG     3510 ATCAAT   G
                         ATGGAG AGATAGGTG
                         |||||| |||||||||
                         TACCTC TCTGTCCAC

                        _____   _
GAM237 NPY2R        TGGAGGAGAAGTTTGGTGG     3521       TA____   IIIC
                         TGGAGGAGA    GGTG
                         ||||||||||   ||||
                         ACCTCCTCT    CCAC
                          TCAAAA  CIII
GAM237 OAS2         ATATCTGAGGAGATATCGGTGGA  3511 TATG       ___   I
                         GAGGAGATA  GGTGG
                         |||||||||  |||||
                         CTCCTCTAT  CCACC
                         A___      AGA   I
GAM237 PACE4        CAATATGGAGAAAGACGAGGTCGA 3515 A      _  _   GGI
                         TATGGAGGA GAT AGGT
                         ||||||||| ||| ||||
                         ATACCTCTT CTG TCCA
                          _       T  C  GII
GAM237 PACE4        CAATATGGAGAAAGACGAGGTCGA 3515 ATCA      _  _   G I
                         ATATGGAGGA GAT AGGT GA
                         |||||||||| ||| |||| ||
                         TATACCTCTT CTG TCCA CT
                         ____       T  C  G  T
GAM237 PTPN1        ATAAATATGGAGTGGAGAGTTG   3513 ATC      GA  T G GA
                         AATATGGAG GA AG TG
                         ||||||||| || || ||
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                           TTATACCTC  CT TC AC
                           TAT        AC  C  A  II
GAM237 PTPN1       ATAAATATGGAGTGGAGAGTTG   3513 C          __       TAGGI
                           AATATGGA  GGAGA
                           IIIIIIII  IIIII
                           TTATACCT  CCTCT
                           T      CA    CAIII
GAM237 RBBP5       CAATATGGA-AATATAGGAGG    3517 _         AG    TGI
                           AATATGGAGG  ATAGG
                           IIIIIIIIII  IIIII
                           TTATACCTTT  TATCC
                           G       A_    TCI
GAM237 RBBP5       CAATATGGA-AATATAGGAGG    3517 ATCA       AG    T
                           ATATGGAGG  ATAGG  GG
                           IIIIIIIII  IIIII  II
                           TATACCTTT  TATCC  CC
                           ____         A_    T
GAM238 ACHE        TGGGAGGCACGGC-CCCCTCCTCC  3542      G    G  GCG  I
                           TGGGAGGCA  GGCTCC  CT  CC
                           IIIIIIIII  IIIIII  II   II
                           ACCCTCCGT  CCGGGG  GA   GG
                           G      _  GGA  I
GAM238 ALPI        GGGAAGAAGGGCCCCGCTGCGCC   3535 TG    C            I
                           GGAGG  AGGGCTCCGCTGCGCC
                           IIIII  IIIIIIIIIIIIIIII
                           CCTTC  TCCCGGGGCGACGCGG
                           __    T        T
GAM238 APBA2       GGGAGGCAGGGGTGACGGCTGC    3533 TG       CTCC__    GCC
                           GGAGGCAGGG    GCTGC
                           IIIIIIIIII    IIIII
                           CCTCCGTCCC    CGACG
                           __       CACTGC   GII
GAM238 CBFA2T2     TGGGAGGCAGAGGTTACCG-TGAGCC 3537          CT__   C C  II
                           TGGGAGGCAGGG    CCG TG GCC
                           IIIIIIIIIII     III II III
                           ACCCTCCGTCTC   GGC AC CGG
                           CAAT   _  T  II
GAM238 CD3Z        GAGGCAGGGAGGCTCCCGCTGC    3525 T__      AGGGC      G
                           GGGAGGC   TCCGCTGC CC
                           IIIIIII   IIIIIIII II
                           CCCTCCG   GGGCGACG GG
                           CGT      A____      _
GAM238 EPHA8       GGGGGGCAGGGCTGGGCAGCTGGGC 3532 T  A      CC___   C CII
                           GGG GGCAGGGCT   GCTG GC
                           III IIIIIIIII   IIII II
                           CCC CCGTCCCGA   CGAC CG
                           _  _       CCCGT   C AII
GAM238 FANCF       TGGGAGGCAGAGGTTGCACTGAGC  3538          CTC_   C CI
                           TGGGAGGCAGGG   CGCTG GC
                           IIIIIIIIIII    IIIII II
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                         ACCCTCCGTCTC   GTGAC CG
                             CAAC    T  II
GAM238 FGFR2         TGGGAGGCATGGTCTCC-CTGC   3536      G _   G  GCC
                        TGGGAGGCA GG CTCC CTGC

                        IIIIIIIII II IIII IIII
                        ACCCTCCGT CC GAGG GACG
                             A A  _    III
GAM238 HMGE         AGGCAGGGCCCTGCTGAGC      3524 TGGGAGGC    C   C
                          AGGGCTC GCTG GC

                          IIIIIIII IIII II
                          TCCCGGG CGAC CG
                        _____         A  T
GAM238 HMOX1        GGCAGGGCTGACCCCTTCGCC     3529 TGGGA AG    GC  G
                           GGC  GGCTCC  TGC CC

                           III  IIIIII  III II
                           CCG  CTGGGG  GCG GG
                        _____  A_    AA  G
GAM238 IRAK1        GGAGGCAGGGTTCCACTCTGCC     3528 TGGG     C    GC
                          AGGCAGGG TCCGCT  GCC

                          IIIIIIII IIIIII  III
                          TCCGTCCC AGGTGA  CGG
                        ____        A   GA
GAM238 LENG4       GGCAGGCAGAGCAGTGTCCGCTGCG 3531 TG G      ____      CCII
                          G AGGCAGGGC   TCCGCTGCG

                          I IIIIIIIII   IIIIIIIII
                          C TCCGTCTCG   AGGCGACGC
                        __ G     TCAC      AIII
GAM238 MAP4        TGTGGGGCAGGGCTGCTGCTGCCCC 3540 TG_ A      CC   _  II
                          GG GGCAGGGCT GCTGC GCC

                          II IIIIIIIII IIIII III
                          CC CCGTCCCGA CGACG CGG
                        ACA _       __   A  GG
GAM238 PVRL2       TGGGAGGCAGTGTTCCACT      3541          GGC    GCGC
                          TGGGAGGCAG  TCCGCT

                          IIIIIIIIII  IIIIII
                          ACCCTCCGTC  AGGTGA
                          ACA     IIIC
GAM238 RAB36       TGGGAGGCAGAGGTTGCACTGAGCC 3539          CTC_   C  II
                          TGGGAGGCAGGG  CGCTG GCC

                          IIIIIIIIIII   IIIII III
                          ACCCTCCGTCTC   GTGAC CGG
                             CAAC    T  II
GAM238 SAS         GGGAGGCAGAGGTTGCGGTGAGCC 3530 TG      CTC_ C C  I
                          GGAGGCAGGG  CG TG GCC

                          IIIIIIIII   II II III
                          CCTCCGTCTC   GC AC CGG
                        __      CAAC  C  T  C
GAM238 SREBF2      GGAGGCAGGGGCTTGGCAGC      3526 TGGG      _ CC T GC
                          AGGCAGGG CT  GC GC

                          IIIIIIII II  II II
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                        TCCGTCCC GA  CG CG
                        ____      C  AC T AA
GAM238 SURF4            GGGAGGCA-GGCTCGGGGCTGGGCC 3534 TG      G  C__  C  I
                        GGAGGCAGG CTC  GCTG GCC
                        |||||||| |||  |||| |||
                        CCTCCGTCC GAG  CGAC CGG
                        __      _  CCC   C  C
GAM238 WASF3           GGAG-CAGGGCTCCTTTGCAGCC  3527 TGGGA      GC  _
                        GGCAGGGCTCC TGC GCC
                        |||||||||| ||| |||
                        TCGTCCCGAGG ACG CGG
                        ____          AA  T
GAM239 ADAM29          TGGGAGGGTGTCACCCGAGGT    3561    ___       CAGGTG
                        TGGGAGG  TCACCCGAGGT
                        |||||||  ||||||||||
                        ACCCTCC  AGTGGGCTCCA
                        CAC          IIIGTG
GAM239 ADAM29          TGGGAGGGTGTCACCCGAGGT    3561    ___       III
                        TGGGAGG  TCACCCGAGG
                        |||||||  |||||||||
                        ACCCTCC  AGTGGGCTCC
                        CAC          AII
GAM239 ALDH1B1         GGGTGGATCACCTGAGGTCAGG   3552 T GA   C       TG
                        GG GGTCACC GAGGTCAGG
                        || ||||||| |||||||||
                        CC CTAGTGG CTCCAGTCC
                        _ AC    A     TI
GAM239 ALDH1B1         GGGTGGATCACCTGAGGTCAGG   3552 GGA    C     I
                        GGTCACC GAGGTCAG
                        ||||||| ||||||||
                        CTAGTGG CTCCAGTC
                        CAC    A    I
GAM239 CLCN7           GGGAGGTCACCCTCGAGGCCGGG  3554 G       __   AGI
                        AGGTCACCC GAGGTC
                        ||||||||| ||||||
                        TCCAGTGGG CTCCGG
                        _     AG   CII
GAM239 CLCN7           GGGAGGTCACCCTCGAGGCCGGG  3554 TG      __   A TGI
                        GGAGGTCACCC GAGGTC GG
                        ||||||||||| |||||| ||
                        CCTCCAGTGGG CTCCGG CC
                        __     AG    C CII
GAM239 COX15           TGGGCGGATTACCTGAGGTCAGG  3565  A TC_ C     TGI
                        TGGG GG  ACC GAGGTCAGG
                        |||| ||  ||| |||||||||
                        ACCC CC  TGG CTCCAGTCC
                        G TAA  A      III
GAM239 COX15           TGGGCGGATTACCTGAGGTCAGG  3565 G A TC_ C       I
                        GG GG  ACC GAGGTCAG
                        || ||  ||| |||||||||
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                              CC CC   TGG CTCCAGTC
                              _  G  TAA  A      I
GAM239  DFFB          GGCAGATCACCTGAGGTCAGG    3555 G     C     I
                          G AGGTCACC GAGGTCAG
                          | |||||||| |||||||||
                          C TCTAGTGG CTCCAGTC
                            G       A      I
GAM239  DFFB          GGCAGATCACCTGAGGTCAGG    3555 TG G    C      TG
                          G AGGTCACC GAGGTCAGG
                          | |||||||| |||||||||
                          C TCTAGTGG CTCCAGTCC
                          __ G      A      TI
GAM239  DFFB          TGGGCGGATCACCTGAGGTCAGG   3563  A _  C     TGI
                          TGGG GG TCACC GAGGTCAGG
                          |||| || ||||| |||||||||
                          ACCC CC AGTGG CTCCAGTCC
                            G  T  A     III
GAM239  DFFB          TGGGCGGATCACCTGAGGTCAGG   3563 GA    C     I
                          GG  GGTCACC GAGGTCAG
                          ||  ||||||| |||||||||
                          CC  CTAGTGG CTCCAGTC
                          GC      A      I
GAM239  FCAR          TGGGTGGATCACCTGAGGTCAGG   3568  A _  C     TGI
                          TGGG GG TCACC GAGGTCAGG
                          |||| || ||||| |||||||||
                          ACCC CC AGTGG CTCCAGTCC
                            A  T  A     III
GAM239  FCAR          TGGGTGGATCACCTGAGGTCAGG   3568 GA    C     I
                          GG  GGTCACC GAGGTCAG
                          ||  ||||||| |||||||||
                          CC  CTAGTGG CTCCAGTC
                           AC     A      I
GAM239  GNE          GGGCGGATCACCTGAGGTCAGG     3551 T GA   C      TG
                          GG  GGTCACC GAGGTCAGG
                          ||  ||||||| |||||||||
                          CC  CTAGTGG CTCCAGTCC
                          _ GC      A      TI
GAM239  GNE          GGGCGGATCACCTGAGGTCAGG     3551 GGA    C     I
                             GGTCACC GAGGTCAG
                             ||||||| |||||||||
                             CTAGTGG CTCCAGTC
                           CGC      A      I
GAM239  HLCS         GGTGGATCAC--GAGGTCAGG     3547 ___A   CC     I
                          G GGTCAC  GAGGTCAG
                          | ||||||  |||||||||
                          C CTAGTG  CTCCAGTC
                          CCA _   __      I
GAM239  HLCS         GGTGGATCAC--GAGGTCAGG     3547 TGGGA   CC     T
                           GGTCAC  GAGGTCAGG
                           ||||||  |||||||||
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                              CTAGTG  CTCCAGTCC
                            AC___     __       T
GAM239  HYAL4         GGCAGATCACTTGAGGTCAGG     3556 G      CC      I
                          G AGGTCAC  GAGGTCAG
                          | |||||||  ||||||||
                          C TCTAGTG  CTCCAGTC
                            G     AA      I
GAM239  HYAL4         GGCAGATCACTTGAGGTCAGG     3556 TG G     CC       TG
                          G AGGTCAC  GAGGTCAGG
                          | |||||||  |||||||||
                          C TCTAGTG  CTCCAGTCC
                          __ G     AA       TI
GAM239  IL11         GGAGGATCACCTGAGGTCAGG      3545 GA    C      I
                          GGTCACC GAGGTCAG
                          ||||||| ||||||||
                          CTAGTGG CTCCAGTC
                          TC    A      I
GAM239  IL11         GGAGGATCACCTGAGGTCAGG      3545 TG A    C       TG
                          GG GGTCACC GAGGTCAGG
                          || ||||||| |||||||||
                          TC CTAGTGG CTCCAGTCC
                          __ _     A      TC
GAM239  KCNJ15        TCACTCCGCAGGTCAGGTG       3558    _ _      III
                          TCAC CCG AGGTCAGGT
                          |||| ||| |||||||||
                          AGTG GGC TCCAGTCCA
                           A   G      CII
GAM239  MEFV         TGGGTGCATCACCTGAGGTCAGG    3566    AG_    C      TGI
                          TGGG  GTCACC GAGGTCAGG
                          ||||  |||||| |||||||||
                          ACCC  TAGTGG CTCCAGTCC
                           ACG      A      III
GAM239  MEFV         TGGGTGCATCACCTGAGGTCAGG    3566 GAG    C      I
                          GG  GTCACC GAGGTCAG
                          || |||||| ||||||||
                          CC  TAGTGG CTCCAGTC
                           ACG     A      I
GAM239  MEFV         GGGTGGATCACCTGAGGTCAGG     3552 GGA    C      I
                          GGTCACC GAGGTCAG
                          ||||||| ||||||||
                          CTAGTGG CTCCAGTC
                          CAC     A      I
GAM239  MEFV         GGGTGGATCACCTGAGGTCAGG     3552 T GA    C       TG
                          GG GGTCACC GAGGTCAGG
                          || ||||||| |||||||||
                          CC CTAGTGG CTCCAGTCC
                          _ AC     A      TI
GAM239  MHC2TA       TGGGTGGATCACCCGAGGTCA      3562 A _          GGTG
                          TGGG GG TCACCCGAGGTCA
                          |||| || ||||||||||||
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                              ACCC CC AGTGGGCTCCAGT
                                A T         IIIG
GAM239  MHC2TA          TGGGTGGATCACCCGAGGTCA   3562  GA           I
                              GG  GGTCACCCGAGGTC

                              II IIIIIIIIIIIII
                              CC  CTAGTGGGCTCCAG
                                AC          I
GAM239  MICB           GGCAGATCACCTGAGGTCAGG   3555  G     C     I
                              G AGGTCACC GAGGTCAG

                              I IIIIIIII IIIIIIII
                              C TCTAGTGG CTCCAGTC
                                G     A    I
GAM239  MICB           GGCAGATCACCTGAGGTCAGG   3555  TG G     C      TG
                              G AGGTCACC GAGGTCAGG

                              I IIIIIIII IIIIIIIII
                              C TCTAGTGG CTCCAGTCC
                                __G     A    TI
GAM239  MLANA            GGCAGATCACCTGAGGTCAGG   3555  G     C     I
                              G AGGTCACC GAGGTCAG

                              I IIIIIIII IIIIIIII
                              C TCTAGTGG CTCCAGTC
                                G     A    I
GAM239  MLANA            GGCAGATCACCTGAGGTCAGG   3555  TG G     C      TG
                              G AGGTCACC GAGGTCAGG

                              I IIIIIIII IIIIIIIII
                              C TCTAGTGG CTCCAGTCC
                                __G     A    TI
GAM239  MPL         TGGGTGGATCACCCGAGGTTAGG   3567  A _       C TGI
                              TGGG GG TCACCCGAGGT AGG

                              IIII II IIIIIIIIIII III
                              ACCC CC AGTGGGCTCCA TCC
                                A T       A III
GAM239  MPL         TGGGTGGATCACCCGAGGTTAGG   3567  GA          CAGI
                              GG  GGTCACCCGAGGT

                              II IIIIIIIIIIIII
                              CC  CTAGTGGGCTCCA
                                AC          ATCI
GAM239  NCOA6           GGGTGGATCACTTGAGGTCAGG   3553  GGA     CC      I
                              GGTCAC  GAGGTCAG

                              IIIIII IIIIIIIII
                              CTAGTG  CTCCAGTC
                                CAC     AA    I
GAM239  NCOA6           GGGTGGATCACTTGAGGTCAGG   3553  T GA     CC      TG
                              GG  GGTCAC  GAGGTCAGG

                              II IIIIII IIIIIIIII
                              CC  CTAGTG  CTCCAGTCC
                                _ AC     AA    TI
GAM239  NDRG3           GGTGGATCACCTGAGGTCAGG   3548  _ A     C      I
                              G GGTCACC GAGGTCAG

                              I IIIIIIII IIIIIIII
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                              C CTAGTGG CTCCAGTC
                              A _     A      I
GAM239 NDRG3          GGTGGATCACCTGAGGTCAGG    3548 TGGGA    C      TG
                          GGTCACC GAGGTCAGG
                          ||||||| |||||||||
                          CTAGTGG CTCCAGTCC
                          AC___     A    TC
GAM239 PABPN1       TGGGAA---ACCCGAGGTCA    3569     GTC       GG
                          TGGGAG  ACCCGAGGTCA
                          ||||||  |||||||||||
                          ACCCTT  TGGGCTCCAGT
                             ___         ||
GAM239 PABPN1       TGGGAA---ACCCGAGGTCA    3569 _  GTC
                          GGGAG   ACCCGAGGTC
                          |||||   ||||||||||
                          CCCTT   TGGGCTCCAG
                          A     ___
GAM239 PDE6B        GGTGATCACCTGAGGTCAGG     3550 GA    C     I
                          GGTCACC GAGGTCAG
                          ||||||| ||||||||
                          CTAGTGG CTCCAGTC
                          CA    A     I
GAM239 PDE6B        GGTGATCACCTGAGGTCAGG     3550 TGGGA    C     T
                          GGTCACC GAGGTCAGG
                          ||||||| |||||||||
                          CTAGTGG CTCCAGTCC
                          A___    A    T
GAM239 PIK3CD       GGGTGGATCACCTGAGGTCAGG    3552 GGA    C     I
                          GGTCACC GAGGTCAG
                          ||||||| ||||||||
                          CTAGTGG CTCCAGTC
                          CAC    A    I
GAM239 PIK3CD       GGGTGGATCACCTGAGGTCAGG    3552 T GA    C      TG
                          GG  GGTCACC GAGGTCAGG
                          ||  ||||||| |||||||||
                          CC  CTAGTGG CTCCAGTCC
                          _ AC    A    TI
GAM239 SAS          GGGTGGATCACCTGAGGTCAGG    3552 GGA    C     I
                          GGTCACC GAGGTCAG
                          ||||||| ||||||||
                          CTAGTGG CTCCAGTC
                          CAC    A    I
GAM239 SAS          GGGTGGATCACCTGAGGTCAGG    3552 T GA    C      TG
                          GG  GGTCACC GAGGTCAGG
                          ||  ||||||| |||||||||
                          CC  CTAGTGG CTCCAGTCC
                          _ AC    A    TI
GAM239 SCML2        TGGGCGGATCACCTGAGGTCAGG    3563 A _  C      TGI
                          TGGG GG TCACC GAGGTCAGG
                          |||| || |||||| |||||||||
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                        ACCC CC AGTGG CTCCAGTCC
                         G  T   A       III
GAM239 SCML2        TGGGCGGATCACCTGAGGTCAGG  3563  GA      C      I
                        GG  GGTCACC GAGGTCAG
                        II  IIIIIIII IIIIIIIII
                        CC  CTAGTGG CTCCAGTC
                         GC     A       I
GAM239 SH3BP2      TGGGCGGATCAGTTGAGGTCAGG  3564   A _  CCC      TGI
                        TGGG GG TCA  GAGGTCAGG
                        IIII II III  IIIIIIIII
                        ACCC CC AGT  CTCCAGTCC
                         G  T  CAA       III
GAM239 SH3BP2      TGGGCGGATCAGTTGAGGTCAGG  3564  GA    CCC       I
                        GG  GGTCA  GAGGTCAG
                        II  IIIII  IIIIIIIII
                        CC  CTAGT  CTCCAGTC
                         GC    CAA      I
GAM239 SH3BP2      TGGGCAGATCACCTGAGGTCAGG  3559   _     C      TGI
                        TGGG AGGTCACC GAGGTCAGG
                        IIII IIIIIIIII IIIIIIIII
                        ACCC TCTAGTGG CTCCAGTCC
                          G      A       III
GAM239 SH3BP2      TGGGCAGATCACCTGAGGTCAGG  3559  G      C      I
                        GG AGGTCACC GAGGTCAG
                        II IIIIIIII IIIIIIIII
                        CC TCTAGTGG CTCCAGTC
                          G     A        I
GAM239 SH3GL3      GGCGGATCAC--GAGGTCAGG    3546 ___ A    CC     I
                         G GGTCAC  GAGGTCAG
                         I IIIIII  IIIIIIIII
                         C CTAGTG  CTCCAGTC
                        CCG _     __        I
GAM239 SH3GL3      GGCGGATCAC--GAGGTCAGG    3546 TGGGA    CC      T
                          GGTCAC  GAGGTCAGG
                          IIIIII  IIIIIIIII
                          CTAGTG  CTCCAGTCC
                        GC___     __        T
GAM239 SHOX        GGCAGATCACCTGAGGTCAGG    3555 G      C      I
                         G AGGTCACC GAGGTCAG
                         I IIIIIIII IIIIIIIII
                         C TCTAGTGG CTCCAGTC
                           G     A        I
GAM239 SHOX        GGCAGATCACCTGAGGTCAGG    3555 TG G    C      TG
                         G AGGTCACC GAGGTCAGG
                         I IIIIIIII IIIIIIIII
                         C TCTAGTGG CTCCAGTCC
                        __ G     A        TI
GAM239 SHOX        GGGTGGATCACCTGAGGTCAGG   3552 GGA    C      I
                          GGTCACC GAGGTCAG
                          IIIIIII IIIIIIIII
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                        CTAGTGG CTCCAGTC
                     CAC       A      I
GAM239 SHOX          GGGTGGATCACCTGAGGTCAGG   3552 T GA      C      TG
                        GG  GGTCACC GAGGTCAGG
                        || ||||||| |||||||||
                        CC  CTAGTGG CTCCAGTCC
                      _  AC       A      TI
GAM239 SLA2          TGGGTGGATCACCTGAGGTCAGG   3568   A _   C      TGI
                        TGGG GG TCACC GAGGTCAGG
                        |||| || ||||| |||||||||
                        ACCC CC AGTGG CTCCAGTCC
                          A  T   A      III
GAM239 SLA2          TGGGTGGATCACCTGAGGTCAGG   3568  GA      C      I
                        GG  GGTCACC GAGGTCAG
                        || ||||||| |||||||||
                        CC  CTAGTGG CTCCAGTC
                          AC       A      I
GAM239 SMAC          GGGTGGATCACTTGAGGTCAGG    3553 GGA     CC     I
                         GGTCAC  GAGGTCAG
                         ||||||  |||||||||
                         CTAGTG  CTCCAGTC
                       CAC     AA      I
GAM239 SMAC          GGGTGGATCACTTGAGGTCAGG    3553 T GA     CC      TG
                        GG  GGTCAC  GAGGTCAGG
                        || ||||||  |||||||||
                        CC  CTAGTG  CTCCAGTCC
                      _  AC     AA      TI
GAM239 SPN          GGTAGATCACCTGAGGTCAGG      3557 GG        C      I
                         AGGTCACC GAGGTCAG
                         |||||||| |||||||||
                         TCTAGTGG CTCCAGTC
                       CA        A      I
GAM239 SPN          GGTAGATCACCTGAGGTCAGG      3557 TGGG      C      TG
                         AGGTCACC GAGGTCAGG
                         |||||||| |||||||||
                         TCTAGTGG CTCCAGTCC
                       CA__      A      TI
GAM239 SULT2B1       TGGGTGGATCACCTGAGGTCAGG   3568   A _   C      TGI
                        TGGG GG TCACC GAGGTCAGG
                        |||| || ||||| |||||||||
                        ACCC CC AGTGG CTCCAGTCC
                          A  T   A      III
GAM239 SULT2B1       TGGGTGGATCACCTGAGGTCAGG   3568  GA      C      I
                        GG  GGTCACC GAGGTCAG
                        || ||||||| |||||||||
                        CC  CTAGTGG CTCCAGTC
                          AC       A      I
GAM239 TAPBP         TGGGCAGATCACCTGAGGTCAGG   3559   _     C      TGI
                        TGGG AGGTCACC GAGGTCAGG
                        |||| ||||||| |||||||||
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                              ACCC TCTAGTGG CTCCAGTCC
                                 G    A       III
GAM239  TAPBP          TGGGCAGATCACCTGAGGTCAGG   3559  G      C      I
                              GG AGGTCACC GAGGTCAG
                              || |||||||| ||||||||
                              CC TCTAGTGG CTCCAGTC
                                 G    A      I
GAM239  TGFB1          GGGGGTGCGCCCGAGGTCTGG      3549 GA  CA_       AGI
                               GGT  CCCGAGGTC
                               |||  |||||||||
                               CCA  GGGCTCCAG
                                C_  CGC      ACI
GAM239  TGFB1          GGGGGTGCGCCCGAGGTCTGG      3549 T  AG CA      A TG
                               GGG  GT CCCGAGGTC GG
                               ||| || ||||||||| ||
                               CCC  CG GGGCTCCAG CC
                               _ A_ C_      A CC
GAM239  TNFRSF10B        GGTGGATCACCTGAGGTCAGG      3548 _ A     C      I
                                G GGTCACC GAGGTCAG
                                | |||||||| |||||||||
                                C CTAGTGG CTCCAGTC
                                A_    A    I
GAM239  TNFRSF10B        GGTGGATCACCTGAGGTCAGG      3548 TGGGA    C      TG
                                 GGTCACC GAGGTCAGG
                                 ||||||| ||||||||||
                                 CTAGTGG CTCCAGTCC
                               AC___    A    TC
GAM239  TPMT           TGGGTAGATCACCTGAGGTCAGG   3560   _     C      TGI
                              TGGG AGGTCACC GAGGTCAGG
                              |||| |||||||| ||||||||||
                              ACCC TCTAGTGG CTCCAGTCC
                                A    A       III
GAM239  TPMT           TGGGTAGATCACCTGAGGTCAGG   3560  G      C      I
                              GG AGGTCACC GAGGTCAG
                              || |||||||| ||||||||
                              CC TCTAGTGG CTCCAGTC
                               A    A    I
GAM239  TRPV1          TGGGCGGATCACCTGAGGTCAGG   3563   A _   C      TGI
                              TGGG GG TCACC GAGGTCAGG
                              |||| || ||||| ||||||||||
                              ACCC CC AGTGG CTCCAGTCC
                                G T  A      III
GAM239  TRPV1          TGGGCGGATCACCTGAGGTCAGG   3563  GA     C      I
                              GG  GGTCACC GAGGTCAG
                              ||  ||||||| |||||||||
                              CC  CTAGTGG CTCCAGTC
                               GC    A    I
GAM239  TUFT1          TGGGTGGATCACCTGAGGTCAGG   3568  A _   C      TGI
                              TGGG GG TCACC GAGGTCAGG
                              |||| || ||||| ||||||||||
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                          ACCC CC AGTGG CTCCAGTCC
                            A  T   A        III
GAM239  TUFT1          TGGGTGGATCACCTGAGGTCAGG   3568  GA      C      I
                          GG  GGTCACC GAGGTCAG
                          II  IIIIIIII IIIIIIII
                          CC  CTAGTGG CTCCAGTC
                            AC       A       I
GAM239  VHL            TGGGCGGATCACCTGAGGTCAGG   3563  A _    C       TGI
                          TGGG GG TCACC GAGGTCAGG
                          IIII II IIIII IIIIIIIII
                          ACCC CC AGTGG CTCCAGTCC
                             G T   A        III
GAM239  VHL            TGGGCGGATCACCTGAGGTCAGG   3563  GA      C      I
                          GG  GGTCACC GAGGTCAG
                          II  IIIIIII IIIIIIII
                          CC  CTAGTGG CTCCAGTC
                            GC       A       I
GAM240  ABCC1         AAAACTCCTCCGTGGGAAGCACC   3572  TAAC _       C_   TTI
                          AC CCTCCGTGGGA CACC
                          II IIIIIIIIIII IIII
                          TG GGAGGCACCCT GTGG
                          TT__ A          TC  TII
GAM240  FCN2          CACCCTCCGCTGGAAAACCT      3576  TAACAC    G  CC
                            CCTCCGT GGA  ACCT
                            IIIIIII III  IIII
                            GGAGGCG CCT  TGGA
                        _____      A   TT
GAM240  HOXB3         AACACCCTCCTCTGAGCCCA       3574  TA      G_  A  CCT
                          ACACCCTCC TGGG CCA
                          IIIIIIIII IIII III
                          TGTGGGAGG ACTC GGT
                          __      AG   G  CII
GAM240  NYX          CACCCAGCCGTGGGACC-CCT       3575  TAACA CT       A
                          CC  CCGTGGGACC CCT
                          II  IIIIIIIIII III
                          GG  GGCACCCTGG GGA
                        _____  TC       _
GAM240  SFRP5         AACACCCTCCAGTAGGGCC        3573  TA      _   A ACCT
                          ACACCCTCC GTGGG CC
                          IIIIIIIII IIIII II
                          TGTGGGAGG CATCC GG
                            __       T   C  CIII
GAM240  SOST          CCCTGCCCCGTGGGACC-CCT      3577  TAACACC        A
                          CTCCGTGGGACC CCT
                          IIIIIIIIIIII III
                          GGGGCACCCTGG GGA
                        _____      _
GAM241  KIF1B         TAACTGTTGCAGTTCTATGCTCAC   3582       C___  __    CGGTGI
                          TAACTGTTGT  CTA CTCAC
                          IIIIIIIIII  III IIIII
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                          ATTGACAACG   GAT  GAGTG
                           TCAA   AC    IIIGTG
GAM241  KIF1B      TAACTGTTGCAGTTCTATGCTCAC  3582        C___  __   IIIG
                           TAACTGTTGT   CTA  CTCA
                           IIIIIIIII   III  IIII
                          ATTGACAACG   GAT  GAGT
                            TCAA   AC   GIII
GAM241  PDE4D        TACCTGTT-TCTTT-TCACCGGTG  3583 AA_   G  CTAC       I
                          CTGTT TC   TCACCGGT
                          IIIII II   IIIIIIII
                          GACAA AG   AGTGGCCA
                          ATG   _  AAA_      I
GAM241  PDE4D        TACCTGTT-TCTTT-TCACCGGTG  3583 TAA   G  CTAC
                          CTGTT TC   TCACCGGTG
                          IIIII II   IIIIIIIII
                          GACAA AG   AGTGGCCAC
                          ATG   _  AAA_
GAM241  PPT2       CTGTTGTC---CTCACAGG      3580       TAC   CG
                          CTGTTGTCC  TCAC
                          IIIIIIIII  IIII
                          GACAACAGG  AGTG
                             ___    TC
GAM241  PPT2       CTGTTGTC---CTCACAGG      3580 TAACTG    TAC   C
                          TTGTCC  TCAC G
                          IIIIII  IIII I
                          AACAGG  AGTG C
                          _____   ___   T
GAM241  TCF7       CTGTTGTCC-ACT-ACTGG       3581       T  C  CGI
                          CTGTTGTCC ACT AC
                          IIIIIIIII III II
                          GACAACAGG TGA TG
                          _  _  ACC
GAM241  TCF7       CTGTTGTCC-ACT-ACTGG       3581 TAACTG    T  C  C
                          TTGTCC ACT AC GG
                          IIIIII III II II
                          AACAGG TGA TG CC
                          _____    _  _  A
GAM242  CCNK      GGCACTGATGAGGCTACTC       3592 A         _  II
                          GG ACTGATGAGGTT CT
                          II IIIIIIIIIIII II
                          CC TGACTACTCCGA GA
                           G        T  GI
GAM242  CCNK      GGCACTGATGAGGCTACTC       3592 CAGGA        _  I
                          ACTGATGAGGTT CTC
                          IIIIIIIIIIII III
                          TGACTACTCCGA GAG
                          G___      T  A
GAM242  HPS3      CAGTGAACTGATGTTGTTC       3588 _        AG  TCI
                          CAG GAACTGATG GTTC
                          III IIIIIIIII IIII
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                    GTC CTTGACTAC CAAG
                      A      AA   III
GAM242 HPS3         CAGTGAACTGATGTTGTTC      3588  _        AG  II
                    CAG GAACTGATG GTT
                    ||| ||||||||| |||
                    GTC CTTGACTAC CAA
                      A      AA  GI
GAM242 IGHMBP2         CAGGTACATCATCTGAGGTTCTC   3590    A TGA___        III
                      CAGG AC    TGAGGTTCTC
                      |||| ||    ||||||||||
                      GTCC TG    ACTCCAAGAG
                        A TAGTAG        III
GAM242 IGHMBP2         CAGGTACATCATCTGAGGTTCTC   3590 AGGAACTGA       I
                            TGAGGTTCT
                            |||||||||
                            ACTCCAAGA
                      ATGTAGTAG        I
GAM242 PPP1R12B       GGAACTAAAGATTGAGGTTCT     3591           ____      IIIA
                      GGAACTGA  TGAGGTTC
                      ||||||||  ||||||||
                      CCTTGATT  ACTCCAAG
                        TCTA      AIII
GAM242 PPP1R12B       GGAACTAAAGATTGAGGTTCT     3591 CAGG       ____        CII
                        AACTGA  TGAGGTTCT
                        ||||||  |||||||||
                        TTGATT  ACTCCAAGA
                      ____      TCTA     ACI
GAM242 PRDM2         CAGGTGCACCTGATCTGAGGTTCTC  3589 AGGAA   __       I
                        CTGA TGAGGTTCT
                        |||| |||||||||
                        GACT ACTCCAAGA
                      GTG__ AG       I
GAM242 PRDM2         CAGGTGCACCTGATCTGAGGTTCTC 3589   AA___  __        III
                      CAGG   CTGA TGAGGTTCTC  G
                      ||||   |||| ||||||||||  |
                      GTCC   GACT ACTCCAAGAG  C
                      ACGTG  AG        III
GAM242 RASA1         AGGCAGCTGATGAGGTTGTC       3586 AA_       CTII
                      AGG CTGATGAGGTT
                      ||| |||||||||||
                      TCC GACTACTCCAA
                      GTC        CAGI
GAM242 RASA1         AGGCAGCTGATGAGGTTGTC       3586 CA AA_      C I
                       GG CTGATGAGGTT TC
                       || ||||||||||| ||
                       CC GACTACTCCAA AG
                       __ GTC        C A
GAM242 ZNF18         AGGGGCTGATCTGAGGTTCT       3587 AA  __       III
                      AGG CTGA TGAGGTTC
                      ||| |||| ||||||||
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                    TCC  GACT  ACTCCAAG
                    CC   AG       AII
GAM242 ZNF18        AGGGGCTGATCTGAGGTTCT     3587 CA AA   __       CI
                    GG  CTGA  TGAGGTTCT
                    II  IIII  IIIIIIIII
                    CC  GACT  ACTCCAAGA
                    __  CC   AG       AI
GAM243 AIM2         CAGCCTCCTGATC-CCTG-GGGC   3602 GC      CTC   GA
                    AGCCTCCTG  TCCC  GGGC
                    IIIIIIIII  IIII  IIII
                    TCGGAGGAC  AGGG  CCCG
                    __         T__   AC
GAM243 BMP8         CAGCCACTCCTGCTCTGCCG      3596 _ AGC      C  AGGG
                    GC  CTCCTGCTCT CCG
                    II  IIIIIIIIII III
                    CG  GAGGACGAGA GGC
                    T  GT_         C  CIII
GAM243 CDH23        GCAGCCCGCGTCCCTCTCTCCCGAG 3606     ____  G      GGCII
                    GCAGCC  TCCT CTCTCCCGAG
                    IIIIII  IIII IIIIIIIIII
                    CGTCGG  AGGG GAGAGGGCTC
                    GCGC   A       IIICG
GAM243 COL1A1       GCCTCCTGCTCCGACCCCGAGG    3615 GCAGCC      ___      C
                    TCCTGCTCT  CCCGAGGG
                    IIIIIIIII  IIIIIIII
                    AGGACGAGG  GGGCTCCT
                    _____          CTG      C
GAM243 CRAT         CAGTCTCCTGCTCT--GGAGGGC   3603 GC C       CCC
                    AG CTCCTGCTCT  GAGGGC
                    II IIIIIIIIII  IIIIII
                    TC GAGGACGAGA  CTCCCG
                    __  A          C__
GAM243 DPEP1        GCCTCCTGC-CTCCC-AGG        3617 GCAGCC      T   G
                    TCCTGC CTCCC AGG
                    IIIIII IIIII III
                    AGGACG GAGGG TCC

                    _____      _   _
GAM243 FOXO1A       GCCGCTTGCTCTCCCCAGCGGC    3616 GCAGCCTCC      G _
                    TGCTCTCCC AG GGC
                    IIIIIIIII II III
                    ACGAGAGGG TC CCG
                    CGA_____         G G
GAM243 HMX1         GCCGCGGCCTGCGCTCCCGAGG    3614 A CT  T      GC
                    GC GC  CCTGC CTCCCGAGG
                    II II  IIIII IIIIIIIII
                    CG CG  GGACG GAGGGCTCC
                    G CC    C      II
GAM243 KCNMB4       AGCCTCCTGCACCCTCGGGCGC    3595 GCAG       TCT  GA
                    CCTCCTGC  CCC  GGGC
                    IIIIIIII  III  IIII
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                        GGAGGACG  GGG  CCCG
                     ____        T__    AG
GAM243  KRT18        GCCTCCTGCTCCCCAAAGGG    3620 GCAGCC       C
                        TCCTGCTCTCC GAGGG
                        ||||||||||| |||||
                        AGGACGAGGGG TTCCC
                     _____          T
GAM243  MAP3K7IP1       CAGGC-CCTGCTCTCCCGCAGG   3599 GCA  TC       _   C
                        GCC  CTGCTCTCCCG AGGG
                        ||| ||||||||||| ||||
                        CGG  GACGAGAGGGC TCCT
                     TC_  __       G   I
GAM243  MBTPS1          CAGCCTTTCCAGTTCTCCCGAG   3597 GC   __  TGC      GGC
                        AGCC TCC  TCTCCCGAG
                        |||| ||| |||||||||
                        TCGG AGG  AGAGGGCTC
                        __  AA  TCA      AII
GAM243  MTMR1           GCCTCCTGC-CGCCCGCCGGC    3621 GCAGCC    T T  AG
                        TCCTGC C CCCG GG
                        |||||| | |||| ||
                        AGGACG G GGGC CC
                     _____      _ C  GG
GAM243  NCKAP1          GCAGCCTCCTGC-CTTCCG      3612        TC  CGAGG
                        GCAGCCTCCTGC TCC
                        |||||||||||| |||
                        CGTCGGAGGACG AGG
                           GA  CIIIC
GAM243  PAX5            GCAGCTCCTCACTGCTCTCC     3605    __ _      CGAGGG
                        GCAGC CTC CTGCTCTCC
                        ||||| ||| ||||||||||
                        CGTCG GAG GACGAGAGG
                        AG  T     IIICGG
GAM243  PKIA          GCAGCCTCC-GCTCCCGCCGCGG    3609       T  _  A GC
                        GCAGCCTCC GCTCTC CCG GG
                        ||||||||| |||||| ||| ||
                        CGTCGGAGG CGAGGG GGC CC
                          _    C  G  II
GAM243  PLA2G4C          CAGC-TCCAGGATCTCCCGAGGG   3598 GC  C  TGC_      C
                        AGC TCC   TCTCCCGAGGG
                        ||| |||   |||||||||||
                        TCG AGG   AGAGGGCTCCC
                        __  _  TCCT        T
GAM243  PLCG1          GCA-CCTGCTGCTCTCCAACGAGG   3610  G  C     __   GCI
                        GCA CCT CTGCTCTCC CGAGG
                        ||| ||| ||||||||| |||||
                        CGT GGA GACGAGAGG GCTCC
                         _  C   TT  III
GAM243  PRKY           GCAGCCTCC-GC-CTCCTGAG      3613       T T  C  GG
                        GCAGCCTCC GC CTCC GAG
                        ||||||||| || |||| |||
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                      CGTCGGAGG CG GAGG CTC
                       _  _     A  II
GAM243  PTEN          GCAGGCCGGCCGGCTC-CCCGAGGGC 3604   _ T_ T  T      II
                      GCAG CC  CC GCTC CCCGAGGGC
                      IIII II  II IIII IIIIIIIII
                      CGTC GG  GG CGAG GGGCTCCCG
                         C CC C   _        II
GAM243  PTPRJ         GCCGCCTCCTGCCGTCTCC    3607 A    __     CGAGGG
                      GC GCCTCCTGC TCTCC
                      II IIIIIIIII IIIII
                      CG CGGAGGACG AGAGG
                       G     GC  IIICGG
GAM243  RASGRP2         CAGCCTCCTGC---CCCGA     3600 GC      TCT   G
                       AGCCTCCTGC  CCCGA
                       IIIIIIIIII  IIIII
                       TCGGAGGACG  GGGCT
                         __      ___    G
GAM243  RPL18          GCCTCCTGCTCGGCC-AGG     3619 GCAGCC     TC G
                       TCCTGCTC CC AGG
                       IIIIIIII II III
                       AGGACGAG GG TCC
                         _____       CC _
GAM243  SCN2B          GCCTCCTGC-CTCCCCAGG     3618 GCAGCC    T  G
                       TCCTGC CTCCC AGG
                       IIIIII IIIII III
                       AGGACG GAGGG TCC
                         _____    _  G
GAM243  SNRPA1        GCAGCCTCCCGTTCCCCCG     3611      C    AGGG
                      GCAGCCTCCTG TCTCCCG
                      IIIIIIIIIII IIIIIII
                      CGTCGGAGGGC AGGGGGC
                            A     IIIC
GAM243  ST5          CAGCATC-TGCTCTCC--AGGGC  3601 GC  CTC     CG
                     AGC  CTGCTCTCC AGGG
                     III  IIIIIIIII IIII
                     TCG  GACGAGAGG TCCC
                       __  TA_        __
GAM243  TCF8         GCAGCCTCCTGCACTGGGCCCG   3608        T ___  AGGGC
                     GCAGCCTCCTGC CT  CCCG
                     IIIIIIIIIIII II  IIII
                     CGTCGGAGGACG GA  GGGC
                          T CCC   IIICG
GAM244  ASTN         TAAG-ACCTGTTT--GGCAGC    3640 TA      _  AI
                     AGGACCTGTTTGG GGC
                     IIIIIIIIIIII III
                     TTCTGGACAAACC TCG
                       A_      G II
GAM244  ASTN         TAAG-ACCTGTTT--GGCAGC    3640 TA       GG   A
                     AGGACCTGTTT GGCAGC
                     IIIIIIIIII IIIIII
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                              TTCTGGACAAA  CCGTCG
                              A_           __       I
GAM244 CA7          AGGGCCTGCCCGTGGCAGCAGG   3626 _  A      G      I
                        GG CCTGTTTG GGCAGCAG
                        || |||||||| |||||||||
                        CC GGACGGGC CCGTCGTC
                              C _      A    I
GAM244 CA7          AGGGCCTGCCCGTGGCAGCAGG   3626 TAA  A     G
                        GG CCTGTTTG GGCAGCAGG
                        || |||||||| |||||||||
                        CC GGACGGGC CCGTCGTCC
                              ___ _      A
GAM244 CDK10          CCTTTTTCTGGGGGCAGCAG      3627 C_____ TTT      III
                          CTG  GGGGCAGCA
                          ||| |||||||||
                          GAC  CCCCGTCGT
                       GGAAAAA  ___       CII
GAM244 CDK10          CCTTTTTCTGGGGGCAGCAG      3627 TAAGGAC  TTT
                          CTG  GGGGCAGCAG
                          ||| ||||||||||
                          GAC  CCCCGTCGTC
                       A_____   ___
GAM244 FGFR2           CCTGTTTGGGGACAGGCAG      3628           _ _  III
                          CCTGTTTGGGG CAG CA
                          |||||||||| ||| ||
                          GGACAAACCCC GTC GT
                             T  C  CII
GAM244 GRLF1        TAATGGACTGTGTTCTGGGGCAGC  3637 AA   C_ _        I
                          GGAC  TGT TTGGGGCAG
                          |||| ||| ||||||||||
                          CCTG  ACA GACCCCGTC
                          __  AC  A       I
GAM244 GRLF1        TAATGGACTGTGTTCTGGGGCAGC  3637 TAA_  C_ _         AGGI
                          GGAC  TGT TTGGGGCAGC
                          |||| ||| |||||||||||
                          CCTG  ACA GACCCCGTCG
                       ATTA   AC  A         IIIG
GAM244 HAMP         GACCTATGTTCTGGGGCAGCAGG   3634 ACC   _          I
                          TGT TTGGGGCAGCAG
                          ||| ||||||||||||
                          ACA GACCCCGTCGTC
                          AT_  A       I
GAM244 HAMP         GACCTATGTTCTGGGGCAGCAGG   3634 TAAGGACC  _         I
                          TGT TTGGGGCAGCAGG
                          ||| |||||||||||||
                          ACA GACCCCGTCGTCC
                          AT_____  A      T
GAM244 INHBC        TAAGCCTCTATTTTGGGCAGCAG   3641    GAC   G      GI
                          TAAG  CTGTTT GGGCAGCAG
                          |||| |||||| |||||||||
```

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                                 ATTC   GATAAA CCCGTCGTC
                                 GGA      A        II
GAM244  INHBC          TAAGCCTCTATTTTGGGCAGCAG  3641 AAGGAC    G      I
                                 CTGTTT GGGCAGCA
                                 IIIIII IIIIIIIII
                                 GATAAA CCCGTCGT
                                 TTCGGA    A      I
GAM244  MAGEA12          GACTCTGGTCAGGGCAGCAGG    3633 AC   T TG      I
                                 CTG T GGGCAGCAG
                                 III I IIIIIIIIII
                                 GAC A CCCGTCGTC
                                 GA   C GT       I
GAM244  MAGEA12          GACTCTGGTCAGGGCAGCAGG    3633 TAAGGAC   T TG
                                 CTG T GGGCAGCAGG
                                 III I IIIIIIIIII
                                 GAC A CCCGTCGTCC
                                 _____ C GT
GAM244  MAGEA2           GACTCTGGTCAGGGCAGCAGG    3633 AC   T TG      I
                                 CTG T GGGCAGCAG
                                 III I IIIIIIIIII
                                 GAC A CCCGTCGTC
                                 GA   C GT       I
GAM244  MAGEA2           GACTCTGGTCAGGGCAGCAGG    3633 TAAGGAC   T TG
                                 CTG T GGGCAGCAGG
                                 III I IIIIIIIIII
                                 GAC A CCCGTCGTCC
                                 _____ C GT
GAM244  MAGEA4           GACTCTGCTCAGGGCAGCAGG    3632 AC    TG      I
                                 CTGTT GGGCAGCAG
                                 IIIII IIIIIIIII
                                 GACGA CCCGTCGTC
                                 GA    GT       I
GAM244  MAGEA4           GACTCTGCTCAGGGCAGCAGG    3632 TAAGGAC    TG
                                 CTGTT GGGCAGCAGG
                                 IIIII IIIIIIIIII
                                 GACGA CCCGTCGTCC
                                 _____   GT
GAM244  MAGEA9          GACTCTGGTCAGGGCAGCAG    3630  _   T TG      II
                                 GAC CTG T GGGCAGCA
                                 III III I IIIIIIIII
                                 CTG GAC A CCCGTCGT
                                 A   C GT       CI
GAM244  MAGEA9          GACTCTGGTCAGGGCAGCAG    3630 TAAGGAC   T TG
                                 CTG T GGGCAGCAG
                                 III I IIIIIIIII
                                 GAC A CCCGTCGTC
                                 _____ C GT
GAM244  MSI1          GACGCTGTTGGGGGCAGCAGG    3631 AC    T        I
                                 CTGTT GGGGCAGCAG
                                 IIIII IIIIIIIIII
```

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                        GACAA CCCCGTCGTC
                        GC    C        I
GAM244 MSI1        GACGCTGTTGGGGGCAGCAGG   3631 TAAGGAC    T
                        CTGTT GGGGCAGCAGG
                        |||||  |||||||||||
                        GACAA CCCCGTCGTCC
                        _____         C
GAM244 MYL4       TAAGGTCCT---TGGGGCAG   3639    A GTT    CA
                        TAAGG CCT  TGGGGCAG
                        ||||| |||  ||||||||
                        ATTCC GGA  ACCCCGTC
                          A  ___    II
GAM244 MYL4       TAAGGTCCT---TGGGGCAG   3639 _  A GTT
                         AAGG CCT  TGGGGCA
                         |||| |||  |||||||
                         TTCC GGA  ACCCCGT
                          A  A ___
GAM244 NUP98      AGGATGCTGCTTCTGGCAGCAGG   3625 GGAC     GG      I
                        CTGTTT GGCAGCAG
                        ||||||  |||||||||
                        GACGAA CCGTCGTC
                        CTAC     GA     I
GAM244 NUP98      AGGATGCTGCTTCTGGCAGCAGG   3625 TAAGGAC     GG      I
                        CTGTTT GGCAGCAGG
                        ||||||  |||||||||
                        GACGAA CCGTCGTCC
                        CTAC___    GA      C
GAM244 PCTK1      TGTTTGGGCAGGCAGCAGG    3642      ___      III
                        TGTTTGGG GCAGCAG
                        ||||||||  |||||||
                        ACAAACCC CGTCGTC
                          GTC     CII
GAM244 RAB6A      AGGAGCCCGGCTGGAGGGCAGCAGG 3624 GGA    T   __     I
                        CCTG TTGG GGCAGCAG
                        |||| ||||  |||||||||
                        GGGC GACC CCGTCGTC
                        C__   C  TC      I
GAM244 RAB6A      AGGAGCCCGGCTGGAGGGCAGCAGG 3624 TAA GA   T   __      II
                        G CCTG TTGG GGCAGCAGG
                        | |||| ||||  |||||||||
                        C GGGC GACC CCGTCGTCC
                        ___TC  C  TC       TG
GAM244 SCEL       TAAGGACCTCTATTGAGCAG    3638        GTTTG    CAG
                        TAAGGACCT    GGGCAG
                        |||||||||    ||||||
                        ATTCCTGGA    CTCGTC
                          GATAA    III
GAM244 SCEL       TAAGGACCTCTATTGAGCAG    3638        GTTTG  I
                        AAGGACCT    GGGCA
                        ||||||||    |||||
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                        TTCCTGGA   CTCGT
                          GATAA     I
GAM244 SLA2          CTGTTTATGGAGGCAGCAGG    3629    __ _        III
                        CTGTT TGG GGCAGCAG
                        ||||| ||| |||||||||
                        GACAA ACC CCGTCGTC
                          AT  T     CII
GAM244 SLC22A1       GACCTGTTTTGGGGTGCAG     3635        _  CA  II
                        GACCTGTTT GGGG GCA
                        ||||||||| |||| |||
                        CTGGACAAA CCCC CGT
                          A  A_  CI
GAM244 SLC22A1       GACCTGTTTTGGGGTGCAG     3635 TAAGGACCTG    CA
                          TTTGGGG GCAG
                          ||||||| ||||
                          AAACCCC CGTC
                        ACA_____      A_
GAM244 XPC          GGGCCTGTAGTGGGGCAGCAG   3636 GA    T_       I
                          CCTGT TGGGGCAGCA
                          ||||| ||||||||||
                          GGACA ACCCCGTCGT
                          C_    TC       I
GAM244 XPC          GGGCCTGTAGTGGGGCAGCAG   3636 TAAGGA    T_      G
                          CCTGT TGGGGCAGCAG
                          ||||| |||||||||||
                          GGACA ACCCCGTCGTC
                        _____    TC       G
GAM245 ASTN        TAAG-ACCTGTTT--GGCAGC    3640 TA        GG    A
                        AGGACCTGTTT GGCAGC
                        |||||||||| ||||||
                        TTCTGGACAAA CCGTCG
                        A_        __   I
GAM245 CA7         AGGGCCTGCCCGTGGCAGCAGG    3626 TAA  A      G
                          GG CCTGTTTG GGCAGCAGG
                          || ||||||| |||||||||
                          CC GGACGGGC CCGTCGTCC
                        ___ _        A
GAM245 CDK10        CCTTTTTCTGGGGGCAGCAG     3627 TAAGGAC  TTT
                          CTG GGGGCAGCAG
                          ||| ||||||||||
                          GAC CCCCGTCGTC
                        A_____   ___
GAM245 GRLF1       TAATGGACTGTGTTCTGGGGCAGC  3637 TAA_  C_  _       AGGI
                          GGAC TGT TTGGGGCAGC
                          |||| ||| ||||||||||
                          CCTG ACA GACCCCGTCG
                        ATTA  AC A        IIIG
GAM245 HAMP        GACCTATGTTCTGGGGCAGCAGG   3634 TAAGGACC  _        I
                          TGT TTGGGGCAGCAGG
                          ||| |||||||||||||
```

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                              ACA GACCCCGTCGTCC
                    AT_____    A         T
GAM245  INHBC       TAAGCCTCTATTTTGGGCAGCAG  3641   GAC    G      GI
                        TAAG  CTGTTT GGGCAGCAG
                        |||  |||||| |||||||||
                        ATTC  GATAAA CCCGTCGTC
                         GGA    A      II
GAM245  MAGEA12        GACTCTGGTCAGGGCAGCAGG    3633 TAAGGAC  T TG
                            CTG T GGGCAGCAGG
                            ||| | |||||||||||
                            GAC A CCCGTCGTCC
                        _____ C GT
GAM245  MAGEA2         GACTCTGGTCAGGGCAGCAGG    3633 TAAGGAC  T TG
                            CTG T GGGCAGCAGG
                            ||| | |||||||||
                            GAC A CCCGTCGTCC
                        _____ C GT
GAM245  MAGEA4         GACTCTGCTCAGGGCAGCAGG    3632 TAAGGAC    TG
                            CTGTT GGGCAGCAGG
                            ||||| ||||||||||
                            GACGA CCCGTCGTCC
                        _____  GT
GAM245  MAGEA9         GACTCTGGTCAGGGCAGCAG    3630 TAAGGAC  T TG
                            CTG T GGGCAGCAG
                            ||| | |||||||||
                            GAC A CCCGTCGTC
                        _____ C GT
GAM245  MSI1         GACGCTGTTGGGGGCAGCAGG    3631 TAAGGAC    T
                            CTGTT GGGGCAGCAGG
                            ||||| |||||||||||
                            GACAA CCCCGTCGTCC
                        _____  C
GAM245  MYL4       TAAGGTCCT---TGGGGCAG     3639   A GTT    CA
                        TAAGG CCT  TGGGGCAG
                        ||||| ||| ||||||||
                        ATTCC GGA  ACCCCGTC
                         A ___    II
GAM245  NUP98       AGGATGCTGCTTCTGGCAGCAGG  3625 TAAGGAC    GG    I
                            CTGTTT GGCAGCAGG
                            |||||| ||||||||||
                            GACGAA CCGTCGTCC
                        CTAC___    GA      C
GAM245  RAB6A       AGGAGCCCGGCTGGAGGGCAGCAGG 3624 TAA GA   T  __      II
                          G CCTG TTGG GGCAGCAGG
                          | |||| |||| |||||||||
                          C GGGC GACC CCGTCGTCC
                        ___ TC  C  TC     TG
GAM245  SCEL       TAAGGACCTCTATTGAGCAG     3638      GTTTG    CAG
                        TAAGGACCT   GGGCAG
                        |||||||||   |||||
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                              ATTCCTGGA    CTCGTC
                                GATAA      III
GAM245  SLC22A1       GACCTGTTTTGGGGTGCAG      3635 TAAGGACCTG     CA
                              TTTGGGG  GCAG
                              ||||||| ||||
                              AAACCCC  CGTC
                         ACA_____       A_
GAM245  XPC        GGGCCTGTAGTGGGGCAGCAG      3636 TAAGGA    T_        G
                             CCTGT  TGGGGCAGCAG
                             ||||| ||||||||||
                             GGACA  ACCCCGTCGTC
                        _____        TC       G
GAM246  ABCC3       AAGGAGCCGTTGCGCTGCAGCAGG  3663 A  C    _  G      I
                             GGA CTGTT TG TGCAGCAG
                             ||| ||||| || ||||||||
                             CCT GGCAA GC ACGTCGTC
                        _  C    C G       I
GAM246  ABCC3       AAGGAGCCGTTGCGCTGCAGCAGG  3663 TA   C    _  G       I
                             AGGA CTGTT TG TGCAGCAGG
                             |||| ||||| || |||||||||
                             TCCT GGCAA GC ACGTCGTCC
                        __   C    C G        C
GAM246  ASTN       TAAG-ACCTGTTTG--GCAGC     3674 TA           _ AI
                             AGGACCTGTTTGGT GC
                             |||||||||||||| ||
                             TTCTGGACAAACCG CG
                        A_           T II
GAM246  ASTN       TAAG-ACCTGTTTG--GCAGC     3674 TA          GT   A
                             AGGACCTGTTTG GCAGC
                             |||||||||||| |||||
                             TTCTGGACAAAC CGTCG
                        A_          __   I
GAM246  CD5       GAGCTGTT--GTGCAGCAG        3669  C    TG       I
                             GA CTGTT GTGCAGCA
                             || ||||| ||||||||
                             CT GACAA CACGTCGT
                        C   __       C
GAM246  COL15A1       TATGAACCTGTTTGTTTCAG      3673 AA        GTG I
                             GGACCTGTTTG  CA
                             |||||||||| ||
                             CTTGGACAAAC  GT
                        TA          AAA  I
GAM246  COL15A1       TATGAACCTGTTTGTTTCAG      3673 TAA        GTG  CAG
                             GGACCTGTTTG  CAG
                             |||||||||| |||
                             CTTGGACAAAC  GTC
                        ATA          AAA  III
GAM246  DDX11       TAAGGACCTGTAGCTGTGCAG     3670        TTG_    CAGG
                             TAAGGACCTGT  GTGCAG
                             |||||||||||  ||||||
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                        ATTCCTGGACA   CACGTC
                          TCGA      IIIG
GAM246 DDX11          TAAGGACCTGTAGCTGTGCAG    3670 A        TTG_    I
                        AGGACCTGT   GTGCA
                        |||||||||   |||||
                        TCCTGGACA   CACGT
                          _        TCGA    I
GAM246 DRD1          AGCACCTGTTTGTATACAGCA    3667 GG        _    I
                        ACCTGTTTG GTGCAGC
                        ||||||||| |||||||
                        TGGACAAAC TATGTCG
                          G_       A    I
GAM246 DRD1          AGCACCTGTTTGTATACAGCA    3667 TAAGG       _
                        ACCTGTTTG GTGCAGCAGG
                        ||||||||| ||||||||||
                        TGGACAAAC TATGTCGTTT
                          G____      A
GAM246 GAS7          TAAGG----GTTTGGTGCAG    3672   ACCT       C
                        TAAGG  GTTTGGTGCAG
                        |||||  ||||||||||
                        ATTCC  CAAACCACGTC
                          ____       I
GAM246 GAS7          TAAGG----GTTTGGTGCAG    3672 _   ACCT
                        AAGG   GTTTGGTGCA
                        ||||   ||||||||||
                        TTCC   CAAACCACGT
                        A   ____
GAM246 IL18          CTGTGTAGACTGCAGCAGG     3668   T __      III
                        CTGT TGG  TGCAGCAG
                        |||| |||  ||||||||
                        GACA ATC  ACGTCGTC
                          C   TG     CII
GAM246 RNTRE          TAATGGCCTGATGAGGTGCAGCA   3671 AA A   TTT_     I
                        GG CCTG   GGTGCAGC
                        || ||||   ||||||||
                        CC GGAC   CCACGTCG
                        TA _   TACT        I
GAM246 RNTRE          TAATGGCCTGATGAGGTGCAGCA   3671 TAA_ A   TTT_      GGI
                        GG CCTG   GGTGCAGCA
                        || ||||   |||||||||
                        CC GGAC   CCACGTCGT
                        ATTA _   TACT       III
GAM246 RPL29          AAGGGGCTGC--GGTGCAGCA    3665_ AC   TT      I
                        AGG CTGT  GGTGCAGC
                        ||| ||||  ||||||||
                        TCC GACG  CCACGTCG
                        T  CC  __       I
GAM246 RPL29          AAGGGGCTGC--GGTGCAGCA    3665 TA AC   TT       G
                        AGG CTGT  GGTGCAGCA
                        ||| ||||  |||||||||
```

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                              TCC  GACG  CCACGTCGT
                               __   CC    __       G
GAM246  SCEL          TAAGGACCTCTATTGAGCAG      3638      G TGG  C
                          TAAGGACCT TT  TG AGCAG
                          |||||||| ||  || |||||
                          ATTCCTGGA GA  AC TCGTC
                               _  TA_ _
GAM246  SCEL          TAAGGACCTCTATTGAGCAG      3638      GT_  T  I
                           AAGGACCT  TTGG GCA
                           ||||||||  |||| |||
                           TTCCTGGA  AACT CGT
                             GAT   _   I
GAM246  SCN3A          AAGG---TGTTTGGTGTAG      3664  ACC      CA
                          AAGG  TGTTTGGTG
                          ||||  |||||||||
                          TTCC  ACAAACCAC
                            ___       AT
GAM246  SCN3A          AAGG---TGTTTGGTGTAG      3664 TA  ACC      C C
                           AGG  TGTTTGGTG AG
                           |||  ||||||||| ||
                           TCC  ACAAACCAC TC
                            __  ___     A A
GAM246  SLC22A1         GACCTGTTTTGGGGTGCAG      3635      ___     III
                           GACCTGTTT  GGTGCA
                           |||||||||  ||||||
                           CTGGACAAA  CCACGT
                             ACC     CII
GAM246  SLC7A8      AAGGATCCTAAGTCCTTAGTGCAGCAGG3662 TA   _  ____           III
                          AGGA CCTG   TTTGGTGCAGCAGG
                          |||| ||||   |||||||||||||
                          TCCT GGAT    GAATCACGTCGTCC
                           __   A   TCAG           TII
GAM246  SLC7A8      AAGGATCCTAAGTCCTTAGTGCAGCAGG3662 AGGA   ____           I
                           CCTG   TTTGGTGCAGCAG
                           ||||   |||||||||||||
                           GGAT   GAATCACGTCGTC
                            ____    TCAG         I
GAM246  TEM6        AGGCACTTGGTTTGGTGCATCA     3666 AGGACCT       GI
                             GTTTGGTGCA
                             ||||||||||
                             CAAACCACGT
                          TGAAC__       AG
GAM246  TEM6        AGGCACTTGGTTTGGTGCATCA     3666 TAA G  CT_      G  G
                           G AC  GTTTGGTGCA CAG
                           | ||  |||||||||| |||
                           C TG  CAAACCACGT GTT
                            ___ G  AAC       A A
GAM247  ATP6V0E       CAAAACAGGCAAGTCAAGAAAAGTGG 3688 TACA           AAC____        II
                          AGACAGGCAAG    AAGTGG
                          |||||||||||    ||||||
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                        TTTGTCCGTTC    TTCACC
                   ____          AGTTCTT    AG
GAM247 ATRN          TAAAAGACCATGTTCAAGAACAACTG 3693 TAC    AGG___     G GII
                        AAGAC    CAAGAACAA TG
                        IIIII     IIIIIIIII II
                        TTCTG    GTTCTTGTT AC
                     ATT   GTACAA     G III
GAM247 BLNK          CAGGTCAGGCAATAGAACAAGT   3687 TACAAGA    __      GG
                        CAGGCA  AGAACAAGT
                        IIIIII IIIIIIIII
                        GTCCGT  TCTTGTTCA
                     CCA____     TA    GG
GAM247 BLTR2         TACAAGACAAGAAAGGA-AAG   3694      C  AACAAGTG
                        TACAAGACAGG AAG
                        IIIIIIIIIII III
                        ATGTTCTGTTC TTC
                         T  CTTTCIII
GAM247 CYP17         CAGGCAAGATAGACAGCAGTGG   3690 TACA    G AGAACAA
                           AGACAG CA    GTGG
                           IIIIII II    IIII
                           TCTGTC GT    CACC
                     CTA_    _ _____
GAM247 DPYSL3        AGACAGTCGTGAAGAACAAG    3683 TACAAGACAGGC    TG
                           AAGAACAAG
                           IIIIIIIII
                           TTCTTGTTC
                     TCAGCAC_____     CG
GAM247 EIF4EBP2      ACAGGAAAGGCAAGAA-AACTGG   3682 TA A C     C G
                        CA GA AGGCAAGAA AA TGG
                        II II IIIIIIIII II III
                        GT CT TCCGTTCTT TT ACC
                        __ C T     _ G
GAM247 FLRT2         ACAAGAC---CAAGAACAAG    3679 TA    AGG     T
                        CAAGAC  CAAGAACAAG
                        IIIIII  IIIIIIIIII
                        GTTCTG  GTTCTTGTTC
                        __    ___         T
GAM247 FOXO1A        TACAAGACA---AAG--CAAGTG  3695      _  AACAAGT
                        TACAAGACAG GCAAG
                        IIIIIIIIII IIIII
                        ATGTTCTGTT CGTTC
                         T  ACIIIGG
GAM247 KCNJ1         TACAAGACAAAAGTAAGATCA   3692       __ C  A AGTGG
                        TACAAGACA GG AAGA CA
                        IIIIIIIII II IIII II
                        ATGTTCTGT TC TTCT GT
                        TT A  A IIIGG
GAM247 LARGE         AAG-CAGGCAAGAACCAGAGG   3677 TACAAGA      A T
                        CAGGCAAGAAC AG G
                        IIIIIIIIIII II I
```

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                          GTCCGTTCTTG TC C
                          _____        G  T
GAM247 MTMR2         ACAAGACAGAC-TGAACCAAAGTGG  3678 TA      AA  __    I
                         CAAGACAGGC  GAAC  AAGTGG
                         ||||||||| |||| |||||
                         GTTCTGTCTG  CTTG  TTCACC
                              __      A_   GT   C
GAM247 PCSK1        ACAAGACAGG---GAACAAG    3680 TA     CAA
                        CAAGACAGG  GAACAAGT
                        ||||||||| ||||||||
                        GTTCTGTCC  CTTGTTCG
                          __     ___
GAM247 PIK4CB         CAAGACAGGCAGGGAAAAAG     3686 TACA      A_  C
                         AGACAGGCA  GAA AAGTG
                         ||||||||| ||| |||||
                         TCTGTCCGT  CTT TTCGT
                         ____        CC  T
GAM247 PRKAB1       CAAGCCGCGGCAAGAACGCAAGGGG 3684 TACAAGACA     __  T  II
                         GGCAAGAAC  AAG  GG
                         ||||||||| ||| ||
                         CCGTTCTTG  TTC CC
                      TCGGCG___       CG  _ CG
GAM247 RP42          CAAGACAGGAAACAAAACAGT    3689 TACA     CA__    A  G
                         AGACAGG   AGAACA GTG
                         ||||||| |||||| |||
                         TCTGTCC   TTTTGT CAT
                         ____       TTTG   _  G
GAM247 TEK          TACAAGTTAGAGGCAAGAA    3691     AC__       CAAGTG
                       TACAAG  AGGCAAGAA
                       |||||| |||||||||
                       ATGTTC  TCCGTTCTT
                        AATC      IIIGGT
GAM247 TPI1        ACATGATCCGCAAGAACAAGT    3681 TACAAGACAG        G
                          GCAAGAACAAGTG
                          ||||||||||||
                          CGTTCTTGTTCAT
                       GTACTAGG__        I
GAM247 WNT10B       CAA-ACAGGAACCAAGAACAAGT  3685 TACAA   ___       GG
                        GACAGG  CAAGAACAAGT
                        |||||| |||||||||||
                        TTGTCC  GTTCTTGTTCA
                         _____    TTG     GA
GAM248 ADRBK1       CCAGCCTCCTTGCTGTGCTGCC   3704 TACC    CA_  G
                        AGCCTCC  CTGTG TGCCT
                        ||||||| ||||| |||||
                        TCGGAGG  GACAC ACGGG
                        ____      AAC   G
GAM248 CORO2B        CCAGCACTTACACTGTGGTACCT  3702 TACC _ CC         I
                        AGC CT  CACTGTGGTGCCT
                        ||| || |||||||||||||
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                        TCG GA  GTGACACCATGGA
                        ____   T  AT            A
GAM248 DRG2             TACCAGCCTGGCACTGAGCATGCC  3708      CC     TG_    TI
                        TACCAGCCT CACTG  GTGCC
                        ||||||||| |||||  |||||
                        ATGGTCGGA GTGAC  TACGG
                               CC    TCG    II
GAM248 HDAC5           ACCAGCCTCCCATCAGTGCTG   3699 TA       CTG    CT
                        CCAGCCTCCCA TGGTGC
                        ||||||||||| ||||||
                        GGTCGGAGGGT GTCACG
                          __        A__    AC
GAM248 IRAK1          CCAGCCTCCTCACTGGATGATGCC  3703 TACC     _  __      TI
                        AGCCTCC CACTG TGGTGCC
                        ||||||| ||||| |||||||
                        TCGGAGG GTGAC ACTACGG
                          ____     A  CT   TC
GAM248 JPH3          ACCAGGC--CCACTGTGGTG    3701 TA  CCT       C
                        CCAG CCCACTGTGGTG
                        |||| |||||||||||
                        GGTC GGGTGACACCAC
                          __   C__       A
GAM248 PAX4          ACCACCTCTCCCACTGCCCTGCC  3698 _  AGC       GG   I
                        TACC CTCCCACTGT TGCCT
                        |||| |||||||||| |||||
                        GTGG GAGGGTGACG ACGGG
                          G  A__      GG   I
GAM248 PPARA           CCAGCCTCCAGAACTGTGGTG  3705 TACC     C__       CCT
                        AGCCTCC ACTGTGGTG
                        ||||||| |||||||||
                        TCGGAGG TGACACCAC
                          ____     TCT     TGI
GAM248 SH3BP2         CCAGCCTCGG-CTGTGGTGC    3706 TACC    CCA       C
                        AGCCTC CTGTGGTGC
                        |||||| |||||||||
                        TCGGAG GACACCACG
                          ____    CC_      T
GAM248 SLC39A1      CCAGCCTCCCA-TGT-GAGCCT   3707 TACC     C    T
                        AGCCTCCCA TGTGG GCC
                        ||||||||| ||||| |||
                        TCGGAGGGT ACACT CGG
                          ____    _  _
GAM248 SREBF2       ACCAGCCTCCCAGGGCTGG-GCC  3700 TA       CT _ T
                        CCAGCCTCCCA G TGG GCCT
                        ||||||||||| | ||| ||||
                        GGTCGGAGGGT C ACC CGGG
                          __       CC G  _
GAM249 ARL4         GAGTCT-GGGTCCAAATGAGAA   3716 TAGAA  A  AAG
                        TCT GGG  AAATGAGAA
                        ||| |||  |||||||||
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                            AGA CCC  TTTACTCTT
                        C____   _  AGG
GAM249 CDC25C           AATCTAGGG--GAAAGGAG      3712 TAGAAT    AA   T
                        CTAGGG GAAA GAG
                        ||||||  ||||  |||
                        GATCCC CTTT CTC
                        _____    __   C
GAM249 GPR81            AGAAACTTCAGCCAGGAAATGAGA  3713 TAGAAT____      AGAA    AI
                        CTAGGGA  ATGAGA
                        |||||||  ||||||
                        GGTCCTT  TACTCT
                        CTTTGAAGTC    ____     CI
GAM249 PDE4B            ATCTCAAGGA-GAAATGAG      3715 TAGAATC    A
                        TAGGGA GAAATGAG
                        ||||||| ||||||||
                        GTTCCT CTTTACTC

                        _____    _
GAM249 TDGF1            AATTTAAG-AAGAAAATGAGAA    3711 TAGAATC    AG
                        TAGGGA  AAATGAGAA
                        ||||||  |||||||||
                        ATTCTT  TTTACTCTT
                        A_____     CT
GAM249 TGFBR2           AGAA-CTAG--AAGAAATG      3714 TAGAATCTAG      A
                        GGAAGAAATG
                        ||||||||||
                        TCTTCTTTAC
                        CTTGA_____       A
GAM250 BACE             ATGATCTTGGGATGCTGGAT     3721 CA      CGCC  C  CT
                        TGATCTTG   GCT GAT
                        ||||||||   |||  |||
                        ACTAGAAC   CGA CTA
                        __        CCTA  C  AI
GAM250 BIN1             GATCTTGCGCGCCGCGCTC       3729 CATGAT    C  _ A
                        CTTGCGC GCT CG TCT
                        ||||||| ||| || |||
                        GAACGCG CGG GC AGG
                        _____       _  C G
GAM250 CD83             TGCGCCGCTGCCACGAGCTG     3734 ___    T  T  CC  CGATCT
                        CATGA CT GCG  GCT
                        ||||| || ||| |||
                        GTGCT GA CGT  CGA
                        ACG    C  _  CT  CIIIGT
GAM250 DDX10            ATCATCCACC-CTCGATCTG      3720 CATGATCTTG  G
                        CGCC CTCGATCT
                        |||| ||||||||
                        GTGG GAGCTAGA
                        AG_____    _
GAM250 EGLN1           TCTTGCGCCCCGTTTCGACCT      3731 CATGATCTT G  C_
                        GC CCG  TCGATCTG
                        || ||| |||||||||
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                              CG GGC  AGCTGGAT
                             G_____  G  AA
GAM250 MAP3K8        TGGAGGCACATTCATGGGTC   3732  A  __        GCTTG
                         TG AGGC  GTTCATGGGTC
                         II IIII  IIIIIIIIIII
                         AC TCCG  TAAGTACCCAG
                          C   TG        IIIAG
GAM250 MAP3K8        TGGAGGCACATTCATGGGTC   3732  A  __        III
                          TG AGGC  GTTCATGGGT
                          II IIII  IIIIIIIIII
                          AC TCCG  TAAGTACCCA
                           C   TG        GII
GAM250 MSL3L1       CATGATCTTCTGCTGC-CCATCT  3724      GC C  G  G
                         CATGATCTT GC GCTC ATCT
                         IIIIIIIII II IIII IIII
                         GTACTAGAA CG CGGG TAGA
                          GA  A   _    I
GAM250 NCOA6IP       CATGATCTTTGTC-CTCGCACTG  3726      GCGCCG  AT I
                         CATGATCTT   CTCG CTG
                         IIIIIIIII   IIII III
                         GTACTAGAA   GAGC GAC
                           AACAG_   GT  I
GAM250 NR1I2        GATGGCCTATCCTTGGTCGCTTG   3728 AA  GT_ ATG      I
                           GGC TC GGTCGCTT
                           III II IIIIIIII
                           CCG AG CCAGCGAA
                          A_  GAT GAA       I
GAM250 NR1I2        GATGGCCTATCCTTGGTCGCTTG   3728 TGAA  GT_ ATG       AI
                            GGC TC GGTCGCTTG
                            III II IIIIIIIII
                            CCG AG CCAGCGAAC
                          TA__ GAT GAA       CI
GAM250 PDXK         CACGGTCTC-CGCCGCTCGCTC   3723  A  G     A TG
                          CATG TCTT CGCCGCTCG TC
                          IIII IIII IIIIIIIII II
                          GTGC AGAG GCGGCGAGC AG
                           C   _     G II
GAM250 SLC17A4       GAAGGCAGATATCATGGGTCACT   3727 A_ CGT         I
                           AGG  TCATGGGTCGC
                           III  IIIIIIIIIII
                           TCT  AGTACCCAGTG
                          CG  AT_         I
GAM250 SLC17A4       GAAGGCAGATATCATGGGTCACT   3727 TG    T___        TGAI
                          AAGGCG  TCATGGGTCGCT
                          IIIIII  IIIIIIIIIIII
                          TTCCGT  AGTACCCAGTGA
                           __   CTAT        CIII
GAM250 TGFBR2       AATGCTGTCATGGGTCCCTT    3719 AG GT      G I
                          GC  TCATGGGTC CT
                          II  IIIIIIIII II
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                              CG  AGTACCCAG GA
                              TA AC        G  I
GAM250 TGFBR2       AATGCTGTCATGGGTCCCTT    3719 TGAAG  GT      G   G
                              GC  TCATGGGTC CTT
                              || ||||||||| |||
                              CG  AGTACCCAG GAA
                              A____  AC       G  G
GAM250 UBQLN1       TGTTCAGGCGCCGCTCGCTC    3733 CATGA  TT      A  T
                              TC  GCGCCGCTCG TC
                              || ||||||||| ||
                              AG  CGCGGCGAGC AG
                              A____ TC      G  T
GAM250 USP6         GTTCATGGGAATTCCCTTG     3730         ___  G  III
                              GTTCATGGG  TC CTT
                              |||||||||  || |||
                              CAAGTACCC  AG GAA
                              TTA  G  CII
GAM250 USP6         GTTCATGGGAATTCCCTTG     3730 TGAA  C   ATGG  _   G
                              GG GTTC  GT CGCTT
                              || ||||   || |||||
                              CC TAAG   CA GTGAG
                              ____  T  GGAA  T   I
GAM250 USP6         CATGATCTTGC-TTTCTCCATCT  3725         GCCG  G  G
                              CATGATCTTGC   CTC ATCT
                              |||||||||||   ||| ||||
                              GTACTAGAACG   GAG TAGA
                              AAA_  G   I
GAM250 WHSC1        ATGATCTTG-GTCTCTGGGTACTG  3722 CA       CGCCG  GAT___  I
                              TGATCTTG  CTC    CTG
                              ||||||||  |||    |||
                              ACTAGAAC  GAG    GAC
                              __      CA___  ACCCAT  C
GAM251 CD59         GAA-AGCGT--TCCATGTGAGA    3743  T   CT       C
                              GAA AGCGT TCCATGTGGGA
                              ||| ||||| |||||||||||
                              CTT TCGCA AGGTACACTCT
                              _   __        I
GAM251 CTSH         GAATATTCGTGGTCCATGTGG     3740  G_  CT       GACA
                              GAATA CGT TCCATGTGG
                              ||||| ||| |||||||||
                              CTTAT GCA AGGTACACC
                              AA  CC       IIIA
GAM251 HAP1         GAAAAGCCTCCAACATGTGGGA    3744  T  G  TC      CA
                              GAA AGC TCT CATGTGGGA
                              ||| ||| ||| |||||||||
                              CTT TCG AGG GTACACCCT
                              T  G  TT       II
GAM251 IDH3B        GAATCATCATCATCCATGTGG     3738  AG_  T       GACA
                              GAAT CGTC TCCATGTGG
                              |||| |||| |||||||||
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                    CTTA  GTAG AGGTACACC
                    GTA   T      IIIA
GAM251  PRDM2       GAAGGGGGTTTTCCATGTG    3741 GAATAGC  C      GGAC
                    GT TTCCATGTG
                    II IIIIIIIII
                    CA AAGGTACAC
                    CTTCCCC A      IIIA
GAM251  SLA         GAATTTGAGTCT-CCATGTGG  3739 GAATAGC_  T      GAC
                    GTCT CCATGTGG
                    IIII IIIIIIII
                    CAGA GGTACACC
                    CTTAAACT  _      III
GAM251  STK9        AATTGGTTCTTCCATGAGAGA  3737 GAATAGCG     T    CA
                    TCTTCCATG GGGA
                    IIIIIIIII IIII
                    AGAAGGTAC CTCT
                    TAACCA__     T  CI
GAM251  VANGL2      GAA-AG-GTCCTCCATGTGG   3742   T C       GA
                    GAA AG GTCTTCCATGTGG
                    III II IIIIIIIIIIII
                    CTT TC CAGGAGGTACACC
                    _ _          II
GAM252  ANK2        ATCTTTGG-TCACAAATTA    3753     T   CTI
                    ATCTTTGGT CACAGA
                    IIIIIIIII IIIIII
                    TAGAAACCA GTGTTT
                    _      AAT
GAM252  ANK2        ATCTTTGG-TCACAAATTA    3753 TGAAATCT   T   CT
                    TTGGT CACAGA
                    IIIII IIIIII
                    AACCA GTGTTT
                    _____  _   AA
GAM252  CA5B        TGAAATCTTGATCAGTTCCCAG 3756     ___ TG  A ACTAT
                    TGAAATCT  T GTTC CAG
                    IIIIIIII  I IIII III
                    ACTTTAGA  A CAAG GTC
                    ACT GT   G  IIITA
GAM252  CA5B        TGAAATCTTGATCAGTTCCCAG 3756     ___ TG  ACAIII
                    TGAAATCT  T GTTC
                    IIIIIIII  I IIII
                    ACTTTAGA  A CAAG
                    ACT GT   GGTCII
GAM252  CPSF6       AAATCTTTGATTAAGTAACTAT 3751        CACA  I
                    AATCTTTGGTT  GACTA
                    IIIIIIIIII   IIIII
                    TTAGAAACTAA  TTGAT
                    TTCA   I
GAM252  CPSF6       AAATCTTTGATTAAGTAACTAT 3751 TGAA       CACA
                    ATCTTTGGTT  GACTAT
                    IIIIIIIIII   IIIII
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                      TAGAAACTAA   TTGATA
                   ____           TTCA
GAM252 NAB1        ATCTTCCTGGTTTCCACAGACTA   3752   __   __        IIIT
                      ATCTT TGGT TCACAGACT
                      IIIII IIII IIIIIIIII
                      TAGAA ACCA GGTGTCTGA
                         GG   AA     TIII
GAM252 NAB1        ATCTTCCTGGTTTCCACAGACTA   3752 TGAAATC    __        I
                      TTTGGT TCACAGACTAT
                      IIIIII IIIIIIIIIII
                      GGACCA GGTGTCTGATG
                   A_____    AA       G
GAM252 PABPC4         AAATCTTTGTGGGCGCCGACT   3747 TGAA    GTTCACA_ AT
                      ATCTTTG     GACT
                      IIIIIII     IIII
                      TAGAAAC     CTGA
                   ____        ACCCGCGG  GC
GAM252 PCDHB16       TGAAAAGTT-GGTTCACAGA     3759    TCT        CTA
                      TGAAA TTGGTTCACAGA
                      IIIII IIIIIIIIIIII
                      ACTTT AACCAAGTGTCT
                         TC_       III
GAM252 PCDHB16       TGAAAAGTT-GGTTCACAGA     3759 _  TCT        I
                       GAAA TTGGTTCACAG
                       IIII IIIIIIIIIII
                       CTTT AACCAAGTGTC
                    A  TC_        I
GAM252 PRKWNK3       GAATTCTATTTAGGTTTCACAGACT 3754 AAATCTTT   _    I
                        GGTT CACAGAC
                        IIII IIIIIII
                        CCAA GTGTCTG
                    GATAAAT_   A    I
GAM252 PRKWNK3       GAATTCTATTTAGGTTTCACAGACT 3754 TGAAA  TT___  _      ATII
                        TCT   GGTT CACAGACT
                        III    IIII IIIIIIII
                        AGA    CCAA GTGTCTGA
                    TTA__  TAAAT  A     CIII
GAM252 ROCK2        AAATATTTGTAGTCACAGACTA    3748 AATC   GT_       I
                       TTTG TCACAGACT
                       IIII IIIIIIIII
                       AAAC AGTGTCTGA
                    ATA_  ATC       I
GAM252 ROCK2        AAATATTTGTAGTCACAGACTA    3748 TGAAATC   GT_      TI
                       TTTG TCACAGACTA
                       IIII IIIIIIIIII
                       AAAC AGTGTCTGAT
                    TATA___  ATC      TA
GAM252 RPH3AL       TGAAGTCA--GGTTCACAG       3758   A TTT       ACT
                      TGAA TC GGTTCACAG
                      IIII II IIIIIIIII
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                    ACTT AG  CCAAGTGTC
                     C T__      III
GAM252 RPH3AL       TGAAGTCA--GGTTCACAG      3758   A TTT     I
                     TGAA TC  GGTTCACA
                     |||| ||  ||||||||
                     ACTT AG  CCAAGTGT
                      C T__      C
GAM252 SCN1A        TGAGAGCTTC--TTCACAGACT    3760   AAT  GG       A
                     TGA  CTTT TTCACAGACT
                     ||| |||| ||||||||||
                     ACT  GAAG AAGTGTCTGA
                      CTC  __      I
GAM252 SCN1A        TGAGAGCTTC--TTCACAGACT    3760 _ AAT  GG     I
                      GA  CTTT TTCACAGAC
                      || |||| |||||||||
                      CT  GAAG AAGTGTCTG
                      A CTC  __      I
GAM252 SEDL         GACATCTTTGGTTGTCACACT     3755 AA        __    GAI
                      ATCTTTGGT TCACA
                      ||||||||| |||||
                      TAGAAACCA AGTGT
                      G_      AC  GII
GAM252 SEDL         GACATCTTTGGTTGTCACACT     3755 TGAA      CA G AT
                       ATCTTTGGTT CA ACT
                       |||||||||| || |||
                       TAGAAACCAA GT TGA
                       TG__       CA G AI
GAM252 SLC21A9      AACTCTTTGGTT--CAGACTA    3750 AA_       CA  I
                       TCTTTGGTTCA GACT
                       |||||||||| ||||
                       AGAAACCAAGT CTGA
                       TTG       __  I
GAM252 SLC21A9      AACTCTTTGGTT--CAGACTA    3750 TGAAA     CA
                       TCTTTGGTTCA GACTA
                       |||||||||| |||||
                       AGAAACCAAGT CTGAT
                       G____       __
GAM252 SRD5A2       TGAAATCTTCTGGAAAACAGA    3757      _ TTC   CTAT
                      TGAAATCT TTGG ACAGA
                      |||||||| |||| |||||
                      ACTTTAGA GACC TGTCT
                       A  TTT  IIIT
GAM252 SRD5A2       TGAAATCTTCTGGAAAACAGA    3757 G   _ TTC  I
                       AAATCT TTGG  ACAG
                       |||||| |||| ||||
                       TTTAGA GACC  TGTC
                       _  A  TTT  I
GAM252 SSRP1        AAATCATT--TTCACAGAC      3749    TTTGG     I
                       AAATC  TTCACAGA
                       ||||| |||||||||
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                              TTTAG    AAGTGTCT
                              TAA__        G
GAM252  SSRP1        AAATCATT--TTCACAGAC      3749 TGAA  TTTGG
                         ATC    TTCACAGACT
                         |||    ||||||||||
                         TAG    AAGTGTCTGG
                         ____      TAA__
GAM253  BSG          TGAAACACTTCAGAAGGAA     3777    G       TGGT
                         TGGAATA TTCAGAAGGAA
                         ||||||| |||||||||||
                         ACTTTGT AAGTCTTCCTT
                              G       IIIA
GAM253  BSG          TGAAACACTTCAGAAGGAA     3777    G       II
                         TGGAATA TTCAGAAGGA
                         ||||||| ||||||||||
                         ACTTTGT AAGTCTTCCT
                              G        TI
GAM253  CHD4       TGGAAGATGGGCAGAAGGAA-GGT 3775    TAGTT_      T  AI
                         TGGAA    CAGAAGGAA GGT
                         |||||    |||||||||| |||
                         ACCTT    GTCTTCCTT CCA
                           CTACCC       _  II
GAM253  CHD4       TGGAAGATGGGCAGAAGGAA-GGT 3775    TAGTT_      T  I
                         GGAA    CAGAAGGAA GG
                         ||||    ||||||||| ||
                         CCTT    GTCTTCCTT CC
                           CTACCC      _  I
GAM253  DNAJB9       AATAGTTCACAGAAAATTGT     3764      GA   TGGI
                         ATAGTTCA AGGAA
                         |||||||| |||||
                         TATCAAGT TCTTT
                             G_    TAAC
GAM253  DNAJB9       AATAGTTCACAGAAAATTGT     3764 TGGAAT    GA   TG_
                         AGTTCA AGGAA  GT
                         |||||| ||||| ||
                         TCAAGT TCTTT  CA
                         _____     G_   TAA
GAM253  DRD2       GGAA-AGGCCAGAAGGAAT      3771   T TT       I
                         GGAA AG  CAGAAGGAA
                         |||| ||  |||||||||
                         CCTT TC  GTCTTCCTT
                          _ CG        A
GAM253  DRD2       GGAA-AGGCCAGAAGGAAT      3771 TG  T TT       G
                         GAA AG  CAGAAGGAATG
                         ||| ||  |||||||||||
                         CTT TC  GTCTTCCTTAT
                          __ _ CG        I
GAM253  DTR       TGTAACAGTTCAGA---AATGG    3778 G           GAAI
                         TG AATAGTTCAGAAG
                         || |||||||||||
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                        AC TTGTCAAGTCTTT
                        A          ACCI
GAM253  DTR             TGTAACAGTTCAGA---AATGG   3778  G          GGA    T
                        TG AATAGTTCAGAA  ATGG
                        || ||||||||||    ||||
                        AC TTGTCAAGTCTT  TACC
                        A           ___   I
GAM253  GTF2F1          GAAGATTCCAGAAGGAAGGG     3767 GAATAG          TI
                             TTCAGAAGGAA
                             |||||||||||
                             AGGTCTTCCTT
                        TCTA__          CC
GAM253  GTF2F1          GAAGATTCCAGAAGGAAGGG     3767 TGGAATAG         T
                             TTCAGAAGGAA GGT
                             ||||||||||| |||
                             AGGTCTTCCTT CCG
                        TCTA____           C
GAM253  IHPK1          GGAA-AG--CATGAAGGAATGAGTA 3770 _  T  TCA        TI
                             GAA AGT  GAAGGAATGG
                             ||| |||  ||||||||||
                             CTT TCG  CTTCCTTACT
                        C  _  TA_          CA
GAM253  IHPK1          GGAA-AG--CATGAAGGAATGAGTA 3770 TG  T  TCA        _
                             GAA AGT  GAAGGAATG GTA
                             ||| |||  |||||||| |||
                             CTT TCG  CTTCCTTAC CAT
                        __  _  TA_        T
GAM253  KIF5C          GGAAAAGTGTTCAGAAGGAA     3769   TA__          III
                             GGAA  GTTCAGAAGGA
                             ||||  |||||||||||
                             CCTT  CAAGTCTTCCT
                        TTCA          TII
GAM253  KIF5C          GGAAAAGTGTTCAGAAGGAA     3769 TGGAATA         TGGT
                             GTTCAGAAGGAA
                             ||||||||||||
                             CAAGTCTTCCTT
                        CTTTTCA          TIII
GAM253  MAFG          GGGAGAGATTAGAAGGAAT      3772 _  AT TTC       II
                             GGA AG  AGAAGGAA
                             ||| ||  ||||||||
                             CCT TC  TCTTCCTT
                        C  C_  TAA        AI
GAM253  MAFG          GGGAGAGATTAGAAGGAAT      3772 T  AT TTC        GT
                             GGA AG  AGAAGGAATG
                             ||| ||  ||||||||||
                             CCT TC  TCTTCCTTAT
                        _  C_  TAA          II
GAM253  MMP25         GAATAGTTCCAGAGGCAAT      3766        _  A  AAII
                             GAATAGTTC AGA GG
                             ||||||||| ||| ||
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                    CTTATCAAG TCT CC
                        G  _  GTTA
GAM253  MMP25       GAATAGTTCCAGAGGCAAT      3766 TGGA    _  A  _  GGT
                    ATAGTTC AGA GG AAT
                    ||||||| ||| || |||
                    TATCAAG TCT CC TTA
                    ____       G  _  G  GTI
GAM253  PACSIN1     GAAGAGGACAGA-GGAATGGT     3768 AAT_  TT   A     I
                    AG  CAGA GGAATGG
                    ||  |||| ||||||||
                    TC  GTCT CCTTACC
                    CTTC  CT   _    I
GAM253  PACSIN1     GAAGAGGACAGA-GGAATGGT     3768 TGGAAT TT   A
                    AG  CAGA GGAATGGT
                    ||  |||| ||||||||
                    TC  GTCT CCTTACCA
                    TC____  CT  _
GAM253  PIK3CD      TGGAATAGTCCAAGAAAGA       3776       _    ATGGT
                    TGGAATAGTTCA GAAGGA
                    ||||||||||| ||||||
                    ACCTTATCAGGT CTTTCT
                        T   IIIAT
GAM253  PIK3CD      TGGAATAGTCCAAGAAAGA       3776       _   II
                    TGGAATAGTTCA GAAGG
                    ||||||||||| |||||
                    ACCTTATCAGGT CTTTC
                        T    TI
GAM253  PMP22       GATTAGTGATAATAAGGAATGGTA  3765 AA   TCAG__        I
                    TAGT    AAGGAATGGT
                    ||||    ||||||||||
                    ATCA    TTCCTTACCA
                    __   CTATTA        I
GAM253  PMP22       GATTAGTGATAATAAGGAATGGTA  3765 TGGAA  TCAG__        I
                    TAGT    AAGGAATGGTA
                    ||||    |||||||||||
                    ATCA    TTCCTTACCAT
                    A____   CTATTA        T
GAM253  RAD52       AATAGTTCAGTAATAAATAGT     3763 A     _  G   I
                    TAGTTCAG AA GAATGG
                    |||||||| || ||||||
                    ATCAAGTC TT TTTATC
                    _     A  A    I
GAM253  RAD52       AATAGTTCAGTAATAAATAGT     3763 TGGAAT   _  G    A
                    AGTTCAG AA GAATGGT
                    ||||||| || ||||||
                    TCAAGTC TT TTTATCA
                    _____     A  A   C
GAM253  SLC19A1     TGGACACACTTCAGAAGGA       3774  _  G      ATGGT
                    TGGA ATA TTCAGAAGGA
                    |||| ||| ||||||||||
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                        ACCT TGT AAGTCTTCCT
                          G  G       IIIAT
GAM253  SLC19A1        TGGACACACTTCAGAAGGA     3774   _  G      II
                       TGGA ATA TTCAGAAGG

                      IIII III IIIIIIIII
                       ACCT TGT AAGTCTTCC
                         G  G     TI
GAM253  UPF3A          TAGTTTATAACAGGAATGGTA    3773   CAGA__      III
                       TAGTT   AGGAATGGT

                      IIIII   IIIIIIIII
                      ATCAA   TCCTTACCA
                       ATATTG     TII
GAM253  UPF3A          TAGTTTATAACAGGAATGGTA    3773 TGGAATAGTTCAGA
                              AGGAATGGTA

                            IIIIIIIIII
                            TCCTTACCAT
                      ATATTG_____
GAM254  BACH1         ATTTCACAAACCTGCAGAGTT     3782 CA   TT_        CAT
                       TTTC  AGCCTGCAGAGTT

                      IIII  IIIIIIIIIIIII
                      AAAG  TTGGACGTCTCAA
                       __   TGT         CII
GAM254  BACH1         ATTTCACAAACCTGCAGAGTT     3782 T  TT_        I
                       TTC  AGCCTGCAGAGT

                      III  IIIIIIIIIIII
                      AAG  TTGGACGTCTCA
                       _   TGT          I
GAM254  C18orf1       TCTTAGCCTGTCCAAGTCCAT     3796 C      CA_    I
                       TTAGCCTG  GAGTTCA

                      IIIIIIII  IIIIIII
                      AATCGGAC  TTCAGGT
                       _        AGG      I
GAM254  C18orf1       TCTTAGCCTGTCCAAGTCCAT     3796 CATTTCTT    CA_
                          AGCCTG  GAGTTCAT

                         IIIIII  IIIIIIII
                         TCGGAC  TTCAGGTA
                      _____    AGG
GAM254  C18orf1       TCTTAGCCTGTCCAAGTCCATC    3797 TTTC      CA_    I
                         TTAGCCTG  GAGTTCATC

                         IIIIIIIII  IIIIIIIII
                         AATCGGAC  TTCAGGTAG
                      ____        AGG      C
GAM254  COX6C         ATTTCTTAGCCCACATA-TTCAT   3784 _       TG GA  I
                       TTTCTTAGCC CA GTTCA

                      IIIIIIIIII II IIIII
                      AAAGAATCGG GT TAAGT
                       T      GT A_   I
GAM254  COX6C         ATTTCTTAGCCCACATA-TTCAT   3784 CA      TG GA
                       TTTCTTAGCC CA GTTCAT

                      IIIIIIIIII II IIIIII
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                              AAAGAATCGG GT TAAGTA
                                   GT A_
GAM254 COX6C          TTTCTTAGCCCACATA-TTCAT  3814       TG GA   C
                      TTTCTTAGCC CA GTTCAT
                      IIIIIIIII II IIIIII
                      AAAGAATCGG GT TAAGTA
                           GT A_     I
GAM254 CTSK           CATCTCTTAGCCT-AAGAGTACA  3789       C   T T
                      CATTTCTTAGCCTG AGAGT CA
                      IIIIIIIIIIIII IIIII II
                      GTAGAGAATCGGAT TCTCA GT
                             _   T I
GAM254 CTSK           CATCTCTTAGCCT-AAGAGTACA  3789 _        C   TCI
                      ATTTCTTAGCCTG AGAGT
                      IIIIIIIIIIII IIIII
                      TAGAGAATCGGAT TCTCA
                      G        _   TGI
GAM254 CTSK           TCTTAGCCT-AAGAGTACA      3798 TTTC    C   T
                      TTAGCCTG AGAGT CAT
                      IIIIIIII IIIII III
                      AATCGGAT TCTCA GTG
                      ____     _    T
GAM254 CYP4A11          CTTGGACCT-CAGAGTTCA    3792 TTTCTTA  G     T
                        GCCT CAGAGTTCA
                        IIII IIIIIIIII
                        TGGA GTCTCAAGT
                      CC_____   _       C
GAM254 CYP4A11          CTTGGACCT-CAGAGTTCA    3792 CTTA_  G    II
                        GCCT CAGAGTTC
                        IIII IIIIIIII
                        TGGA GTCTCAAG
                      GAACC   _      TI
GAM254 ELAVL2        ATTTCTTAGGATGCTAAGTAGTCAT 3783    CC A  TCAI
                      TCTTAG TGC GAGT
                      IIIIII III IIII
                      AGAATC ACG TTCA
                      CT A   TCAI
GAM254 ELAVL2        ATTTCTTAGGATGCTAAGTAGTCAT 3783 CA     CC A  __  II
                      TTTCTTAG TGC GAGT TCAT
                      IIIIIIII III IIII IIII
                      AAAGAATC ACG TTCA AGTA
                           __     CT A  TC  AI
GAM254 EPHA3         CATTTCTTATACT-CA-AGATCAT  3790       GC G G T
                      CATTTCTTA CT CA AG TCAT
                      IIIIIIIII II II II IIII
                      GTAAAGAAT GA GT TC AGTA
                           AT _ _ T
GAM254 EPHA3         CATTTCTTATACT-CA-AGATCAT  3790       GC G GA CI
                      CATTTCTTA CT CA GTT
                      IIIIIIIII II II III
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                              GTAAAGAAT GA GT  TAG
                              AT _  TC  TA
GAM254  EYA1              TTTTCAGTCTGCAGAGTACA    3810 TTTC   C      T TC
                              TTAG CTGCAGAGT CA
                              |||| |||||||||| ||
                              AGTC GACGTCTCA GT
                              AA__  A    T TI
GAM254  GNAL          CATCTCTCGTCAGCCTGCAG-CTTCAT3785       ___      AG   II
                              CATTTCTT AGCCTGCAG TTCAT
                              |||||||| |||||||||| |||||
                              GTAGAGAG TCGGACGTC AAGTA
                                 CAG    G_   II
GAM254  GNAL          CATCTCTCGTCAGCCTGCAG-CTTCAT3785 A  _        AG   I
                              TTTC TTAGCCTGCAG TTCA
                              |||| |||||||||| ||||
                              AGAG AGTCGGACGTC AAGT
                              G  C     G_   I
GAM254  GOLGA4          ACTCTTTC-TTCAACTGTGT   3781 _       TTAA   I
                              CTCTTTCTTT TGTG
                              |||||||||| ||||
                              GAGAAAGAAG ACAC
                              T       TTG_  I
GAM254  GOLGA4          ACTCTTTC-TTCAACTGTGT   3781 TGGACT    TTAA
                              CTTTCTTT TGTGT
                              |||||||| |||||
                              GAAAGAAG ACACA
                              _____        TTG_
GAM254  GPT         TTTATTAGGGACCTGCAGAG    3813 CATTTCTTA    TTCA
                              GCCTGCAGAG
                              ||||||||||
                              TGGACGTCTC
                              ATAATCCC_     TCII
GAM254  GPT         TTTATTAGGGACCTGCAGAG    3813 TTTCTTA___     TTCATC
                              GCCTGCAGAG
                              ||||||||||
                              TGGACGTCTC
                              AAATAATCCC     IIICTA
GAM254  GPT         TTTATTAGGGACCTGCAGAG    3813 TTTCTTA___     III
                              GCCTGCAGA
                              |||||||||
                              TGGACGTCT
                              AAATAATCCC     CII
GAM254  GRLF1        TGGTTTCTTCCTTTTTAAT    3807 AC       GTGT
                              TGG TCTTTCTTTTTAAT
                              ||| ||||||||||||||
                              ACC AGAAGGAAAAATTA
                              AA       IIIC
GAM254  GRLF1        TGGTTTCTTCCTTTTTAAT    3807 AC       II
                              TGG TCTTTCTTTTTAA
                              ||| ||||||||||||
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                        ACC  AGAAGGAAAAATT
                         AA           AI
GAM254  GSTM3          GGGCTCTATTATTTTTAATGAGT  3794 T  A    TTC_       T  CI
                        GG CTCT    TTTTTAATG GT
                        || ||||    |||||||||| ||
                        CC GAGA    AAAAATTAC CA
                        _  _    TAAT        T  TI
GAM254  HSPA5          TGAAGTCTATCTTTTTAAT      3805    C  T       GTGT
                        TGGA TCT TCTTTTTAAT
                        |||| ||| ||||||||||
                        ACTT AGA AGAAAAATTA
                             C   T    IIIC
GAM254  HSPA5          TGAAGTCTATCTTTTTAAT      3805    C  T       II
                        TGGA TCT TCTTTTTAA
                        |||| ||| |||||||||
                        ACTT AGA AGAAAAATT
                             C   T    AI
GAM254  LCP1           CATTTCTTATCCAGCATAGATTCAT 3787      G  T  G  _    II
                        CATTTCTTA CC GCA AG TTCAT
                        ||||||||| || ||| || |||||
                        GTAAAGAAT GG CGT TC AAGTA
                             A   T  A  T    II
GAM254  LCP1           CATTTCTTATCCAGCATAGATTCAT 3787 A      G  T  G  _    I
                        TTTCTTA CC GCA AG TTCA
                        ||||||| || ||| || ||||
                        AAAGAAT GG CGT TC AAGT
                        _    A   T  A  T   I
GAM254  MAP2           TGGCTTCTTTC-TTTTAAT     3806   AC        TAAI
                        TGG TCTTTCTTTT
                        ||| ||||||||||
                        ACC AGAAAGAAAA
                         GA        TTAI
GAM254  MAP2           TGGCTTCTTTC-TTTTAAT       3806   AC        TAATGTG
                        TGG TCTTTCTTTT
                        ||| ||||||||||
                        ACC AGAAAGAAAA
                         GA        TTAIIIC
GAM254  MEF2C          TGGTCTCTGATCCTTTTTAATGAGT 3804   A  __        T  CII
                        TGG CTCT TTCTTTTTAATG GT
                        ||| |||| |||||||||||| ||
                        ACC GAGA AGGAAAAATTAC CA
                         A  CT        T  III
GAM254  MEF2C          TGGTCTCTGATCCTTTTTAATGAGT 3804 GA  __        TGI
                        CTCT TTCTTTTTAATG
                        |||| ||||||||||||
                        GAGA AGGAAAAATTAC
                        A_  CT        TII
GAM254  NCALD          TTTTTTCGAGTCTGCAGAGT      3811 ___  TT  C     TCATC
                        TTTC AG CTGCAGAGT
                        |||| || |||||||||
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                              AAAG  TC GACGTCTCA
                         AAA   C_  A       IIICT
GAM254 NT5C2             GACTCTTTCCTTTTCCTCGTGT   3793 A         AA_   I
                           CTCTTTCTTTTT  TGTG
                           IIIIIIIIIIII IIII
                           GAGAAAGGAAAA  GCAC
                           _           GGA   I
GAM254 NT5C2             GACTCTTTCCTTTTCCTCGTGT   3793 TGGA        AA_   C
                           CTCTTTCTTTTT  TGTGT
                           IIIIIIIIIIII IIIII
                           GAGAAAGGAAAA  GCACA
                           ____          GGA   T
GAM254 OXCT              CATTTCTTAACATGTATAG      3786      C CAGAGTTCA
                           CATTTCTTAGC TG
                           IIIIIIIIII II
                           GTAAAGAATTG AC
                             T ATATCIIIT
GAM254 OXCT              CATTTCTTAACATGTATAG      3786      C CAGAII
                           CATTTCTTAGC TG
                           IIIIIIIIII II
                           GTAAAGAATTG AC
                             T ATATCI
GAM254 PDGFRA             TCTTTCTTTTTATTATTTC      3803       A GTII
                           TCTTTCTTTTTA TGT
                           IIIIIIIIIIII III
                           AGAAAGAAAAAT ATA
                             A AAGI
GAM254 SLC6A3             GGACACTTGGCTTTTTAATATG   3795 TG  T  T_        TC
                           GAC CTT CTTTTTAATGTG
                           III III IIIIIIIIIII
                           CTG GAA  GAAAAATTATAC
                           __  T  CC          CI
GAM254 TAL1             TTGCTTGAGCC--CAGAGTTCA    3812 TTT   _  TG      TC
                           CTT AGCC  CAGAGTTCA
                           III IIII  IIIIIIIII
                           GAA TCGG  GTCTCAAGT
                           AAC  C    __        II
GAM254 THBD             TCTTTCTTTTCATACATGT       3800          ATGIII
                           TCTTTCTTTTTA
                           IIIIIIIIIIII
                           AGAAAGAAAAGT
                              ATGTAC
GAM254 TOX             CTTTTTCTTTTTTTAATGTG       3791 TGGAC   CT        T
                           TCTTT TTTTAATGTG
                           IIIII IIIIIIIIII
                           AGAAA AAAATTACAC
                           A____  __         T
GAM254 TRIM9           TCTTTCTTTATTACTTTCTC       3799 TGGACT__        AATGTGT
                           CTTTCTTTTT
                           IIIIIIIIII
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                          GAAAGAGAAG
                       GAAATAAT        AAIIICT
GAM254 TRIM9           TCTTTCTTTCTTTTGTTTC     3802         AA  GTII
                       TCTTTCTTTTT TGT
                       ||||||||||| |||
                       AGAAAGAAAGA ACA
                            AA   AAGI
GAM254 TRPS1           TTCTGTTGTTTGCAGAGTTGAT   3808 CATTTCTTAGCC      CAT
                            TGCAGAGTT
                            |||||||||
                            ACGTCTCAA
                       ACAACAA_____      CTA
GAM254 TRPS1           TTCTGTTGTTTGCAGAGTTGAT   3808 TCTTAGCC       CI
                            TGCAGAGTT
                            |||||||||
                            ACGTCTCAA
                       ACAACAA_     CT
GAM254 TRPS1           TTCTGTTGTTTGCAGAGTTGATC  3809 TTTCTTAGCC      C  I
                            TGCAGAGTT ATC
                            ||||||||| |||
                            ACGTCTCAA TAG
                       AGACAACAA_      C  A
GAM254 XT3             TCTTTCTTTATAACTTGTC      3801        T  G  II
                       TCTTTCTTT TAAT TGT
                       ||||||||| |||| |||
                       AGAAAGAAA ATTG ACA
                           T   A  GI
GAM254 ZNF239          CATTTCTTAATCTCCACAGT      3788     GC G  G  TCA
                       CATTTCTTA CT CA AGT
                       ||||||||| || || |||
                       GTAAAGAAT GA GT TCA
                           TA  G  G  III
GAM254 ZNF239          CATTTCTTAATCTCCACAGT      3788     GC G  G  I
                       ATTTCTTA CT CA AG
                       |||||||| || || ||
                       TAAAGAAT GA GT TC
                          TA  G  G  I
GAM255 APLP2           ACCACAGGT-TACCAGAACCTT   3826 _     C  A   GTI
                       CCACAGGT TAC AGAGC
                       |||||||| ||| |||||
                       GGTGTCCA ATG TCTTG
                       T    _  G   GAI
GAM255 APLP2           ACCACAGGT-TACCAGAACCTT   3826 TAAC    C  A   G
                       CACAGGT TAC AGAGC TT
                       ||||||| ||| ||||| ||
                       GTGTCCA ATG TCTTG AA
                       ____    _  G   G
GAM255 APM1            TTGTGGACA--GGTATTATTTTG  3847 _      AA T       I
                       TGTGGACA G TATTATTTT
                       |||||||| | |||||||||
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                               ACACCTGT  C ATAATAAAA
                               A      __C       I
GAM255  APM1        TTGTGGACA--GGTATTATTTTG  3847 AT      AA T
                               TGTGGACA  G TATTATTTTG
                               |||||||| | ||||||||||
                               ACACCTGT  C ATAATAAAAC
                               __      __C
GAM255  APPBP2        ATTGTGAGATAAATTTTATTATTTT 3829   _ C  G_      GII
                               ATTGTG GA AAA  TTATTATTTT
                               |||||| || ||| ||||||||||
                               TAACAC CT TTT  AATAATAAAA
                                T  A  AA       III
GAM255  ATP6V1A1        TGTG-ACATATGTCATTATTTTG  3842 ATTGTG   AA_
                               GACA  GTTATTATTTTG
                               ||||  |||||||||||
                               CTGT  CAGTAATAAAAC
                               A_____    ATA
GAM255  ATP6V1A1        TGTG-ACATATGTCATTATTTTG  3842 GTG   AA_       I
                               GACA  GTTATTATTTT
                               ||||  ||||||||||
                               CTGT  CAGTAATAAAA
                               CA_   ATA        I
GAM255  C18orf1        ATGGTACACAAAGTTAATGTT   3831 ATT  G       TTATTTTG
                               GTG ACAAAGTTA
                               ||| |||||||||
                               CAT TGTTTCAAT
                               TAC  G        TACAAIII
GAM255  C18orf1        ATGGTACACAAAGTTAATGTT   3831 TT  G       TTAI
                               GTG ACAAAGTTA
                               ||| |||||||||
                               CAT TGTTTCAAT
                               C_  G       TACA
GAM255  CLCN6        AACCACAGGGCAAGACCAGAGC   3820 AC     TCTA  GI
                               CACAGG   CAAGA
                               ||||||   |||||
                               GTGTCC   GTTCT
                               __    C___   GG
GAM255  CLCN6        AACCACAGGGCAAGACCAGAGC   3820 TA     TCT__ A  GTT
                               ACCACAGG   AC AGAGC
                               ||||||||   || |||||
                               TGGTGTCC   TG TCTCG
                               __       CGTTC  G    GII
GAM255  DACH        TAACCACTG--CTACAAGAG    3839    AG T    CG
                               TAACCAC  G CTACAAGAG
                               |||||||  | |||||||||
                               ATTGGTG  C GATGTTCTC
                                A _       II
GAM255  DACH        TAACCACTG--CTACAAGAG    3839 _   AG T    I
                               AACCAC  G CTACAAGA
                               ||||||  | ||||||||
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                         TTGGTG C GATGTTCT
                          A    A_ _      I
GAM255  DDEF1        AACCACAGGATATTTACAA    3817        TC___    III
                         AACCACAGG    TACA
                         |||||||||    ||||
                         TTGTGTCC    ATGT
                          TATAA    TII
GAM255  DDEF1        AACCACAGGATATTTACAA    3817 TA     TC___    GAGCGT
                         ACCACAGG    TACAA
                         ||||||||    |||||
                         TGGTGTCC    ATGTT
                         __      TATAA   GIIITT
GAM255  EGR3        TTTTGGCAACAAAGTTATTTTT   3843  TG          ATI
                         TG GACAAAGTTATT
                         || ||||||||||||
                         AC TTGTTTCAATAA
                          CG        AAI
GAM255  EGR3        TTTTGGCAACAAAGTTATTTTT   3843 A  TG         ATTTTG
                         TTG GACAAAGTTATT
                         ||| ||||||||||||
                         AAC TTGTTTCAATAA
                         A CG        AAAGII
GAM255  EHF        ACTATAGGGATACAAGAGC      3825 ACCAC  TC       II
                          AGG TACAAGAG
                          ||| ||||||||
                          TCC ATGTTCTC
                         TGATA CT      GI
GAM255  EHF        ACTATAGGGATACAAGAGC      3825 TAACCAC  TC      T
                          AGG TACAAGAGCG
                          ||| |||||||||
                          TCC ATGTTCTCGT
                         ATA____ CT       T
GAM255  FCN2        CCACCAGGTCTACACGGAGC     3833   _      A_   III
                         CCAC AGGTCTACA GAG
                         |||| ||||||||| |||
                         GGTG TCCAGATGT CTC
                          G    GC GII
GAM255  FCN2        CCACCAGGTCTACACGGAGC     3833 TAACCA       A_   GT
                          CAGGTCTACA GAGC
                          |||||||||| ||||
                          GTCCAGATGT CTCG
                         G_____     GC AG
GAM255  FMR2        GTGGAAAAAGA-ATTATTTTG    3836 _  C   TT     I
                          TGGA AAAG ATTATTTT
                          |||| |||| ||||||||
                          ACCT TTTC TAATAAAA
                          C   T  T_   I
GAM255  HIF1A        TGG-CAAAGCATTATTATTT    3841 A      __    II
                          TGG CAAAGT TATTATT
                          ||| |||||| |||||||
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                        ACC GTTTCG  ATAATAA
                          _    TA      AI
GAM255  HTR1D           AACCACAGGAATC-CCAAGA    3818        __  A   II
                        AACCACAGG  TCT CAAG
                        ||||||||| ||| ||||
                        TTGGTGTCC  AGG GTTC
                            TT  _   TI
GAM255  HTR1D           AACCACAGGAATC-CCAAGA    3818 TA    __  A   GCGT
                         ACCACAGG  TCT CAAGA
                         |||||||| ||| |||||
                         TGGTGTCC  AGG GTTCT
                           __      TT  _  AIII
GAM255  IL18R1          ATTTTG-ACAAAGTTAATTATTT   3830 ATTGTG    _    TG
                          GACAAAGTTA TTATTT
                          |||||||||| ||||||
                          CTGTTTCAAT AATAAA
                          TAAAA_       T   II
GAM255  IL18R1          ATTTTG-ACAAAGTTAATTATTT   3830 TTGTG     _   I
                          GACAAAGTTA TTATT
                          |||||||||| |||||
                          CTGTTTCAAT AATAA
                          AAAA_       T   I
GAM255  IL18R1          TTCTTGA-ATAGCTATTATTTT   3845 ATTG   CAA       G
                          TGGA  AGTTATTATTTT
                          ||||  |||||||||||||
                          ACTT  TCGATAATAAAA
                          AGA_  A__        A
GAM255  JAG2            AACCACAGGTGCGTCAACAGC    3819 A     CTA_  G I
                          CCACAGGT   CAA AG
                          |||||||| |||| ||
                          GGTGTCCA   GTT TC
                          _      CGCA  G  I
GAM255  JAG2            AACCACAGGTGCGTCAACAGC    3819 TA    CTA_  G  GTT
                          ACCACAGGT   CAA AGC
                          ||||||||| |||| |||
                          TGGTGTCCA   GTT TCG
                          __       CGCA  G  GII
GAM255  KCNJ1           TAACCACAG----AC-AGAGC    3840       GTCT  A
                          TAACCACAG   ACA GAGC
                          ||||||||| ||| ||||
                          ATTGGTGTC   TGT CTCG
                               ____  _
GAM255  KCNJ1           TAACCACAG----AC-AGAGC    3840 _     GTCT  A
                          AACCACAG   ACA GA
                          ||||||||  ||| ||
                          TTGGTGTC   TGT CT
                          A     ____  _
GAM255  KCNJ6           TTGGTGCCAAA-TTATTATTTT   3846 ATTG  ACA_       G
                          TGG  AAGTTATTATTTT
                          |||  ||||||||||||||
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                              ACC   TTTAATAATAAAA
                            ____  ACGG          A
GAM255 KCNJ6          TTGGTGCCAAA-TTATTATTT   3846 TG  ACA_        I
                          TGG  AAGTTATTATTT
                          |||  ||||||||||||
                          ACC   TTTAATAATAAA
                          A_  ACGG          I
GAM255 LEP           GGGCAAAGTTATTTTATTT   3835 _  A       ATTIII
                          GG CAAAGTTATT
                          || ||||||||||
                          CC GTTTCAATAA
                          C _       AATAAA
GAM255 LPHH1         AACCACAGGT---CAAGAG     3821         TAC
                          AACCACAGGTC  AAGA
                          ||||||||||  ||||
                          TTGGTGTCCAG  TTCT

                               ___
GAM255 LPHH1         AACCACAGGT---CAAGAG     3821 TA     TAC   C
                          ACCACAGGTC  AAGAG
                          ||||||||||  |||||
                          TGGTGTCCAG  TTCTC
                          __    ___    A
GAM255 MAN2A2        TAACCACAGGATTCCCCTAGAGC  3838      __ ACA   GTTI
                          TAACCACAGG TCT AGAGC
                          |||||||||| ||| |||||
                          ATTGGTGTCC AGG  TCTCG
                           TA GGA    IIIT
GAM255 MAN2A2        TAACCACAGGATTCCCCTAGAGC  3838 AA     __ ACA  I
                          CCACAGG TCT AGAG
                          ||||||| ||| ||||
                          GGTGTCC AGG  TCTC
                          __    TA GGA  I
GAM255 NAT1         TAACCACAGGCCATCTTTAAAAGA  3837        TAC___  CGTTI
                          TAACCACAGGTC    AAGAG
                          ||||||||||||    |||||
                          ATTGGTGTCCGG    TTTTC
                           TAGAAA   TIIIT
GAM255 NAT1         TAACCACAGGCCATCTTTAAAAGA  3837        TACAAGIIIT
                          TAACCACAGGTC
                          ||||||||||||
                          ATTGGTGTCCGG
                            TAGAAATTTT
GAM255 NR4A2         GGACAAAGTTTCCAAGATTTT    3834        ATTATTTIII
                          GGACAAAGTT
                          ||||||||||
                          CCTGTTTCAA
                           AGGTTCTAAA
GAM255 PEX3         ATT-TGAGACAAATAATTTATTATTTTG3828 A_ T   G___        III
                          TTG GGACAAA   TTATTATTTTG
                          ||| |||||||   ||||||||||
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                              AAC TCTGTTT   AATAATAAAAC
                              TA  _       ATTA        III
GAM255 PEX3        ATT-TGAGACAAATAATTTATTATTTTG3828 TTGT      G___       I
                              GGACAAA   TTATTATTTT
                              IIIIIII   IIIIIIIIII
                              TCTGTTT   AATAATAAAA
                              C___       ATTA      I
GAM255 PPEF1         CACAGGTCTTATTGAAGAGGGTT  3832 ACA   AC___    C I
                              GGTCT   AAGAG GT
                              IIIII   IIIII II
                              CCAGA   TTCTC CA
                              ___       ATAAC   C I
GAM255 PTPN12        ACATGTCTACAAGCAGCGT      3823   G      _    II
                              ACA GTCTACAAG AGCG
                              III IIIIIIIII IIII
                              TGT CAGATGTTC TCGC
                              A       G   AI
GAM255 RAP1       ACAAAGTTATATTTATTTT        3822        TATTTIII
                              ACAAAGTTAT
                              IIIIIIIIII
                              TGTTTCAATA
                              TAAATAAA
GAM255 RNPEPL1        ACCCCAGGAAGCTACAAGAG     3824   A  T__      III
                              ACC CAGG  CTACAAGA
                              III IIII  IIIIIIII
                              TGG GTCC  GATGTTCT
                              G   TTC     CII
GAM255 RNPEPL1        ACCCCAGGAAGCTACAAGAG     3824 TAA A  T__     _ GT
                              CC CAGG  CTACAAGAG C
                              II IIII  IIIIIIIII I
                              GG GTCC  GATGTTCTC G
                              ___ _    TTC      T II
GAM255 SHANK2       TTGTGGACACAACTCAGTATTT    3844 AT      _ G  T   G
                              TGTGGACA AA TTA TATTTT
                              IIIIIIII II III IIIIII
                              ACACCTGT TT AGT ATAAAG
                              __      G G C    I
GAM255 SHANK2       TTGTGGACACAACTCAGTATTT    3844 T      _ G  T  I
                              GTGGACA AA TTA TATT
                              IIIIIII II III IIII
                              CACCTGT TT AGT ATAA
                              _      G G C    I
GAM255 SLC21A3     ATTAGTGAACATT-TTATTATTTTG 3827 ATT_     AAG        I
                              GTGGACA  TTATTATTTTG
                              IIIIIII  IIIIIIIIIII
                              CACTTGT  AATAATAAAAC
                              TAAT    AA_        I
GAM255 SLC21A3     ATTAGTGAACATT-TTATTATTTTG 3827 TT_      AAG       I
                              GTGGACA  TTATTATTTT
                              IIIIIII  IIIIIIIIII
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                          CACTTGT  AATAATAAAA
                          AAT      AA_       I
GAM256 AICDA        TGTAAACTCTAA-GAAAGTG   3857    ACAA      TCT
                    TGTAAAC  AAGAAAGTG
                    |||||||  |||||||||
                    ACATTTG  TTCTTTCAC
                        AGA_        III
GAM256 ANXA4        TGTGAAACACAAAGTAGAAAGT   3854  _   __        GTCTC
                    TGT AAACACAAA  AGAAAGT
                    ||| |||||||||  |||||||
                    ACA TTTGTGTTT  TCTTTCA
                        C    CA    IIICT
GAM256 BAZ2B        TGGAAACTTCAACAAGAAAGTG   3855  T  A_  _       TCTC
                    TG AAAC  CAA AAGAAAGTG
                    || ||||  ||| |||||||||
                    AC TTTG  GTT TTCTTTCAC
                       C  AA  G       IIIC
GAM256 BCL6        AAAGACAAAAGAACCTATCTC   3853 TGTAAAC      AG
                          ACAAAAGAA TGTCTC
                          ||||||||| ||||||
                          TGTTTTCTT ATAGAG
                          C_____       GG
GAM256 CDKN2D        AAACAAGAAGAGAAAGTGTTTC   3851 TGTAAACACAAA      C
                             AGAAAGTGT TC
                             ||||||||| ||
                             TCTTTCACA AG
                          GTTCTTC_____      A
GAM256 MGA        AAACATCAACTAAAAAGTGTCTC   3850 TGTAAACA  A_       I
                             CAA AGAAAGTGTCTC
                             ||| |||||||||||||
                             GTT TTTTTCACAGAG
                          GTA_____  GA        A
GAM256 PIK3C2B       AAACACAAAGAGCAAATGT     3852 TGTAAA       __     CT
                          CACAAAAGA AAGTGT
                          ||||||||| ||||||
                          GTGTTTCT TTTACA
                          _____        CG    TT
GAM256 PROX1        TGGAAA-ACAAAAGAAAATG     3856 TGTAAAC        TCT
                          ACAAAAGAAAGTG
                          |||||||||||||
                          TGTTTTCTTTTAC
                       ACCTTT_          III
GAM257 C18orf1     ATTCCAATCCTCAAAACAA     3861 CATTG  __  A       CG
                          CCA  CC TCAAAACAAG
                          |||  || |||||||||
                          GGT  GG AGTTTGTTT
                          AA___  TA  _       II
GAM257 CASP8       ATTGCCACCAGCTAAAAACA     3860 CA       TC__     AGCG
                          TTGCCACCA  AAAACA
                          |||||||||  ||||||
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                     AACGGTGGT  TTTTGT
                       __   CGAT     AIII
GAM257 CD2AP         ATTGCTAC-AGCAAAACAAG    3862 CA   C CAT      CG
                    TTGC AC  CAAAACAAG
                    IIII II  IIIIIIIII
                    AACG TG  GTTTTGTTC
                      __   A TC_      CI
GAM257 CYP17        CATTGCCACAAGCTGAAAAAGAAG  3871        CATCAAAAC  GCI
                    CATTGCCAC      AAGC
                    IIIIIIIII      IIII
                    GTAACGGTG      TTCG
                    _____  ACT
GAM257 DAG1          GCCAGCCATCAAAAATGAAGCG   3877 CATTGCCA      C__   C
                      CCATCAAAA  AAGCG
                      IIIIIIIII  IIIII
                      GGTAGTTTT  TTCGC
                    C_____       TAC   T
GAM257 DDX11        CATGCCCACCATCACCACA     3872 CAT  _     AA  AGCG
                      TGCC ACCATCA  ACA
                      IIII IIIIIII III
                      ACGG TGGTAGT TGT
                    GT_  G    GG IIIC
GAM257 DEC1         CATTGGCAGTAGCCATCAAAA   3866   C _____      CAAGCGC
                     CATTG CA   CCATCAAAA
                     IIIII II   IIIIIIIII
                     GTAAC GT   GGTAGTTTT
                      C CATC      IIICGCG
GAM257 FANCC         CATTGCCACATACCAAAATAAG  3867     C_   C CGC
                    CATTGCCAC ATCAAAA AAG
                    IIIIIIIII IIIIIII III
                    GTAACGGTG TGGTTTT TTC
                       TA   A III
GAM257 FLT1         CAGTGCTACAAATCAAAACATGC  3868 T C C_     A GCI
                    CA TGC AC ATCAAAACA GC
                    II III II IIIIIIIII II
                    GT ACG TG TAGTTTTGT CG
                     C  A TT     A III
GAM257 GALNT7        TTGTCACCTAAAAAACAAGC    3883 CATTGC  ATC
                      CACC AAAACAAGCG
                      IIII IIIIIIIIII
                      GTGG TTTTGTTCGT
                    CA____   ATT
GAM257 GNRHR         TTACCTACATCAAAACTAAG   3881 CATT AC     _ CG
                     GCC CATCAAAAC AAG
                     III IIIIIIIII III
                     TGG GTAGTTTTG TTC
                    ____  AT    A AA
GAM257 IRS1         GCCCCAACCAAAACAAGCG   3879 CATTGCCACC
                      ATCAAAACAAGCG
                      IIIIIIIIIIIII
```

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                              TGGTTTTGTTCGC
                       GT_____
GAM257  ITGA11         CATTTCTACC-TCAAAACAAG   3876   GCC  A       CG
                       CATT  ACC TCAAAACAAG
                       ||||  ||| ||||||||||
                       GTAA  TGG AGTTTTGTTC
                        AGA  _        ||
GAM257  MADH4          CATTGCCACCTTTGCAGAACA   3869       AT__ A   AGCGC
                       CATTGCCACC   CA AACA
                       ||||||||||   || ||||
                       GTAACGGTGG   GT TTGT
                         AAAC  C   |||CG
GAM257  MAOB           ATTTCTACCATCAAAA-AAG   3863 CATTGCC      C  CG
                          ACCATCAAAA AAG
                          |||||||||| |||
                          TGGTAGTTTT TTC
                       AAAGA__        _  AI
GAM257  MARK3          CAATGCGAGGGTCAAAACAA   3874  T  CACCA      GCG
                       CA TGC   TCAAAACAA
                       || |||   |||||||||
                       GT ACG   AGTTTTGTT
                        T  CTCCC       |||
GAM257  MECP2          GCCCACTTTAAAACAAGCGC   3880 CATTGCCACCATC
                            AAAACAAGCG
                            ||||||||||
                            TTTTGTTCGC
                       TGAAA_____
GAM257  PDE4D          CATTGTCCAC-ATCAAAAC   3865    _  C      AAGC
                       CATTG CCAC ATCAAAAC
                       ||||| |||| ||||||||
                       GTAAC GGTG TAGTTTTG
                         A  _     |||C
GAM257  RERE           CATTTCAACAGACAAAACAAGC  3870   GC C T_      GCI
                       CATT  CA CA  CAAAACAAGC
                       ||||  || ||  ||||||||||
                       GTAA  GT GT  GTTTTGTTCG
                        AA  T  CT       |||
GAM257  STX1A          GCCACCATCCCAAACATGC    3878 CATTGCCA   A_   A
                         CCATC AAACA GCG
                         ||||| ||||| |||
                         GGTAG TTTGT CGT
                       _____  GG   A
GAM257  TRPM7          CATCACCCTCATCAAAACAA   3875  TG AC       GCG
                       CAT CC CATCAAAACAA
                       ||| || |||||||||||
                       GTA GG GTAGTTTTGTT
                        GT GA       |||
GAM257  UVRAG          TTGCCACCA-CCTACCAAGC   3882 CATT      AAAA  G
                         GCCACCATC  CAAGC
                         ||||||||||  |||||
```

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                        CGGTGGTGG   GTTCG
                        ____        ATG_   G
GAM257  WHSC1L1      ATTGTGACCATTAA--CAAGCGC   3864 CA  CC    CAA
                        TTG  ACCAT  AACAAGCGC
                        |||  |||||  |||||||||
                        AAC  TGGTA  TTGTTCGCG
                        __   AC   A__
GAM257  ZNF80        CATTGTATTCATCAAAACA      3873     CCAC       AGCG
                        CATTG  CATCAAAACA
                        |||||  ||||||||||
                        GTAAC  GTAGTTTGT
                        ATAA       |||C
GAM258  ABCD3        GCTCATTTGGAGTTTAATACCA    3896       A ___      |||
                        GCTCATTTG AG  AATACC
                        ||||||||| ||  ||||||
                        CGAGTAAAC TC  TTATGG
                        C  AAA     T||
GAM258  ABCD3        GCTCATTTGGAGTTTAATACCA    3896 TAGC      A ___       CAA
                        TCATTTG AG  AATACCA
                        ||||||| ||  |||||||
                        AGTAAAC TC  TTATGGT
                        ____       C  AAA     TT|
GAM258  APLP2        AGCTCATTTAAAAAGGGAATAC    3888         ATA|||G
                        AGCTCATTTGAAGA
                        ||||||||||||||
                        TCGAGTAAATTTTT
                        CCCTTAT
GAM258  APLP2        AGCTCATTTAAAAAGGGAATAC    3888 TA         ____       CACAA
                        GCTCATTTGAA  GAATAC
                        ||||||||||   |||||
                        CGAGTAAATTT  CTTATG
                        __       TTCC     A|||A
GAM258  CD164        AGCTCATTTGTAGACTTGCAAAA   3890       A ATAC CA|
                        GCTCATTTG AGA   CA
                        ||||||||| |||   ||
                        CGAGTAAAC TCT   GT
                        A  GAAC TT|
GAM258  CD164        AGCTCATTTGTAGACTTGCAAAA   3890 TA     A ATAC CAA|
                        GCTCATTTG AGA   CA
                        ||||||||| |||   ||
                        CGAGTAAAC TCT   GT
                        __       A  GAAC TTTA
GAM258  CRIM1        AGCTTTTTTGAAGAAAACAAAAA   3891  CA       T CACA|
                        GCT TTTGAAGAA AC
                        ||| ||||||||| ||
                        CGA AAACTTCTT TG
                        AA     T TTTT|
GAM258  CRIM1        AGCTTTTTTGAAGAAAACAAAAA   3891 TA CA      T CACAA|
                        GCT TTTGAAGAA AC
                        ||| ||||||||| ||
```

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                          CGA  AAACTTCTT TG
                          __   AA       T TTTTTG
GAM258  CYP4F3            TCATTTGATGAAGAATAACTCAA  3897 CATT        CCACAI
                              TGAAGAATA
                              IIIIIIIII
                              ACTTCTTAT
                          AACT        TGAGTI
GAM258  CYP4F3            TCATTTGATGAAGAATAACTCAA  3897 TAGCTCATT       CCACAAI
                              TGAAGAATA
                              IIIIIIIII
                              ACTTCTTAT
                          AACT_____       TGAGTTA
GAM258  CYP4F3            GCACATTTTGAAGAA---CACAA   3895 T   _     CACI
                            GC CATTT GAAGAATAC
                            II IIIII IIIIIIIII
                            CG GTAAA CTTCTTGTG
                             T   A    TTII
GAM258  CYP4F3            GCACATTTTGAAGAA---CACAA   3895 TAGCTCA        CACA
                             TTTGAAGAATAC
                             IIIIIIIIIIII
                             AAACTTCTTGTG
                           TGTA___       TTTT
GAM258  DNMT1             ATTTGAAGAAATATTACAA     3892        TACCACAII
                             ATTTGAAGAA
                             IIIIIIIIII
                             TAAACTTCTT
                              TATAATGTT
GAM258  FZD8           TCATT--AAGAATACC-CAA    3898    TG     ACI
                           TCATT AAGAATACC
                           IIIII IIIIIIIII
                           AGTAA TTCTTATGG
                            __     GTT
GAM258  PCSK1             AGTTCCCTT-AAGAATACCA     3889 G___  ATTTG      I
                             CTC   AAGAATACC
                             III   IIIIIIIII
                             GGG   TTCTTATGG
                          TCAA  AA___       I
GAM258  PCSK1             AGTTCCCTT-AAGAATACCA     3889 TAG  ATTTG      CA
                             CTC   AAGAATACCA
                             III   IIIIIIIIII
                             GGG   TTCTTATGGT
                           CAA  AA___        TI
GAM258  SCML2             CATATGAAGAATAAACACA     3893 T     C_ II
                             CAT TGAAGAATA CAC
                             III IIIIIIIII III
                             GTA ACTTCTTAT GTG
                              T   TT TI
GAM258  SEL1L           AGCTTCTTTTCAATGAATACCACA  3886 GC A  G _      I
                            TC TTT AA GAATACCAC
                            II III II IIIIIIIII
```

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                              AG AAA TT CTTATGGTG
                              A_  A  G  A         I
GAM258  SEL1L      AGCTTCTTTTCAATGAATACCACA  3886 TA  _A  G  _       AI
                              GCT C TTT AA GAATACCACA
                              ||| | ||| || ||||||||||
                              CGA G AAA TT CTTATGGTGT
                              __  A A  G  A        GI
GAM258  TP63       AGCTCATTTGCATGCATGCAAAAA  3887 TA       AAGAATACCACAAI
                              GCTCATTTG
                              |||||||||
                              CGAGTAAAC
                              __        GTACGTACGTTTTT
GAM258  ZNF266     CTCATTTGAAG-TTACTCAC     3894        AA  _  II
                              CTCATTTGAAG  TAC CA
                              ||||||||||| ||| ||
                              GAGTAAACTTC  ATG GT
                                A_  A  GI
GAM258  ZNF266     CTCATTTGAAG-TTACTCAC     3894 TAGCTC    AA  _  A
                              ATTTGAAG  TAC CAC
                              |||||||| ||| |||
                              TAAACTTC  ATG GTG
                              _____       A_  A  G
GAM259  BRCA1      TCGCTTGAGCCTAGGAGGTCA    3906 A    AC_     TCI
                              TC CTTGGG  AGGAGGTCA
                              || |||||| |||||||||
                              AG GAACTC  TCCTCCAGT
                               C   GGA      III
GAM259  BRCA1      TCGCTTGAGCCTAGGAGGTCA    3906 CA    AC_    I
                              CTTGGG  AGGAGGTC
                              |||||| ||||||||
                              GAACTC  TCCTCCAG
                              C_   GGA      I
GAM259  DLEC1      TCACTTGGGCCCAGCAGGCCAT   3903     A_  G   CI
                              TCACTTGGG  CAG AGGTCAT
                              ||||||||| ||| |||||||
                              AGTGAACCC  GTC TCCGGTA
                                GG  G      II
GAM259  DLEC1      TCACTTGGGCCCAGCAGGCCAT   3903 C    A_  G   I
                              ACTTGGG  CAG AGGTCA
                              ||||||| ||| ||||||
                              TGAACCC  GTC TCCGGT
                                _   GG  G    I
GAM259  LZTR1      TCACATCGAACCGCAGGAGGTCAT  3905  _  A__     CII
                              TCAC TTGGG  CAGGAGGTCAT
                              |||| ||||| |||||||||||
                              AGTG AGCTT  GTCCTCCAGTA
                                T   GGC       III
GAM259  LZTR1      TCACATCGAACCGCAGGAGGTCAT  3905 CAC   A__      I
                              TTGGG  CAGGAGGTCA
                              ||||| ||||||||||
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                                    AGCTT  GTCCTCCAGT
                                    T__     GGC        I
GAM259 MYCL2          TCACCTAGGTCAGGAGGTCA     3908       A       TC
                             TCACTTGGG CAGGAGGTCA
                             |||||||| ||||||||||
                             AGTGGATCC GTCCTCCAGT
                                 A        II
GAM259 MYCL2          TCACCTAGGTCAGGAGGTCA     3908       A       I
                             CACTTGGG CAGGAGGTC
                             ||||||||| |||||||||
                             GTGGATCC GTCCTCCAG
                                 A        I
GAM259 RAD52          TCACTTGGGCCCAAGAGGT      3902       A_      CATC
                             TCACTTGGG CAGGAGGT
                             |||||||||| ||||||||
                             AGTGAACCC GTTCTCCA
                                 GG       IIIC
GAM259 RAD52          TCACTTGGGCCCAAGAGGT      3902       A_      II
                             TCACTTGGG CAGGAGG
                             |||||||||| |||||||
                             AGTGAACCC GTTCTCC
                                 GG       AI
GAM259 SLC21A3        TCACTTGGGAAGCCCAAGGGGTCA  3904        ____   A   TCII
                             TCACTTGGGA   CAGG GGTCA
                             ||||||||||   |||| |||||
                             AGTGAACCCT   GTTC CCAGT
                                TCGG   C   IIIC
GAM259 SLC21A3        TCACTTGGGAAGCCCAAGGGGTCA  3904 CACT   ____   A   I
                                TGGGA   CAGG GGTC
                                |||||   |||| ||||
                                ACCCT   GTTC CCAG
                                ____    TCGG  C   I
GAM259 TNFAIP2        TCACTTGAACCAGGAGGTC       3907       GA      ATC
                             TCACTTGG CAGGAGGTC
                             |||||||| |||||||||
                             AGTGAACT GTCCTCCAG
                                 TG       III
GAM259 TNFAIP2        TCACTTGAACCAGGAGGTC       3907       GA      II
                             TCACTTGG CAGGAGGT
                             |||||||| ||||||||
                             AGTGAACT GTCCTCCA
                                 TG       GI
GAM259 WARS          ACTGGGTGACAGGAGGGCA       3901   T _     TCII
                             ACT GG GACAGGAGG
                             ||| || |||||||||
                             TGA CC CTGTCCTCC
                                 C A     CGTI
GAM259 WARS          ACTGGGTGACAGGAGGGCA       3901 TCACTT _     T  TC
                             GG GACAGGAGG CA
                             || ||||||||| ||
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                          CC CTGTCCTCC GT
                     AC____   A      C CT
GAM260  CELL         AGGTCTTGGCA---CTCTTG    3912 TGAG     G TGC
                        GTCTTGG A  CTCTTG
                        ||||||| |  ||||||
                        CAGAACC T  GAGAAC
                             ____     G ___
GAM260  HIP1         TGAGGTCTTGCTATGATGCC    3915        G___      TCTTGC
                        TGAGGTCTTG  GATGCC
                        ||||||||||  ||||||
                        ACTCCAGAAC  CTACGG
                                GATA    IIIGCG
GAM260  PCDH15       TCTTGCCAAGGCTGCCTCTTGC  3914 TGAGGT  T  A
                        CT GGG TGCCTCTTGCG
                        || ||| |||||||||||
                        GG TCC ACGGAGAACGT
                             _____  T G
GAM260  RHO          AGGTCTTGGTGGATGTCCCTT   3911 TGAG     __   C   GCG
                        GTCTTGG GATG CTCTT
                        ||||||| |||| |||||
                        CAGAACC CTAC GGGAA
                             ____    AC   A   GAI
GAM260  USP6         GGTCTTGGGTTGTGACTTG     3913 TGAGGT    A CCT   C
                        CTTGGG TG  CTTG
                        |||||| ||  ||||
                        GAACCC AC  GAAC
                             _____  A ACT   C
GAM260  ZNF136       TGAGGTCTTGCTATG--TTTTGC 3916        GG  CCTC   G
                        TGAGGTCTTG ATG  TTGC
                        |||||||||| |||  ||||
                        ACTCCAGAAC TAC  AACG
                               GA  AA__   I
GAM261  AVP          CCAAGAAGA---GGGTAAG     3921 TACC     T_   AAG
                        AAGAAGAG TGGGA
                        |||||||| |||||
                        TTCTTCTC ATTCT
                             ____    CC   CII
GAM261  LPP          AAGAAGTACTCCCCTGGGAAAGCA 3919 TACCAAGAAGAG      CI
                        TTGGGAAAGCA
                        |||||||||||
                        GACCCTTTCGT
                        TCATGAGGG___         CG
GAM261  OGT          CAAGAAGAGTTAG--AAGC    3920 TACCAA       AA
                        GAAGAGTTGGG AGC
                        |||||||||| |||
                        CTTCTCAATCT TCG
                             _____
GAM262  ACCN1        CTTCTTTCCAGCACTGGGGCCA  3939 ____ A       III
                        CTTCT  TAG GCTGGGGCC
                        |||||  ||| |||||||||
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                             GAAGA   GTC TGACCCCGG
                             AAG   G      TII
GAM262  ACCN1        CTTCTTTCCAGCACTGGGGCCA   3939 CAAGTC   T  A
                          TTCT AG GCTGGGGCCA
                          |||| || |||||||||
                          AAGG TC TGACCCCGGT
                          _____    _ G
GAM262  ADAM19       CAAGTGT-CTCAGAGCTGGGGC   3937     CT         CA
                         CAAGT TCTTAGAGCTGGGGC
                         ||||| |||||||||||||
                         GTTCA AGAGTCTCGACCCCG
                             C_       II
GAM262  ADAM19       CAAGTGT-CTCAGAGCTGGGGC   3937 _  CT          I
                          AAGT TCTTAGAGCTGGGG
                          |||| |||||||||||||
                          TTCA AGAGTCTCGACCCC
                          G  C_         I
GAM262  B3GAT1       TCTTCAGTAG-GCTGGGGCC    3944    T_ A     II
                         TCTTC TAG GCTGGGGC
                         ||||| ||| ||||||||
                         AGAAG ATC CGACCCCG
                          TC  _    GI
GAM262  B3GAT1       TCTTCAGTAG-GCTGGGGCC    3944 CAAGTCTTCT A
                              TAG GCTGGGGCC
                              ||| ||||||||||
                              ATC CGACCCCGG
                         GTC_____  _
GAM262  B4GALT3      GTCTTCTTAGGGATCATGGGG   3942         AGC___  III
                         GTCTTCTTAG   TGGG
                         ||||||||||   ||||
                         CAGAAGAATC   ACCC
                           CCTAGT   CII
GAM262  B4GALT7      TCCTGTCAGAGCTGGGCCCA    3946  C       G  I
                         CTT TTAGAGCTGGG CC
                         ||| |||||||||| ||
                         GGA AGTCTCGACCC GG
                           C       G  I
GAM262  B4GALT7      TCCTGTCAGAGCTGGGCCCA    3946 CAAGTCTTC      G
                           TTAGAGCTGGG CC
                           |||||||||| ||
                           AGTCTCGACCC GG
                         C_____     G
GAM262  CSF1R        CAAGT-TTC--AGAGCTGGG    3936    CTTC      GC
                         CAAGT TTAGAGCTGGG
                         ||||| |||||||||||
                         GTTCA AGTCTCGACCC
                           A___      II
GAM262  CSF1R        CAAGT-TTC--AGAGCTGGG    3936 _  CTTC
                          AAGT TTAGAGCTGG
                          |||| ||||||||||
```

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                        TTCA   AGTCTCGACC
                        G  A___
GAM262 EXT1       AGTGCATCTTGCAGCTGGGGC   3930_ CT  AG      I
                        GT TCTT AGCTGGGG
                        || |||| ||||||||
                        CG AGAA TCGACCCC
                        A T_  CG      I
GAM262 EXT1       AGTGCATCTTGCAGCTGGGGC   3930 CAA CT  AG      CA
                        GT TCTT AGCTGGGGC
                        || |||| |||||||||
                        CG AGAA TCGACCCCG
                        A__ T_  CG      CG
GAM262 HPRT1       CAAAACTTCTTAGATGCTG      3935   T     _   GGGCC
                        CAAG CTTCTTAGA GCTG
                        |||| ||||||||| ||||
                        GTTT GAAGAATCT CGAC
                        T      A  IIIAC
GAM262 HPRT1       CAAAACTTCTTAGATGCTG      3935   T     _  II
                        CAAG CTTCTTAGA GCT
                        |||| ||||||||| |||
                        GTTT GAAGAATCT CGA
                        T      A  CI
GAM262 IL17R      AAGT-TCCTTCATGGCTGGGGCCA 3924  C   AGA_     I
                        AGT TTCTT  GCTGGGGCC
                        ||| |||||  |||||||||
                        TCA AGGAA  CGACCCCGG
                        _   GTAC      I
GAM262 IL17R      AAGT-TCCTTCATGGCTGGGGCCA 3924 CAAG   TTAGA      I
                        TCTTC  GCTGGGGCCA
                        |||||  ||||||||||
                        GGAAG  CGACCCCGGT
                        TCAA  TAC__      A
GAM262 IL1F5      AGCCTTCTTAGAGACTGGATCCA  3931 CAAGT     _  GG  I
                        CTTCTTAGAG CTGG  CCA
                        |||||||||| |||| |||
                        GAAGAATCTC GACC  GGT
                        G____       T  TA  T
GAM262 IL1F5      AGCCTTCTTAGAGACTGGATCCA  3931 GT       _  GG  I
                        CTTCTTAGAG CTGG  CC
                        |||||||||| |||| ||
                        GAAGAATCTC GACC  GG
                        G_        T  TA  I
GAM262 ITGA5     AAGGCTTCAGGGAGGCTGGGGCC   3925 A T  TTA  _     I
                        G CTTC  GAG CTGGGGC
                        | ||||  ||| |||||||
                        C GAAG  CTC GACCCCG
                        C _ TCC  C      I
GAM262 ITGA5     AAGGCTTCAGGGAGGCTGGGGCC   3925 CA T  TTA  _      AI
                        AG CTTC  GAG CTGGGGCC
                        || ||||  ||| ||||||||
```

```
                              TC GAAG  CTC GACCCCGG
                             __  C  TCC  C      AI
GAM262 MLLT2        CAA-TCTGTTTTAGAGCTGG    3934 CA    TC_        GGCC
                        AGTCT  TTAGAGCTGG
                        |||||  ||||||||||
                        TTAGA  AATCTCGACC
                        G_  CAA      IIIA
GAM262 MLLT2        CAA-TCTGTTTTAGAGCTGG    3934 CA    TC_      II
                        AGTCT  TTAGAGCTG
                        |||||  |||||||||
                        TTAGA  AATCTCGAC
                        G_  CAA      CI
GAM262 MMP19        AGCCCTCGTAGA-CTGGGGCCA   3932 _    T  G       I
                       GTCTTC TAGA CTGGGGCC
                       |||||| |||| |||||||||
                       CGGGAG ATCT GACCCCGG
                        T   C   _    I
GAM262 MMP19        AGCCCTCGTAGA-CTGGGGCCA   3932 CAAGT  T  G
                         CTTC TAGA CTGGGGCCA
                         |||| |||| ||||||||||
                         GGAG ATCT GACCCCGGT
                        G____    C   _
GAM262 MX2         GTCTCCCTGTCAGAGCTGGGG    3941 ___          III
                        GTCTTCT  TAGAGCTGGG
                        |||||||  ||||||||||
                        CAGAGGG  GTCTCGACCC
                          ACA        CII
GAM262 MX2         GTCTCCCTGTCAGAGCTGGGG    3941 CAAG  C        CCA
                         TCTT TTAGAGCTGGGG
                         |||| ||||||||||||
                         GGGA AGTCTCGACCCC
                        A___   C      CTA
GAM262 MYO1D       CAAGGCCTTCTCAGCAGCTGGGGC  3933 _    _        CAI
                        CAAG TCTTCTTAG AGCTGGGGC
                        |||| ||||||||| |||||||||
                        GTTC GGAAGAGTC TCGACCCCG
                          C    G      III
GAM262 MYO1D       CAAGGCCTTCTCAGCAGCTGGGGC  3933 AA       _      I
                         GTCTTCTTAG AGCTGGGG
                         |||||||||| |||||||||
                         CGGAAGAGTC TCGACCCC
                        C_      G     I
GAM262 PLCG1       CTTCATCCAGAGCTGGGGC     3940 __          III
                         CTTC TTAGAGCTGGGG
                         |||| ||||||||||||
                         GAAG GGTCTCGACCCC
                          TA      GII
GAM262 PLCG1       CTTCATCCAGAGCTGGGGC     3940 CAAGTCTTC        C
                          TTAGAGCTGGGGC
                          |||||||||||||
```

```
                              GGTCTCGACCCCG
                         A_____            T
GAM262 PPP1R12B          AAGTCTTCTTAAACTTGGGG    3928        GC   I
                         AGTCTTCTTAGA TGGG
                         |||||||||||| ||||
                         TCAGAAGAATTT ACCC
                               GA   I
GAM262 PPP1R12B          AAGTCTTCTTAAACTTGGGG    3928 CA      GC   CC
                         AGTCTTCTTAGA TGGGG
                         |||||||||||| |||||
                         TCAGAAGAATTT ACCCC
                         __        GA   AI
GAM262 PRKG2             AAGT-TGCTGAGAGCTGGGG    3927 _ CTT T       I
                         AGT  CT AGAGCTGGG
                         |||  || |||||||||
                         TCA  GA TCTCGACCC
                         T  AC_ C     I
GAM262 PRKG2             AAGT-TGCTGAGAGCTGGGG    3927 CA CTT T     CC
                         AGT  CT AGAGCTGGGG
                         |||  || ||||||||||
                         TCA  GA TCTCGACCCC
                         __   AC_ C       TI
GAM262 PROS1            AAG-CTTTTCGGAGCTGGGG    3926 _ T  C TA     I
                         AG CTT T GAGCTGGG
                         || ||| | |||||||||
                         TC GAA A CTCGACCC
                         T _ A GC     I
GAM262 PROS1            AAG-CTTTTCGGAGCTGGGG    3926 CA T  C TA      CC
                         AG CTT T GAGCTGGGG
                         || ||| | ||||||||||
                         TC GAA A CTCGACCCC
                         __ _ A GC     CI
GAM262 RFX2             TCTTAAAGGGACTGGGGCCA    3943       ___       III
                         TCTTAGAG CTGGGGCC
                         |||||||| ||||||||
                         AGAATTTC GACCCCGG
                             CCT     TII
GAM262 RFX5            CAAGTCTTC----ACCTGGAGCCA 3938        TTAGAG
                         CAAGTCTTC   CTGGGGCC
                         |||||||||   ||||||||
                         GTTCAGAAG   GACCTCGG
                             TG____
GAM262 RFX5            CAAGTCTTC----ACCTGGAGCCA 3938 _      TTAGAG
                         AAGTCTTC   CTGGGGCC
                         ||||||||   ||||||||
                         TTCAGAAG   GACCTCGG
                         G    TG____
GAM262 SLC29A1          TCATCTCGGGGCTGGGGCCA    3945 CT  AGA       I
                         TCTT GCTGGGGCC
                         |||| |||||||||
```

```
                              AGAG   CGACCCCGG
                           GT    CCC         I
GAM262 STK4              AAGCCTGGGTGGAGCTGGGGCC   3929     TCTTA        I
                           AGTCT    GAGCTGGGGC
                           |||||    ||||||||||
                           TCGGA    CTCGACCCCG
                             CCCAC        I
GAM262 STK4              AAGCCTGGGTGGAGCTGGGGCC   3929 CA    TCTTA        A
                           AGTCT    GAGCTGGGGCC
                           |||||    |||||||||||
                           TCGGA    CTCGACCCCGG
                           __    CCCAC        G
GAM263 AANAT           GATACCCAGTGTTCCCTCCA      3959 AGAA   ACGA        T
                           ACC   GTTCCCTCCAT
                           |||   |||||||||||
                           TGG   CAAGGGAGGTG
                           TA__  GTCA        I
GAM263 APC            AGGAAGGAAGACTTCCCTCCA      3953 AGAAACCAC  G      TTT
                             GA TTCCCTCCA
                             || |||||||||
                             CT AAGGGAGGT
                           TCCTTCCTT  G       III
GAM263 AQP6          AGAAAGTA--AGTTCCCTCC       3951    CCAC        AT
                           AGAAA   GAGTTCCCTCC
                           |||||   |||||||||||
                           TCTTT   TTCAAGGGAGG
                             CA__        II
GAM263 CASP8          GAAAACAC---TTCCCTCCA      3957 A    C GAG        T
                           GAAAC AC  TTCCCTCCA
                           ||||| ||  |||||||||
                           TTTTG TG  AAGGGAGGT
                           _   _  ___        C
GAM263 DAXX          AACCTCGCATGGTTCCCTCC       3949 AGAAACCACGA       ATT
                             GTTCCCTCC
                             |||||||||
                             CAAGGGAGG
                           GAGCGTAC___        CGG
GAM263 FGFR3          GAATTCACGGCTTCCCTCCA      3958 AGAAAC   AG       TT
                            CACG TTCCCTCCA
                            |||| |||||||||
                            GTGC AAGGGAGGT
                           TTAA__  CG        TI
GAM263 OPA1          AGAAATGAAGATCTCCCTCCAT     3954     CCAC G       TT
                           AGAAA   GA TTCCCTCCAT
                           |||||   || |||||||||||
                           TCTTT   CT GAGGGAGGTA
                             ACTT  A       II
GAM263 PAICS         GAAA--ATGAGTTCCCTTCAT      3960 AGAAACCAC      C T
                           GAGTTCCCT CAT
                           ||||||||| |||
```

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                            CTCAAGGGA GTA
                  TTTTA____           A C
GAM263  RAD54B         AGAAACCACTGG--CCCTGCA    3952       GAGTT  C TT
                       AGAAACCAC    CCCT CA
                       ||||||||    |||| ||
                       TCTTTGGTG    GGGA GT
                         ACC__    C II
GAM263  RTDR1          AGAAACCACTCACTGCCTCC    3950       GAGTTC   ATT
                       AGAAACCAC    CCTCC
                       |||||||||    |||||
                       TCTTTGGTG    GGAGG
                          AGTGAC    III
GAM263  WIF1         AGAAAC----AGGTCCCTCCATT   3955    CACG  T
                     AGAAAC   AG TCCCTCCATT
                     ||||||   || ||||||||||
                     TCTTTG   TC AGGGAGGTAA
                        ____     C
GAM263  WT1         GAAA--ATGAATTCCCCTCCATTT  3956 AGAAACCAC       _
                       GAGTTCCC TCCATTT
                       |||||||| |||||||
                       CTTAAGGG AGGTAAA
                     TTTTA____          G
GAM264  AKAP13         CAGGTTCAGTACTGCCCTCC    3965          __  G III
                       CAGGTTCAGTA GCC TC
                       ||||||||||| ||| ||
                       GTCCAAGTCAT CGG AG
                         GA  G GII
GAM264  AKAP13         CAGGTTCAGTACTGCCCTCC    3965 TGCCAG      __  G CC
                          GTTCAGTA GCC TCC
                          |||||||| ||| |||
                          CAAGTCAT CGG AGG
                        _____     GA  G  AC
GAM264  AOC3        AGGTTCAGT----GTCCCC      3963       AGCC
                       AGGTTCAGT   GTCCC
                       |||||||||   |||||
                       TCCAAGTCA   CAGGG

                          ____
GAM264  BDKRB2         CCAGGTTCATT--CCCTCC    3967       GTAG  G  I
                       CCAGGTTCA   CC TC
                       |||||||||   || ||
                       GGTCCAAGT   GG AG
                         AA__  G G
GAM264  BDKRB2         CCAGGTTCATT--CCCTCC    3967 TGCC     GTAG  G  C
                          AGGTTCA   CC TCC
                          |||||||   || |||
                          TCCAAGT   GG AGG
                        ____       AA__  G T
GAM264  BDKRB2         TGCCAGGTTC--TAGCCCTCC    3974       AG   G  CC
                       TGCCAGGTTC TAGCC TCC
                       |||||||||| ||||| |||
```

```
                      ACGGTCCAAG ATCGG AGG
                         __    G  II
GAM264 BDKRB2         TGCCAGGTTC--TAGCCCTCC    3974 _      AG    G  I
                        GCCAGGTTC TAGCC TC
                        |||||||||| ||||| ||
                        CGGTCCAAG ATCGG AG
                        A        __   G  I
GAM264 C4B           CCAGGTTCAGGTTCC-TCCC     3968 _      TAG  G  I
                         CAGGTTCAG  CC TCC
                         ||||||||| || |||
                         GTCCAAGTC  GG AGG
                         G      CAA _   I
GAM264 C4B           CCAGGTTCAGGTTCC-TCCC     3968 TGCC     TAG  G   C
                          AGGTTCAG  CC TCCC
                          |||||||| || ||||
                          TCCAAGTC  GG AGGG
                        ____       CAA _   T
GAM264 CDY2         TGACAGCTTGCTCAGTAGCC     3972 T____  CAG        III
                          GC  GTTCAGTAGC
                          ||  ||||||||||
                          CG  CGAGTCATCG
                        ACTGT AA_       GII
GAM264 GNB5        GCC-GCTCCAGCAGCCGTCCCC    3970 _  AGG             I
                         CC  TTCAGTAGCCGTCCC
                         ||  ||||||||||||||
                         GG  AGGTCGTCGGCAGGG
                       C CG_           I
GAM264 GORASP1      CAGGTGATGAGGGGCCGTCCCC   3964 A_  TC TA       I
                        GGT AG GCCGTCCC
                        ||| || |||||||||
                        CTA TC CGGCAGGG
                       CA  C_ CC     I
GAM264 GORASP1      CAGGTGATGAGGGGCCGTCCCC   3964 TGCCA TC TA      C
                        GGT AG GCCGTCCCC
                        ||| || |||||||||
                        CTA TC CGGCAGGGG
                      CA___  C_ CC      T
GAM264 IL6R        TTAAGTAAAAGCCGTCCCC     3976 TTC  ___         III
                        AGT AGCCGTCCC
                        ||| ||||||||||
                        TCA TCGGCAGGG
                      AAT TTT      GII
GAM264 MECP2       CAGGTTCAGAAGCCATGTCC    3966         T  CIII
                        CAGGTTCAG AGCCGT
                        ||||||||| ||||||
                        GTCCAAGTC TCGGTA
                          T   CAGG
GAM264 MECP2       CAGGTTCAGAAGCCATGTCC    3966 TGCCAG   T __ CC
                         GTTCAG AGCC GTCC
                         |||||| |||| ||||
```

```
                        CAAGTC TCGG CAGG
                        _____     T   TA  AG
GAM264 MPDU1         TGCCTGAGTCATTCTCCGTCCCCC  3975   A GT  GTAG      I
                        TGCC G TCA   CCGTCCCCC
                        ||||  |  |||    |||||||||
                        ACGG C AGT   GGCAGGGGG
                          A TC  AAGA      I
GAM264 MPDU1         TGCCTGAGTCATTCTCCGTCCCCC  3975   A GT  GTAG      I
                        GCC G TCA   CCGTCCCC
                        ||| |  |||   ||||||||
                        CGG C AGT   GGCAGGGG
                          A TC  AAGA      I
GAM264 PLCB2         GCCAGGG--AGTGGCCGTCCCC  3971 _   TTC  A     I
                        CCAGG  AGT GCCGTCCC
                        |||||   |||  |||||||||
                        GGTCC  TCA CGGCAGGG
                          C   C__  C     I
GAM264 PLCB2         GCCAGGG--AGTGGCCGTCCCC  3971 TG   TTC  A
                        CCAGG  AGT GCCGTCCCC
                        |||||   |||  ||||||||||
                        GGTCC  TCA CGGCAGGGG
                          __   C__  C
GAM264 TCF1         GCCAGGTTCTCAGCAGCAGGCCC  3969 CC   __     C_  CI
                        AGGT  TCAGTAGC  GTC
                        ||||  ||||||||  |||
                        TCCA  AGTCGTCG  CGG
                          __   AG      TC  II
GAM264 TCF1         GCCAGGTTCTCAGCAGCAGGCCC  3969 TG    __     C_   CCCI
                        CCAGGT  TCAGTAGC  GTCC
                        ||||||  |||||||||  ||||
                        GGTCCA  AGTCGTCG  CGGG
                          __    AG      TC  TIII
GAM264 ZNF180       TGCCAGGTTGAAAAGTCGT      3973       C T C  CCCC
                        TGCCAGGTT AG AG CGT
                        ||||||||| || || |||
                        ACGGTCCAA TT TC GCA
                          C T A  IIIC
GAM264 ZNF180       TGCCAGGTTGAAAAGTCGT      3973       C T C  II
                        TGCCAGGTT AG AG CG
                        ||||||||| || || ||
                        ACGGTCCAA TT TC GC
                          C T A  AI
GAM265 ABCA1       TAATTTGAAATC---TGAA      3982 TGTA       AGT
                        ATTTGAAATC  TGAA
                        |||||||||  ||||
                        TAAACTTTAG  ACTT
                        _____   ___
GAM265 AS3        TAATTTGAAATTGGTTTGAA      3981 TGTA     CAG_  TT
                        ATTTGAAAT  TTGAA
                        |||||||||   |||||
```

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                          TAAACTTTA   AACTT
                  ____           ACCA    TA
GAM265  CPNE3       TGTAATTTGATGAATTA-TTCAA  3984       AATCAGT    T
                    TGTAATTTGA    TGAATT
                    |||||||||     ||||||
                    ACATTAAACT    ACTTAA
                  _____           T
GAM265  DDX15      TAATTTATGAAATCAGAATGGAAT  3980 TGTAATT      TT__   TTI
                       TGAAATCAG   GAAT
                       |||||||||   ||||
                       ACTTAGTC    CTTA
                    TAAAT__       TTAC  TAI
GAM265  DIAPH2     TGTAATTTGAAAGCAGATTAACTT  3987        T  TTG   I
                    TGTAATTTGAAA CAG   AATTT
                    |||||||||||| |||   |||||
                    ACATTAAACTTT GTC   TTGAA
                         C   TAA   I
GAM265  KLRC4      TATTATGAAGTCAGTTGAAT    3983 TGTAATT   A      T
                       TGAA TCAGTTGAAT
                       |||| |||||||||||
                       ACTT AGTCAACTTA
                    AAT____      C       T
GAM265  TEM8       TGTAATTTGAGAAGGATTGTGAA  3985       AATCA  AATTTI
                    TGTAATTTGA    GTTG
                    ||||||||||    ||||
                    ACATTAAACT    TAAC
                       CTTCC   ACTTII
GAM265  TNC        GTAGACTTCAAATCAGTTG    3979 TGTA   G      AATT
                       ATTT AAATCAGTTG
                       |||| |||||||||||
                       TGAA TTTAGTCAAC
                    ATC_   G       AIII
GAM265  TRPM6      TGAAATTTGAAATCCAAATGTATTT  3986  T      AGT_ A  II
                    TG AATTTGAAATC   TG ATTT
                    || ||||||||||    || ||||
                    AC TTAAACTTTAG   AC TAAA
                       T      GTTT A  II
GAM266  ATP11B     TTAACTTTTC-CCATGAAA     3996 TT     G    CA
                    TAACTTTTC CCATGGAA
                    ||||||||| |||||||||
                    ATTGAAAAG GGTACTTT
                       __      _      TI
GAM266  B4GALT5    GCCATGCT-GA---TGAAAAG   3994 TTGC    GAAC
                    CATGCTG   GTGAAAA
                    |||||||   |||||||
                    GTACGAC   TACTTTT
                     ____
GAM266  BCL2       CCATGCTCCA-CGTGAAAA     3991 TTGCCA   GGA
                    TGCT  ACGTGAAAA
                    ||||  |||||||||
```

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                      ACGA  TGCACTTTT
              _____      GG_
GAM266 CLN5       TTTAACTTTATGCACCAAGGAAGAA 4003      T__   T  CAACII
                  TTTAACTTT  CGCCA GGAA
                  |||||||||  ||||| ||||
                  AAATTGAAA  GTGGT CCTT
                     TAC   T  CTTIII
GAM266 CSNK1A1      TTAACTTTTCCACTTGAAAAAA  3998 TT       _ CA   CAAC
                   TAACTTTTC GC  TGGAA
                   ||||||||| ||  |||||
                   ATTGAAAAG TG  ACTTT
                      __        G A_    TTTA
GAM266 EIF2C1      CCATGCTGG-ACTTGAGAGGG   3993 TTGCCA     ACG  AA
                     TGCTGGA  TGA  AG
                     |||||||  ||| ||
                     ACGACCT  ACT  TC
                   _____       GA_  C_
GAM266 GPC4       TTTAACTTTTTG--AT-GAACA  4006       CGCCATG   A
                  TTTAACTTTT     GAACA
                  ||||||||||     |||||
                  AAATTGAAAA     CTTGT
                     ACTA___     I
GAM266 IL1RN      TTGCCATGCAAGAATGGGAACAGG  4000      T  CGT  A I
                  TTGCCATGC GGAA  GAA AGG
                  ||||||||| ||||  ||| |||
                  AACGGTACG TCTT  CTT TCC
                     T   ACC   G  I
GAM266 IMPA1      TGGCATGGT--AACGTGAAA   3995 TTGCCAT _  _      A
                       GC TGG AACGTGAAA
                       || ||| |||||||||
                       CG ACC TTGCACTTT
                     C_____ T  A      A
GAM266 MEN1       TTTAACTTTTATCTACCTGAAACA 4002      C___  A   ACI
                  TTTAACTTTT  GCC TGGAACA
                  ||||||||||  ||| |||||||
                  AAATTGAAAA  TGG ACTTGT
                     TAGA   _      III
GAM266 NXF3       CCATACTTTATTGTGAAAAGG   3992 TTGCCA   GGAAC
                     TGCT  GTGAAAAGG
                     ||||  |||||||||
                     ATGA  CACTTTTCC
                        _____    AATAA
GAM266 OGT       AACTTAGTTGACCATGGAAC   3990 TTTAACTTTC      AA
                       GCCATGGAAC
                       ||||||||||
                       TGGTACCTTG
                     AATCAAC____       AG
GAM266 PCDHB4       TTTAA-TATTAGCATTCATGGAACA 4004 TTTAACTTTTC ___      ACI
                        GC  CATGGAACA
                        || |||||||||
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                          CG  GTACCTTGT
                    AAATTATAAT_ TAA        III
GAM266  PPARBP      TTTAACTTTCTTTCTGGCACAGGAACAA4001        C_____ _ T    CIII
                    TTTAACTTTT    GC CA GGAACAA
                    IIIIIIIII    II II IIIIIII
                    AAATTGAAAG    CG GT CCTTGTT
                      AAAGAC T _    IIIC
GAM266  RRM2B       TTTAACTTTTTACAAAGGAGCA  4005      CG CAT  A AC
                    TTTAACTTTT C  GGA CA
                    IIIIIIIII I  III II
                    AAATTGAAAA G  CCT GT
                      AT TTT  C II
GAM266  SPTBN1      TTGC-ATGCTGGAATTTCACTGAAAAGG3999   C       ___ _        III
                    TTGC ATGCTGGAA  CG TGAAAAGG
                    IIII IIIIIIIII  II IIIIIIII
                    AACG TACGACCTT  GT ACTTTCC
                     _      AAA G      III
GAM266  SRY         TTAACTTTT-GTAATGAAAC   3997 TT    CGCC    AA
                    TAACTTTT  ATGGAAC
                    IIIIIIII  IIIIIIII
                    ATTGAAAA  TACTTTG
                     __    CAT_   AI
GAM267  APOL1       GGTAAGAGCGATGGGACTGT   4013 _   A TCAT     GT
                    TGGGA GT  TGGGACTGT
                    IIIII II  IIIIIIIII
                    ATTCT CG  ACCCTGACA
                    C  _ CT__     AI
GAM267  APOL1       GGTAAGAGCGATGGGACTGT   4013 GG  TTCAT    I
                      AAG   TGGGACTG
                      III   IIIIIIII
                      TTC   ACCCTGAC
                    CA TCGCT    I
GAM267  C21orf33    TGGGAAGTTGCCATTTTGGGA   4014      __  __    CTGTGTC
                    TGGGAAGT TCAT TGGGA
                    IIIIIIII IIII IIIII
                    ACCCTTCA GGTA ACCCT
                     AC   AA   IIICTGT
GAM267  C21orf33    TGGGAAGTTGCCATTTTGGGA   4014      __  __    IIIT
                    TGGGAAGT TCAT TGGG
                    IIIIIIII IIII IIII
                    ACCCTTCA GGTA ACCC
                     AC   AA   TIII
GAM267  KLRC4       TGTGATGT-CA--GGGACTGTG   4017 GG_ A T TT
                    GA GT CA  GGGACTGT
                    II II II  IIIIIIIII
                    CT CA GT  CCCTGACA
                    ACA  A _ __
GAM267  KLRC4       TGTGATGT-CA--GGGACTGTG   4017 TGG A T TT     T
                    GA GT CA  GGGACTGTG
                    II II II  IIIIIIIII
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                          CT CA GT  CCCTGACAC
                        ACA  A _ __         I
GAM267 NR2E1         GAAGTTCATCTGATACTGT    4011         GGG_  II
                        GAAGTTCATT  ACTG
                        |||||||||  ||||
                        CTTCAAGTAG  TGAC
                          ACTA  AI
GAM267 NR2E1         GAAGTTCATCTGATACTGT    4011 TGGGAA    GGG_   G
                          GTTCATT  ACTGT T
                          ||||||  ||||| |
                          CAAGTAG  TGACA G
                        _____      ACTA  G
GAM267 PIGN        TGGGAAGTT--GTGCGACTG    4015      CAT G  TG
                        TGGGAAGTT  TG GACTG
                        |||||||||  || |||||
                        ACCCTTCAA  AC CTGAC
                          C__ G  II
GAM267 PIGN        TGGGAAGTT--GTGCGACTG    4015 _      CAT G  I
                          GGGAAGTT  TG GACT
                          ||||||||  || ||||
                          CCCTTCAA  AC CTGA
                        A     C__ G  I
GAM267 RBP3        AAGCTCCCTGG-ACTGTGT    4009      ATTG     I
                          AAGTTC  GGACTGTG
                          ||||||  ||||||||
                          TTCGAG  CCTGACAC
                          GGA_      A
GAM267 TCF12       GGAAGTTCAAAGTGATTATGTC   4012      TT _ C  I
                        GAAGTTCA  GG GA TGTGT
                        ||||||||  || || |||||
                        CTTCAAGT  TC CT ATACA
                          T_ A A  I
GAM267 TCF12       GGAAGTTCAAAGTGATTATGTC   4012 TGGG    TT _ C
                          AAGTTCA  GG GA TGTGTC
                          |||||||  || || |||||
                          TTCAAGT  TC CT ATACAG
                        ____      T_ A A
GAM267 TCIRG1      TGGGAAGTTC--CGGGCCTG    4016      AT  A TG
                        TGGGAAGTTC  TGGG CTG
                        ||||||||||  |||| |||
                        ACCCTTCAAG  GCCC GAC
                          __  G  II
GAM267 TCIRG1      TGGGAAGTTC--CGGGCCTG    4016      AT  ACI
                        TGGGAAGTTC  TGGG
                        ||||||||||  ||||
                        ACCCTTCAAG  GCCC
                          __  GGA
GAM267 USP6        AAGTTCATTTGCA-TGTGT    4010       GGGAC  I
                        AAGTTCATT  TGTG
                        |||||||||  ||||
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                        TTCAAGTAA   ACAC
                          ACGT_   A
GAM268  ACOX3           AATCTGCAATTT--CTTTT    4030 TGAAAT      GA
                          CTGCAATTT CTTTT
                          ||||||||| |||||
                          GACGTTAAA GAAAA

                          ‾‾‾‾‾‾   ‾‾
GAM268  ARCN1           TGAAAT-TA-AACTTGACTTTTA 4035    C C        G
                          TGAAAT TG AATTTGACTTTTA
                          |||||| || ||||||||||||
                          ACTTTA AT TTGAACTGAAAAT
                             _ _           |
GAM268  B3GAT1          AAAACTGTA-TTTGACTTTTA   4024 TGAAAT  CA
                          CTG ATTTGACTTTTA
                          ||| |||||||||||
                          GAC TAAACTGAAAAT
                        TT____  A_
GAM268  CUL3            GAAATCTGC-ATTT--CTTTT   4031 TG      A  GA
                          AAATCTGCA TTT CTTTT
                          ||||||||| ||| |||||
                          TTTAGACGT AAA GAAAA

                          __      _  __
GAM268  DGKB            AATCTGCAATTATGATCATTGTAG 4028 TGAAAT     _ CTTTTAGI
                          CTGCAATT TGA
                          |||||||| |||
                          GACGTTAA ACT
                          _____      T AGTAACAT
GAM268  LAMP2           GAAATCTGC-ATT--AATTTTAG  4032 TG       AT  C
                          AAATCTGCA TTGA TTTTA
                          ||||||||| |||| |||||
                          TTTAGACGT AATT AAAAT

                          __      __  _
GAM268  NEBL            AAATATGTA--TTGACTTTTA    4025 TGAAATCTGCAAT
                          TTGACTTTTA
                          ||||||||||
                          AACTGAAAAT
                        TATACAT_____
GAM268  PMCHL1          TGAGAATCTGCAATTT-ACT     4034  _          ACTTTTA
                          TGA AATCTGCAATTTG
                          ||| |||||||||||||
                          ACT TTAGACGTTAAAT
                             C       GAIIIGA
GAM268  PTER            TGTAATAT--ATTTGACTTTTA   4036 TGAAATCTGCAA       G
                          TTTGACTTTTA
                          |||||||||||
                          AAACTGAAAAT
                        ACATTATATA__       I
GAM268  RAB6A           AAATCTGCATAATATTGAGTTTTA 4021 TGAA    AT___  C  GI
                          ATCTGCA TTGA TTTTA
                          |||||| |||| |||||
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                         TAGACGT    AACT AAAAT
                    ____          ATTAT   C    AA
GAM268  RANBP2           AAGCTGCAATTTTACATTT    4029 TGAAAT      G  T  A
                        CTGCAATTT AC TTT
                        ||||||||| || |||
                        GACGTTAAA TG AAA
                    _____          A  T  C
GAM268  RGS5             AAATCTGCACTTTTGACTGTAAG  4022 TGAA    A_      TTTAGI
                        ATCTGCA  TTTGACT
                        ||||||| |||||||
                        TAGACGT AAACTGA
                    ____      GA     CATTCA
GAM268  SGCB             GAAATCTGCATCTTTCCTTTTAG  4033 TG       A  GA    I
                        AAATCTGCA TTT  CTTTTAG
                        ||||||||| ||| |||||||
                        TTTAGACGT GAA  GAAAATC
                    __        A  AG    T
GAM268  SLC4A7           AAATCACCTGCAATTTTACTT    4020 TGAA      G   TTAG
                        ATCTGCAATTT ACTT
                        ||||||||||| ||||
                        TGGACGTTAAA TGAA
                    TAG_          A  CAII
GAM268  SOCS5            AAATCTGCAATTTAGGTTTCAG   4026 TGAA       AC
                        ATCTGCAATTTG TTTTAG
                        ||||||||||| ||||||
                        TAGACGTTAAAT AAAGTC
                              CC
GAM268  SOCS5            AAACTGAAACATGTGACTTTTAG  4027 _    C CAATT          I
                        TGAAAT TG   TGACTTTTAG
                        |||||| ||   ||||||||||
                        ACTTTG AC   ACTGAAAATC
                    G   T _____     G
GAM268  SORCS3           TGAAGGCAGACATTTGACTTTAAG  4037    ATCT ____       TAGI
                        TGAA  GCA  ATTTGACTTT
                        ||||  |||  ||||||||||
                        ACTT  CGT  TAAACTGAAA
                        C___   CTG       TTCI
GAM268  UBL3             AAATCAGCT-TTTGACTTT    4023 TGAA  T  AA      T
                        ATC GC  TTTGACTTT
                        ||| || |||||||||
                        TAG CG  AAACTGAAA
                    ____      T  A_      T
GAM269  CDH11            TCACGCAGA-CCTC-TCTTGGG   4047        CGCA _ C  T
                        TCACGCAGATC  TC CT GG
                        |||||||||| || || ||
                        AGTGCGTCTGG  AG GA CC
                        ____      A  A  C
GAM269  CDKN1A           CGC-GAACACGCATCCTCG     4044 TCACGCA TC       G
                           GA CGCATCCTCG
                           || |||||||||
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```
                              TT  GCGTAGGAGC
                         C_____ GT        G
GAM269  IDH3G            CACGCAGATACGC-T-CTCG    4043 TC     C  ATC   G
                          ACGCAGAT CGC   CTCG
                          |||||||| |||  ||||
                          TGCGTCTA GCG   GAGC
                          __     T A__  G
GAM269  IGFBP4           CGCTGCGCCGCATCCTCGG     4045 TCAC  AGAT
                           GC   CCGCATCCTCGGT
                           ||   ||||||||||||
                           CG   GGCGTAGGAGCCG
                         A___  C___
GAM269  NEK6             TCACAGCAGATCCGAGTCCACGTGTG 4046  _      CA  T _  ||
                          TCAC GCAGATCCG TCC CG GTG
                          |||| ||||||||| ||| || |||
                          AGTG CGTCTAGGC AGG GC CAC
                           T     TC T A  ||
GAM269  NLGN2            TCACGGATATC-G--TCCTCGGTG  4051   CAG  CGCA
                          TCACG ATC   TCCTCGGTG
                          ||||| |||   |||||||||
                          AGTGC TAG   AGGAGCCAC
                           CTA  C___
GAM269  SLC38A2          TCACGCAGA--CG--TCTTCAGTG  4049      CCGCA C
                          TCACGCAGAT   TC TCGGT
                          ||||||||||   || |||||
                          AGTGCGTCTG   AG AGTCA
                                C____ A
GAM269  TGFB1            CACAGAGATCCGCAGTCCTC      4042 TC  C     _    GGT
                           ACG AGATCCGCA TCCTC
                           ||| |||||||||| |||||
                           TGT TCTAGGCGT AGGAG
                           __   C      C  A||
GAM269  TXN             TCACGCAGAT-GGCA-ACTGGGT    4048       CC  TC  C  G
                          TCACGCAGAT GCA  CT GGT
                          |||||||||| |||  || |||
                          AGTGCGTCTA CGT  GA CCA
                           C_  T_  C  I
GAM269  UCN             TCACGCAGA-CAGTGCCCT-GGTG   4050       CC_ AT  C
                          TCACGCAGAT GC CCT GGTG
                          |||||||||| || ||| ||||
                          AGTGCGTCTG  CG GGA CCAC
                           TCA  __  _
GAM269  VENTX2          CACTGCAGGGCCCCAGCATCCTCG   4041 TCAC   A__  _      GTGI
                           GCAG  TCC GCATCCTCG
                           ||||  ||| |||||||||
                           CGTC  GGG CGTAGGAGC
                           TGA_  CCG  T     GIII
GAM269  ZNF264          ACGCAGGGCCGCCGCCTCCTCGGTG  4040 TCAC  AT___  A       II
                           GCAG    CCGC TCCTCGGTG
                           ||||    |||| |||||||||
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```
                        CGTC    GGCG AGGAGCCAC
                        ____      CCGGC   G      CG
GAM270 BRF2          AGCCTTCAG-AGACTCCTG    4054 TCAG    C C    C
                        CCTTCAG AG CTCCTG
                        ||||||| || ||||||
                        GGAAGTC TC GAGGAC
                        ____      _  T    C
GAM270 CA11          TCAGCCTTCTGCTGCCCCC    4062       A A    TGCC
                        TCAGCCTTC GC GCCTCC
                        ||||||||| || ||||||
                        AGTCGGAAG CG CGGGGG
                             A A    IIIC
GAM270 CD3E          TTCACCATGAGGCTGAG-GAA    4067 TCATTG  T      C
                        ACC TGAGGCTGAG GA
                        ||| ||||||||| ||
                        TGG ACTCCGACTC CT
                        _____      T       _
GAM270 COL9A1        CAGCCTTGGTC--CCTCCTGCCC    4057 TC    CAGCAG
                        AGCCTT    CCTCCTGCCC
                        ||||||    ||||||||||
                        TCGGAA    GGAGGACGGG
                        __      CCAG__
GAM270 EN2           TCAGCCTTCGGC--CCTCCCGC    4063      A AG      C
                        TCAGCCTTC GC  CCTCCTGC
                        ||||||||| ||  |||||||||
                        AGTCGGAAG CG  GGAGGGCG
                             C __    I
GAM270 GJB3          CACTG-CCT-GAGGCTGAGGGA    4059 TC   A T      C
                        ATTG CCT GAGGCTGAG GA
                        |||| ||| ||||||||| ||
                        TGAC GGA CTCCGACTC CT
                        __   _  _      C
GAM270 HSPB3         CAGCCTTGAACAGCCTCCT    4056 TC    C      GCC
                        AGCCTT AGCAGCCTCCT
                        |||||| ||||||||||||
                        TCGGAA TTGTCGGAGGA
                        __      C      AII
GAM270 KCNF1         GCCCTC-GCAGCCTCC-GCCC    4061 TCAGCCTTCA      T
                        GCAGCCTCC GCC
                        ||||||||| |||
                        CGTCGGAGG CGG
                        GAG_____      _
GAM270 KCNMB4        CAGCCGCTTCAG-AGCCTCCTGC    4055 TC  __  C      CC
                        AGCC TTCAG AGCCTCCTGC
                        |||| ||||| ||||||||||
                        TCGG AAGTC TCGGAGGACG
                        __   CG  _      TI
GAM270 LSS          TCACT-ACCTTGAGGCCGTGC    4064  A      A GA
                        TCATTG CCTTGAGGCTG GC
                        |||||| ||||||||||| ||
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                        AGTGAT GGAACTCCGGC CG
                               _            A  II
GAM270   PPP1R12B        CTTCATCCAGACTCCTGCCC      4060 TCAGCCTTCAG   C
                             CAG CTCCTGCC
                             ||| ||||||||
                             GTC GAGGACGG
                          AG_____  T
GAM270   PRSS11          CATTGACCTTTGGGTGCTGA      4058 TC     GAG__   GCGA
                           ATTGACCTT   GCTGA
                           |||||||||   |||||
                           TAACTGGAA   CGACT
                            __      ACCCA   GIII
GAM270   TIAL1          TTGTCCTTGGGGAGGCTGAGC      4066 TCATTGA  ___       AA
                            CCTT GAGGCTGAGCG
                            |||| ||||||||||||
                            GGAA CTCCGACTCGT
                          A_____  CCC      GG
GAM270   TNFRSF10B        TGAGCCCTGAGGCTGAGCG      4065 TCATTGA         A
                            CCTTGAGGCTGAGCG
                            |||||||||||||||
                            GGGACTCCGACTCGC
                          _____        A
GAM271   A1BG           CAGCC-CAC--TCAGCCCTG      4079    T  CT     I
                           CAGCC CAC  TCAGCCC
                           ||||| ||| |||||||
                           GTCGG GTG  AGTCGGG
                           _  __       A
GAM271   A1BG           CAGCC-CAC--TCAGCCCTG      4079 TC   T  CT
                            AGCC CAC  TCAGCCCTG
                            |||| ||| |||||||||
                            TCGG GTG  AGTCGGGAC
                                 __    _  __
GAM271   ALDH3A2        CAGGATGATAAAGAATG-AAT      4088     T    CAATTC
                           CAGGATGAT GAGGATG
                           ||||||||| |||||||
                           GTCCTACTA TTCTTAC
                               T    TTAIII
GAM271   ALK           CAGCCTCACCCTTC-GCTCT      4075         CA CCII
                           CAGCCTCACCTT GC
                           |||||||||||| ||
                           GTCGGAGTGGGA CG
                             AG AGAI
GAM271   ALK           CAGCCTCACCCTTC-GCTCT      4075 TC     CA C GT
                           AGCCTCACCTT GC CT
                           |||||||||| || ||
                           TCGGAGTGGGA CG GA
                           __        AG A GI
GAM271   ATM           CAGGAGG-TTGAGGATGCA      4086   TGA      ATT
                           CAGGA TTGAGGATGCA
                           ||||| |||||||||||
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                    GTCCT  AACTCCTACGT
                    CC_          III
GAM271 BAK1         CAGCCACCCCTTCAGCCTCCTGT   4076 G  TCA       _ GI
                    CC  CCTTCAGCC CT
                    II  IIIIIIIII II
                    GG  GGAAGTCGG GG
                    _ TGG        A AI
GAM271 BAK1         CAGCCACCCCTTCAGCCTCCTGT   4076 TC   TCA      __  II
                    AGCC  CCTTCAGCC CTGT
                    IIII  IIIIIIIII IIII
                    TCGG  GGAAGTCGG GACA
                     __  TGG        AG AI
GAM271 BPHL         CAGGTTGGAGTGCAGTGATGCAATT 4083   AT_ T _ _      CGII
                    CAGG  GA TG AG GATGCAATT
                    IIII  II II II IIIIIIIII
                    GTCC  CT AC TC CTACGTTAA
                    AAC  C  G  A      IIIG
GAM271 BUB3         CAGGATGATTAGGTGGACCTGCAAT 4084         A__ __      TCGII
                    CAGGATGATTG GGA TGCAAT
                    IIIIIIIIII III IIIIII
                    GTCCTACTAAT CCT ACGTTA
                     CCA GG   IIIGC
GAM271 C1orf1       CAGGACTCAATAAGGGATGCAATT 4082      GAT_ _     CGI
                    CAGGAT  TGAGG ATGCAATT
                    IIIIII  IIIII IIIIIIII
                    GTCCTG  ATTCC TACGTTAA
                     AGTT    C      III
GAM271 CKMT1        CAGG--GAGGGAGGATGCAA    4087   AT TT      TT
                    CAGG GA GAGGATGCAA
                    IIII II IIIIIIIIII
                    GTCC CT CTCCTACGTT
                     __ CC       II
GAM271 CYP3A4       GGGTG-TTGAGGATGGAAT      4094 CAGGA A      C  T
                    TG TTGAGGATG AAT
                    II IIIIIIIII III
                    AC AACTCCTAC TTA
                    C____ _      C  C
GAM271 DIAPH2       AGGA-GATAATGGATGCAATT     4071 CA  T  TGA       C
                    GGA GAT  GGATGCAATT
                    III III  IIIIIIIIII
                    CCT CTA  CCTACGTTAA
                     __ _ TTA       T
GAM271 ELAVL4       GGATGATTG-TAAAGCAAATC     4095 CAGG     AG T  T
                    ATGATTG GA GCAA TC
                    IIIIIII II IIII II
                    TACTAAC TT CGTT AG
                     ____       AT _ T
GAM271 EXT2         CAGCCTCACATTCAGACCT        4078 TC     C   C GT
                    AGCCTCAC TTCAG CCT
                    IIIIIIII IIIII III
```

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                          TCGGAGTG AAGTC GGA
                          __      T    T  GI
GAM271 EXT2        CAGCCTCACATTCAGACCT    4078       C   _ CII
                       CAGCCTCAC TTCAG CC
                       ||||||||| ||||| ||
                       GTCGGAGTG AAGTC GG
                             T     T  AII
GAM271 FCN2        TCACCCCCACCTTCAGCTCCTG    4102  G         _   TI
                       TCA CCTCACCTTCAGC CCTG
                       ||| ||||||||||||| ||||
                       AGT GGGGTGGAAGTCG GGAC
                           G     A   II
GAM271 FCN2        TCACCCCCACCTTCAGCTCCTG    4102 CAG          _  I
                       CCTCACCTTCAGC CCT
                       ||||||||||||| |||
                       GGGGTGGAAGTCG GGA
                       TG_          A  I
GAM271 FCRH3       TCAGCCTCACATACCCTGCAGCCC    4097        ____    _    TGTII
                       TCAGCCTC  ACCTT CAGCCC
                       ||||||||  ||||| ||||||
                       AGTCGGAG  TGGGA GTCGGG
                              TGTA    C    IIITG
GAM271 FCRH3       TCAGCCTCACATACCCTGCAGCCC    4097        ____    _    IIIG
                       TCAGCCTC  ACCTT CAGCC
                       ||||||||  ||||| |||||
                       AGTCGGAG  TGGGA GTCGG
                              TGTA    C    GIII
GAM271 FOLH1       GCCTCGCTTATCAGCCCTG    4090     ACCT_     II
                       GCCTC    TCAGCCCT
                       |||||    ||||||||
                       CGGAG    AGTCGGGA
                            CGAAT       CI
GAM271 FOLH1       GCCTCGCTTATCAGCCCTG       4090 TCA  CTCACCT
                       GC    TCAGCCCTGT
                       ||    ||||||||||
                       CG    AGTCGGGACG
                       AG_ AAT____
GAM271 HAL         TCAGGTCTCTCCTTCAGCC     4096    C_ A      CTGT
                       TCAG CTC CCTTCAGCC
                       |||| ||| |||||||||
                       AGTC GAG GGAAGTCGG
                        CA  A      IIIT
GAM271 HAL         TCAGGTCTCTCCTTCAGCC     4096    C_ A    II
                       TCAG CTC CCTTCAGC
                       |||| ||| ||||||||
                       AGTC GAG GGAAGTCG
                        CA  A    GI
GAM271 HSPA8       TCAGCCTCATCCTCCCCAGGACCCCTGT4098        _    AG_____    III
                       TCAGCCTCA CCTTC    CCCTGT A
                       ||||||||| |||||    ||||| |
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                        AGTCGGAGT GGAGG     GGGACA  T
                          A     GGTCCTG      III
GAM271  HSPA8            TCAGCCTCATCCTCCCCAGGACCCCTGT4098 AG_   A  TCA    GI
                          CCTC CCT  GCCCT
                          IIII III  IIIII
                          GGAG GGG  TGGGG
                          GTA  _  TCC    AI
GAM271  MAFG            GCTTCACCTTCAAGGCCTTGT    4091  C         __  C III
                          GC TCACCTTCA  GCC TG
                          II IIIIIIIII III II
                          CG AGTGGAAGT  CGG AC
                           A    TC A AII
GAM271  MAFG            GCTTCACCTTCAAGGCCTTGT    4091 TCAGCC      __  C  I
                          TCACCTTCA  GCC TGT
                          IIIIIIIII III III
                          AGTGGAAGT  CGG ACA
                          _____        TC  A  A
GAM271  MEN1            TCGGCCTCACCTCTCTGCTCCTGT  4101  A      _ A _   II
                          TC GCCTCACCT TC GC CCTGT
                          II IIIIIIIII II II IIIII
                          AG CGGAGTGGA AG CG GGACA
                           C    G A A  II
GAM271  MEN1            TCGGCCTCACCTCTCTGCTCCTGT  4101 CA      _ A _   I
                          GCCTCACCT TC GC CCTG
                          IIIIIIIII II II IIII
                          CGGAGTGGA AG CG GGAC
                           __     G A A  I
GAM271  PAFAH1B1        ATCATCTGAGGATGCAATTC     4072 CAGGATGA
                          TTGAGGATGCAATTC
                          IIIIIIIIIIIIIII
                          GACTCCTACGTTAAG
                          A_____
GAM271  PDE4B           CAGCAACAGCTTCAGCCCT      4077    CT C      II
                          CAGC  CA CTTCAGCCC
                          IIII  II IIIIIIIII
                          GTCG  GT GAAGTCGGG
                           TT  C      AI
GAM271  PDE4B           CAGCAACAGCTTCAGCCCT      4077 TC  CT C     GT
                          AGC  CA CTTCAGCCCT
                          III  II IIIIIIIIII
                          TCG  GT GAAGTCGGGA
                           __  TT  C      GI
GAM271  PHLDA3          CATCTTCATCCTCAGCCCTG     4080 AGCC  C      I
                          TCA CTTCAGCCCT
                          III IIIIIIIIII
                          AGT GGAGTCGGGA
                          TAGA  A      I
GAM271  PHLDA3          CATCTTCATCCTCAGCCCTG     4080 TCAGCC  C
                          TCA CTTCAGCCCTGT
                          III IIIIIIIIIIII
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                        AGT GGAGTCGGGACG
                      TAGA__    A
GAM271 PRX            AGCCTCACCATCCACCTCTG    4070        T A  _  II
                      AGCCTCACC TC GCC CT
                      ||||||||| || ||| ||
                      TCGGAGTGG AG TGG GA
                          T  G   A  CI
GAM271 PRX            AGCCTCACCATCCACCTCTG    4070 TCAG    T A  _  T
                       CCTCACC TC GCC CTG
                       ||||||| || ||| |||
                       GGAGTGG AG TGG GAC
                       ___       T G  A  C
GAM271 PRX            TCAGCCTCAGCCCCCACCC      4100        _   G  TGT
                      TCAGCCTCA CCTTCA CCC
                      ||||||||| |||||| |||
                      AGTCGGAGT GGGGGT GGG
                           C    _  III
GAM271 PRX            TCAGCCTCAGCCCCCACCC      4100        _    GCII
                      TCAGCCTCA CCTTCA
                      ||||||||| ||||||
                      AGTCGGAGT GGGGGT
                           C    GGGI
GAM271 PRX            TCAGCCTCAGC-CCA-CCCT     4103        _  TCA    G
                      TCAGCCTCA CCT  GCCCT
                      ||||||||| |||  |||||
                      AGTCGGAGT GGG  TGGGA
                           C  ___   I
GAM271 PRX            TCAGCCTCAGC-CCA-CCCT     4103 _      _  TCA  I
                       CAGCCTCA CCT  GCCC
                       |||||||| |||  ||||
                       GTCGGAGT GGG  TGGG
                       A    C  ___   I
GAM271 RB1           CAGAATAATTTTGAGATGCAATT   4085        GA_      CGI
                     CAGGATGATT  GGATGCAATT
                     ||||||||||  ||||||||||
                     GTCTTATTAA  TCTACGTTAA
                         AAC        III
GAM271 RLBP1           ATGATTGAGAAAATG-AATTCG  4073 CAGGA  TT    C
                       TGA  GAGGATG AATTCG
                       |||  ||||||| ||||||
                       ACT  CTTTTAC TTAAGC
                     A____   __    _
GAM271 RNTRE           CAGG-TCAGTGATGATGCAATT  4089   ATGAT  G      CG
                       CAGG   TGA GATGCAATT
                       ||||   ||| |||||||||
                       GTCC   ACT CTACGTTAA
                        AGTC_  A      II
GAM271 RUNX1         TCAGCCTCACCCCTCTAGCCCT    4099        _ _    GTI
                     TCAGCCTCACCT TC AGCCCT
                     |||||||||| || |||||
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                        AGTCGGAGTGGG AG TCGGGA
                            G  A      III
GAM271  RUNX1          TCAGCCTCACCCCTCTAGCCCT   4099 CA        _ _    I
                        GCCTCACCT TC AGCCC
                        |||||||||| || |||||
                        CGGAGTGGG AG TCGGG
                            __      G  A    I
GAM271  SFRS1          GGAT-ATTACAAGAATGCAATTC   4093 CAGGATGATT
                            GAGGATGCAATTCG
                            ||||||||||||||
                            TTCTTACGTTAAGT
                        TATAATG___
GAM271  SMAC           CAGGAACCTAAATGAGGATGCA   4081    ___  T        ATTCG
                        CAGGA  TGA TGAGGATGCA
                        |||||   ||| ||||||||||
                        GTCCT  ATT ACTCCTACGT
                            TGG  T       IIIGC
GAM271  SPAG4          GCCTC--CTTCAGCCGCTG      4092   CA      _  I
                        GCCT  CCTTCAGCC CT
                        ||||  ||||||||| ||
                        CGGA  GGAAGTCGG GA
                            __        C C
GAM271  SPAG4          GCCTC--CTTCAGCCGCTG      4092 TCAGCCTCA        _
                            CCTTCAGCC CTG
                            ||||||||| |||
                            GGAAGTCGG GAC
                        A_____          C
GAM271  TP63           ATGATACAGTGATGCAATT     4074 CAGGATGATTG _      C
                            AG GATGCAATT
                            || |||||||||
                            TC CTACGTTAA
                        ATG_____ A     A
GAM272  ABCB8          TGTGAGCAGGAGCAGCCGC     4120         TCCAC   CCT
                        TGTGAGCAGG   CGGCC
                        ||||||||||   |||||
                        ACACTCGTCC   GTCGG
                            TC___    CGI
GAM272  ACP5           TGTGAGCAGGGTC--CCGGC    4115         TCCA    CCC
                        TGTGAGCAGG   CCGGC
                        ||||||||||   |||||
                        ACACTCGTCC   GGCCG
                            CAG_    III
GAM272  ASTN           TGTGAGCAGGGCCA-AGGCTCC  4124        T  CC  C TA
                        TGTGAGCAGG CCA  GGC CC
                        |||||||||| |||  ||| ||
                        ACACTCGTCC GGT  CCG GG
                            C T_  A II
GAM272  B4GALT5        TGTGAGCA-GTGCACCTGGGCTCT  4119       GTC  __  CCCTAI
                        TGTGAGCAG  CACC  GGC
                        ||||||||   ||||  |||
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                    ACACTCGTC GTGG CCG
                      AC_    AC   AGAIII
GAM272 CSK            GTGAGCAGGGGCACCAGGTCC   4113 TG     TC    CC TA
                      TGAGCAGG CACCGG CC
                      |||||||| |||||| ||
                      ACTCGTCC GTGGTC GG
                         __      CC    CA  TI
GAM272 GNGT2          TGAGGCAAGTCCTAGACCGGCCCCTA 4114 TGTGA      ___        II
                        GCAGGTCC ACCGGCCCCTA
                        |||||||| ||||||||||
                        CGTTCAGG TGGCCGGGGAT
                      TC___    ATC      TG
GAM272 HIVEP3         GAGCAGGTCATCAGGGCCC      4108 TGTGAG    CACC_   CT
                        CAGGTC   GGCCC
                        |||||| |||||
                        GTCCAG   CCGGG
                        _____    TAGTC    TG
GAM272 HOXB6          GAGCAGGTCTCCTGGCTCC      4109 TGTGAG   CA _ _
                        CAGGTC CC GGC CCCT
                        |||||| || ||| ||||
                        GTCCAG GG CCG GGGG
                        _____    A_ A  A
GAM272 KCNA5          AGC-GGTCGGCCGGCCCCT      4106 TGTGAGCAG  CA
                          GTC CCGGCCCC
                          ||| ||||||||
                          CAG GGCCGGGG
                        _____    CC
GAM272 LAPTM5         TGTGAGCAGCT-CACAGGCCC    4122       G  C  C   CT
                        TGTGAGCAG TC AC GGCCC
                        ||||||||| || || |||||
                        ACACTCGTC AG TG CCGGG
                            G _ T   II
GAM272 MYO15A         TGTGAGCAGACCCGACTGGCCC   4117        GT _ C   CTA
                        TGTGAGCAG CC AC GGCCC
                        ||||||||| || || |||||
                        ACACTCGTC GG TG CCGGG
                           TG C A   III
GAM272 PTGIR          GAGCAGGTCGGCCAGGCCACT    4107 TGTGAG    CA _  C A
                        CAGGTC CC GGCC CT
                        |||||| || |||| ||
                        GTCCAG GG CCGG GA
                        _____    CC T  T C
GAM272 PTHR1          TGTCAGCAGGTCCA---GCCCC   4123  G      CCG   T
                        TGT AGCAGGTCCA  GCCCC
                        ||| |||||||||| |||||
                        ACA TCGTCCAGGT CGGGG
                          G     ___  I
GAM272 PTTG1IP        GTGGGCAGGTCCAGCAGTGCCACT 4110 TG A     CCG__ C AI
                        TG GCAGGTCCA   GCC CT
                        || |||||||| |||| ||
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                          AC CGTCCAGGT    CGG GA
                          __  C        CGTCA  T CI
GAM272 RAD9               TGTGAGCAGGATCCTGGGGCC   4116        _ ACC   CCTA
                          TGTGAGCAGG TCC  GGCC
                          |||||||||| ||| ||||
                          ACACTCGTCC AGG  CCGG
                              T  ACC   IIIA
GAM272 SLC17A5            GTGAGCAGGTGTACTCGCCACCT  4111 TG      CC CG  _  AI
                          TGAGCAGGT AC GCC CCT
                          ||||||||| || ||| |||
                          ACTCGTCCA TG CGG GGA
                              __     CA AG  T  CI
GAM272 SMOH              TGGGAGCAGGTCCTTCCAGCCCC  4118 T      A_     TAI
                          TG GAGCAGGTCC CCGGCCCC
                          || |||||||||| ||||||||
                          AC CTCGTCCAGG GGTCGGGG
                              C     AA     III
GAM272 TLR4              TGTGAGCAG---CAGTGGCCC   4121       GTC CC   C
                          TGTGAGCAG CA GGCCC
                          ||||||||| || |||||
                          ACACTCGTC GT CCGGG
                              ___  CA   I
GAM272 TRPV1            GTGAGCAGGCCTAGCAGGGCCC  4112 TG      CACC__   CTA
                          TGAGCAGGTC    GGCCC
                          |||||||||     |||||
                          ACTCGTCCGG    CCGGG
                              __      ATCGTC   TII
GAM273 AGM1              AGTACTGCCATTATTATTG    4127  G G       II
                          AG AC GCCATTATTGTT
                          || || |||||||||||
                          TC TG CGGTAATAATAA
                              A  A      CI
GAM273 AGM1              AGTACTGCCATTATTATTG    4127 TATGAGGACG
                          GCCATTATTGTTG
                          |||||||||||||
                          CGGTAATAATAAC
                          GA_____
GAM273 CASQ2             TATGA--ACTCCAATTATTGTTG  4134 ATGA  GG  _    I
                          GGAC CCA TTATTGTT
                          |||| ||| |||||||||
                          CTTG GGT AATAACAA
                          ATA_  A_  T    I
GAM273 CASQ2             TATGA--ACTCCAATTATTGTTG  4134 TATGA  GG  _     G
                          GGAC CCA TTATTGTTG
                          |||| ||| |||||||||
                          CTTG GGT AATAACAAC
                          ATA__  A_  T    I
GAM273 CLASP1            TATGAGGACGTCCAGCAATGTT   4133       G T T  GG
                          TATGAGGACG CCA TA TGTT
                          |||||||||| ||| || ||||
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                        ATACTCCTGC GGT GT ACAA
                          A   C   T   II
GAM273 CLASP1         TATGAGGACGTCCAGCAATGTT  4133      G  T  T  I
                        ATGAGGACG CCA TA TGT
                        IIIIIIIII III II III
                        TACTCCTGC GGT GT ACA
                          A   C   T   I
GAM273 ESR1          GAGGACGGCCAGGGACTGTTG  4129 TATGAG    TT_    G
                          GACGGCCA ATTGTTG
                          IIIIIIII  IIIIIII
                          CTGCCGGT TGACAAC
                          _____      CCC    G
GAM273 ESR1          GAGGACGGCCAGGGACTGTTG  4129 A       TT_    I
                          GGACGGCCA ATTGTT
                          IIIIIIIII IIIIII
                          CCTGCCGGT TGACAA
                          _      CCC    I
GAM273 GAS7          TGACGACAGGGCCATTATAGT  4135  G  __      TGIII
                          TGA GAC GGCCATTAT
                          III III IIIIIIIII
                          ACT CTG CCGGTAATA
                           G   TC     TCAII
GAM273 GAS7          TGACGACAGGGCCATTATAGT  4135 TATGAG  __      T TGG
                          GAC GGCCATTAT GT
                          III IIIIIIIII II
                          CTG CCGGTAATA CA
                        TG____  TC     T CAI
GAM273 IL17BR       TGAAGATG--CTTTATTGTTG  4136 _   CG CA      I
                          GAGGA GC TTATTGTT
                          IIIII II IIIIIIII
                          CTTCT CG AATAACAA
                           A   A_ A_    I
GAM273 IL17BR       TGAAGATG--CTTTATTGTTG  4136 TATG  CG  CA
                          AGGA GC TTATTGTTG
                          IIII II IIIIIIIII
                          TTCT CG AATAACAAC
                          ____   A_ A_
GAM273 PCDHA9        TAGGAGGAGCTTCATTATTGTT  4132 AT   CG __      I
                          GAGGA GC CATTATTGT
                          IIIII II IIIIIIIII
                          CTCCT CG GTAATAACA
                        TC    __ AA     I
GAM273 PCDHA9        TAGGAGGAGCTTCATTATTGTT  4132 TAT   CG __      GG
                          GAGGA GC CATTATTGTT
                          IIIII II IIIIIIIII
                          CTCCT CG GTAATAACAA
                        ATC    __ AA      II
GAM273 SHANK2        TATGAGGACTGGAATTTTT  4131        _ CCATTATII
                          TATGAGGAC GG
                          IIIIIIIII II
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                                      ATACTCCTG CC
                                      A  TTAAAAAII
GAM273 SLC17A4    TATCATGATGGAATCATTATTGTT  4130 _  _  CGGC        I
                                      ATGA GGA   CATTATTGT
                                      |||| |||  |||||||||
                                      TACT CCT  GTAATAACA
                                      G  A TA__       I
GAM273 SLC17A4    TATCATGATGGAATCATTATTGTT  4130 ___   _  CGGC      GGI
                                      TATGA GGA   CATTATTGTT
                                      ||||| |||  |||||||||
                                      GTACT CCT   GTAATAACAA
                                      ATA  A TA__      III
GAM273 UGT1A1     ATGAGGACTGACCATTATTG     4128        _      II
                                      ATGAGGAC GGCCATTATT
                                      |||||||| |||||||||
                                      TACTCCTG CTGGTAATAA
                                          A     CI
GAM273 UGT1A1     ATGAGGACTGACCATTATTG     4128 TA   _       TTG
                                      TGAGGAC GGCCATTATTG
                                      ||||||| ||||||||||
                                      ACTCCTG CTGGTAATAAC
                                      __     A      CII
GAM273 UGT1A4     ATGAGGACTGACCATTATTG     4128        _      II
                                      ATGAGGAC GGCCATTATT
                                      |||||||| |||||||||
                                      TACTCCTG CTGGTAATAA
                                          A     CI
GAM273 UGT1A4     ATGAGGACTGACCATTATTG     4128 TA   _       TTG
                                      TGAGGAC GGCCATTATTG
                                      ||||||| ||||||||||
                                      ACTCCTG CTGGTAATAAC
                                      __     A      CII
GAM273 UGT1A9     ATGAGGACTGACCATTATTG     4128        _      II
                                      ATGAGGAC GGCCATTATT
                                      |||||||| |||||||||
                                      TACTCCTG CTGGTAATAA
                                          A     CI
GAM273 UGT1A9     ATGAGGACTGACCATTATTG     4128 TA   _       TTG
                                      TGAGGAC GGCCATTATTG
                                      ||||||| ||||||||||
                                      ACTCCTG CTGGTAATAAC
                                      __     A      CII
GAM274 GFRA1      GTAATCTTCGAGAGCTCGAA     4140       _ T GGAIII
                                      GTAATCTTC AG GT
                                      ||||||||| || ||
                                      CATTAGAAG TC CG
                                          C  T AGCTTI
GAM274 ZFP161     TCAGAGTAACTCTGATCAG      4141      _  __    TGTGGAA
                                      TCAGAGTAA TCT  TCAG
                                      ||||||||| |||  ||||
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                        AGTCTCATT AGA  AGTC
                           G  CT   IIITAAG
GAM274  ZFP161       TCAGAGTAACTCTGATCAG      4141        T  CAIII
                        TCAGAGTAA CTT
                        IIIIIIIII III
                        AGTCTCATT GAG
                         _  ACTAG
GAM274  ZNF80        AAGCTTCCACAGTGTGGAA     4139 AA___   T       III
                        TCT CAGTGTGGA
                        III IIIIIIIII
                        AGG GTCACACCT
                        TTCGA  T     TII
GAM275  ANK1         TCTAATGTG--CAGACTGCA     4154      ATA      CG
                        TCTAATGTG AGGCTGCA
                        IIIIIIIII IIIIIIII
                        AGATTACAC TCTGACGT
                             G__      II
GAM275  ATP11A       TGTGCAGGAGGCTGCACGTT     4156 TCTAATGTGATA
                           AGGCTGCACGT
                           IIIIIIIIIII
                           TCCGACGTGCA
                        TCC_____
GAM275  CORO2B        TCTAC-GTGCATAAGGCTGAAAGT  4153   A  _       CACGTTI
                        TCTA TGTG ATAAGGCTG
                        IIII IIII IIIIIIIII
                        AGAT GCAC TATTCCGAC
                         _  G       TTTCAII
GAM275  KCNJ3       ATGTGATAATACATGCCCGTT     4145 TCTAATGT   G _ A
                        GATAA GC TGC CGTT
                        IIIII II III IIII
                        CTATT TG ACG GCAA
                        _____  A T  G
GAM275  KCNK2       TCTTAGGTAA-AAGGCTGCA     4155  AAT  T     CGT
                        TCT  GTGA AAGGCTGCA
                        III  IIII IIIIIIIII
                        AGA  CATT TTCCGACGT
                         ATC  _     III
GAM275  MOCS1       TAAGCTGA-AAGGCTGCAAGT     4151 TCTAAT GAT     C
                        GT  AAGGCTGCA GT
                        II  IIIIIIIII II
                        CG  TTCCGACGT CA
                        T_____  ACT      T
GAM275  MYO3A       TACTGTGTCCAGGCTGCAC     4150 TCTAA  ATA      GT
                        TGTG  AGGCTGCAC
                        IIII  IIIIIIIII
                        ACAC  TCCGACGTG
                        G____  AGG      AC
GAM275  NLGN1       CTTATGTGATAATGGTGTAC     4149 TCTA       _ C C GT
                        ATGTGATAA GG TG AC
                        IIIIIIIII II II II
```

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                      TACACTATT CC AC TG
                      AA__      A _ A GI
GAM275 NOTCH3         TCTATTCTGCCATAAGGCTG   4152  A__  G      CACGT
                      TCTA  TGT ATAAGGCTG
                      |||| ||| |||||||||
                      AGAT  ACG TATTCCGAC
                      AAG   G      IIITT
GAM275 PFKL           AAGGTGACAGGTGCTGCACGT  4144 TCTAAT   AG_      T
                      GTGATA  GCTGCACGT
                      |||||| |||||||||
                      CACTGT  CGACGTGCA
                      _____    CCA    C
GAM275 PITPNB         CTAATGTGATTTGACTGCA    4148 TC     AA    CGT
                      TAATGTGAT GGCTGCA
                      ||||||||| |||||||
                      ATTACACTA CTGACGT
                      __         AA    CII
GAM275 SLC21A3        ATGTAACAAACCTGCACGTT   4146 TCTAATGT   G
                      GATAAG CTGCACGT
                      |||||| ||||||||
                      TTGTTT GACGTGCA
                      _____      G
GAM275 SPARC          CTAATGTGAAAAGAAACTGCAC 4147 TC    T  __     GTT
                      TAATGTGA AAG  GCTGCAC
                      |||||||| ||| |||||||
                      ATTACACT TTC  TGACGTG
                      __        T  TT   AII
GAM276 CAPZA1         TGAGGAAGAGTAA---TTTGAAA 4165       _  CCT   C
                      TGAGGAAGA TAAT  TTGAAA
                      ||||||||| |||| ||||||
                      ACTCCTTCT ATTA  AACTTT
                      C  ___     I
GAM276 COX7A2L        TGAGGCAAATAACCCTTTGAAA 4175   A        CA
                      TGAGG AGATAATCCTTTGAAA
                      ||||| ||||||||||||||
                      ACTCC TTTATTGGGAAACTTT
                      G              II
GAM276 CYP7A1         TGAGGAAGAAAAT-CTCTGA   4172     T  C   AAC
                      TGAGGAAGA AATC TTTGA
                      ||||||||| |||| |||||
                      ACTCCTTCT TTAG AGACT
                      T   _   III
GAM276 ECT2           TGTGAAAGATA-TCACACTTTGAAACA4169 TGA     __ TC      II
                      GGAAGATA A CTTTGAAACA
                      |||||||| | ||||||||||
                      CTTTCTAT T GAAACTTTGT
                      ACA   AG GT     II
GAM276 FBXL5          TGAGGAAGAAAATCTCTTGTAA 4174     T  C   AAACA
                      TGAGGAAGA AATC TTTG
                      ||||||||| |||| ||||
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                         ACTCCTTCT TTAG GAAC
                           T   A    ATTII
GAM276 FMR1          GAGGAAGATCAAACTTTATTGAAAC 4163 TG      AATC  ___     AII
                         AGGAAGAT   CTT  TGAAAC
                         IIIIIIII   III  IIIIII
                         TCCTTCTA   GAA  ACTTTG
                             __   GTTT  ATA    AII
GAM276 GOLGA5           AGCAGGATAATCCTATTGGCAAAC  4160 TGAGGAA      _  __    AI
                          GATAATCCT TTG  AAAC
                          IIIIIIIII III  IIII
                          CTATTAGGA AAC  TTTG
                         GTC____     T  CG   GA
GAM276 HTR4          TGAGGAGGGTCGTTCCTTTGAAACA 4168     AGATAA_        II
                         TGAGGA    TCCTTTGAAACA
                         IIIIII    IIIIIIIIIIII
                         ACTCCT    AGGAAACTTTGT
                           CCCAGCA            II
GAM276 IL10RA       TGAGCAA-ATAATCCTTTATGATACA 4170   GA       __  A II
                         TGAG AGATAATCCTT TGA ACA
                         IIII IIIIIIIIIII III III
                         ACTC TTTATTAGGAA ACT TGT
                            G_       AT A  II
GAM276 IRTA2       TGAGGAAGAATAAGCCCTTTTGTTACA4164      _  _    GAA_ III
                         TGAGGAAGA TAA TCCTTT   ACA
                         IIIIIIIII III IIIIII   III
                         ACTCCTTCT ATT GGGAAA   TGT
                          T  C   ACAA  III
GAM276 ITPKA        TGAGGAAGA-AGCCCTTTG   4171      TAA    AAA
                         TGAGGAAGA  TCCTTTG
                         IIIIIIIII  IIIIIII
                         ACTCCTTCT  GGGAAAC
                           TC_    III
GAM276 MSX2         GAGGGAGAGGAAACCCTTTGAAACA 4162 T____    GATA        II
                          GAGGAA  ATCCTTGAAACA
                          IIIIII  IIIIIIIIIIII
                          CTCCTT  TGGGAAACTTTGT
                         TCCCT    ____         TI
GAM276 MTF1        TGAGGAAGAAAATACCATTAAAA  4167     T _ T   CAI
                         TGAGGAAGA AAT CC TTGAAA
                         IIIIIIIII III II IIIIII
                         ACTCCTTCT TTA GG AATTTT
                           T  T T     III
GAM276 NDUFA5         AGAAATATCATC-TTTGAAACA    4161 TGAGGAAGATAATC
                            CTTTGAAACA
                            IIIIIIIIII
                            GAAACTTTGT
                         TTTATAGTA_____
GAM276 PIR51        TGAG-AAGATAATTCTTATAAACA 4176   G     C  TG  I
                         TGAG AAGATAAT CTT  AAACA
                         IIII IIIIIIII III  IIIII
```

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                    ACTC TTCTATTA GAA  TTTGT
                       _    A  TA     I
GAM276 SMOH         TGAGGAAGAAGAGCC-TTGAA    4173      TAATC     AC
                    TGAGGAAGA    CTTTGAA
                    |||||||||    |||||||
                    ACTCCTTCT    GGAACTT
                       TCTC_      II
GAM276 UBE2V1       AAGATAAATTTCCTTTGAA    4159 TGAGGAAGATAA      AC
                            TCCTTTGAA
                            |||||||||
                            AGGAAACTT
                    TTTAA_____      AC
GAM276 ZNF80        TGAGGAAGATATTTCCTGTG    4166      A_  T AAAC
                    TGAGGAAGATA  TCCT TG
                    |||||||||| |||| ||
                    ACTCCTTCTAT AGGA AC
                         AA   C  IIIA
GAM277 CAPN5        CCAGGGAGGGGAGGGGGAA    4185 T CCA     CAAAT  A
                      GG  GGGAGGG   GGAA
                      ||  |||||||   ||||
                      CC  CCCTCCC   CCTT
                      C TC_       _____  G
GAM277 CDK5R2       AGGAACGGAAAATGGAAAG    4179 TGGCCA__      AATGGAAA
                          GGGAGGGCA
                          |||||||||
                          CCTTTCCGT
                    GCCTTTTA     CCIIIGAA
GAM277 DLX4         TGGCCAGGGCCCGGGCAGAAGG    4197      A__  AAT AAAG
                    TGGCCAGGG  GGGCA  GG
                    ||||||||| ||||| ||
                    ACCGGTCCC  CCCGT  CC
                        GGG   CTT IIIG
GAM277 FZD8         GCCAGGGAGGGCTCCAAAT    4189 TGGC      AAATGGAAA
                       CAGGGAGGGC
                       ||||||||||
                       GTCCCTCCCG
                       _____        AGGTTTAGA
GAM277 GGT2         GGCCAGGGAGGCCACCTGGA    4193 TG     G AA  AA
                      GCCAGGGAGG CA TGGA
                      ||||||||||| || ||||
                      CGGTCCCTCC GT ACCT
                          __    G GG  CI
GAM277 GPRC5B       GCCAGGGA-GGCAAATCGGTAAG    4190 TGGC    G  _ A
                      CAGGGAGG CAAAT GG AAG
                      ||||||||| ||||| || |||
                      GTCCCTCC GTTTA CC TTC
                      ____      _  G A
GAM277 HPCAL1       GCCAGGGAGGGAGCAAGGTGGA    4188 TGGC     __  A_  AAG
                      CAGGGAGG GCAA TGGA
                      ||||||||| |||| ||||
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                        GTCCCTCC CGTT ACCT
                        ____    CT   CC   CCI
GAM277 MAG              TGGC-AGGGAGGGGCAGCTGGGAAG 4198   C      _ AA  A  I
                        TGGC AGGGAGGG CA TGG AAG
                        |||| |||||||| || ||| |||
                        ACCG TCCCTCCC GT ACC TTC
                        _     C CG  C  I
GAM277 NGFR             GGCCAGGGAGGG--GGTGGAAAG  4195 TG      CAAA
                        GCCAGGGAGGG  TGGAAAG
                        |||||||||||  |||||||
                        CGGTCCCTCCC  ACCTTTC
                        __         CC__
GAM277 PCSK2            TGGGGAGGGAGGGCGGTGGGAAAG 4201  CC      AAAT   I
                        TGG AGGGAGGGC  GGAAAG
                        ||| ||||||||| ||||||
                        ACC TCCCTCCCG  CCTTTC
                        CC      CCAC   I
GAM277 PGR             CCAGGGAGGGAGGGAAAAGGGAAG  4183 T CCA    C  T  AGI
                        GG  GGGAGGG AAA GGAA
                        ||  |||||||| ||| ||||
                        CC  TCCTCCC TTT CCTT
                        C ___       T  C  CCT
GAM277 PKD2L1           GCCAGCAGAGAGCAAATGGAAAG  4187 T  CAG           I
                        GGC  GGAGGGCAAATGGAAAG
                        |||  ||||||||||||||||
                        TCG  TCTCTCGTTTACCTTTC
                        G ___          C
GAM277 POLR2E          GGCCAGGGAGGGGGACAGAGAGAG  4196 TG      CAA   AAGI
                        GCCAGGGAGGG ATGGA
                        ||||||||||| |||||
                        CGGTCCCTCCC TGTCT
                        __        C__  CTCT
GAM277 PTN            CAGGGAGGGAACGGAAGGGAAA   4180 T__ CCA    C    AAG
                        GG  GGGAGGG AAATGGA
                        ||  ||||||| |||||||
                        CC  CCTTCCC TTTACCT
                        CTC TTG     _    III
GAM277 SLC8A2          TGGC-ACTGAGGGCAAAAGGAA   4199   CAGG     T  AG
                        TGGC  GAGGGCAAA GGAA
                        ||||  ||||||||| ||||
                        ACCG  CTCCCGTTT CCTT
                        TGA_     T  II
GAM277 SNAP25          CAGGGAGGG-AA--GGAAAG    4181 T_ CC      AATGGAA
                        GG AGGGAGGGCA
                        || |||||||||
                        CC TCCTTTCTGT
                        CT CT       CIIIGAA
GAM277 SOX11          TGGAAAGGGAGGGCAGAGAGAAAG  4200  CC       AAT   I
                        TGG AGGGAGGGCA GGAAAG
                        ||| ||||||||| ||||||
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                    ACC  TCCCTCCCGT  TCTTTC
                    TT        CTC     I
GAM277 SUFU         CAGGGAGGG-AAA--GAAAG    4182 TGGCC    C  T AA
                    AGGGAGGG AAA GG
                    |||||||| ||| ||
                    TCCCTTTC TTT CC
                    C____        _  C AT
GAM277 SUPT5H       CCAGGGAGGGAAAAGATGGAAA   4184 TGGCCA    C __
                    GGGAGGG AA ATGGAAAG
                    ||||||| || ||||||||
                    CCCTCCC TT TACCTTTT
                    _____        T TC
GAM277 TGM7         GCCAGGGAGGGCAGCTGGA      4191 TGGC      AA  AA
                    CAGGGAGGGCA TGGA
                    |||||||||| ||||
                    GTCCCTCCCGT ACCT
                    ____        CG  CC
GAM277 THRA         GGCCAGGGAGTGGCAGGTGG     4192 TG     _ AA  AAA
                    GCCAGGGAG GGCA TGG
                    ||||||||| |||| |||
                    CGGTCCCTC CCGT ACC
                    __        A  CC  CII
GAM277 TULP3        GGGCAGGGAGGGGAAGGGGA     4194 T C     C AT  AA
                    GGC AGGGAGGG AA GGA
                    ||| |||||||| || |||
                    CCG TCCCTCCC TT CCT
                    _ _        C CC  CI
GAM277 USP18        CCAGGAACGG-AAATGGAAA     4186 TGGCCA   G C
                    GGGA GG AAATGGAAA
                    |||| || |||||||||
                    CCTT CC TTTACCTTT
                    _____    G _
GAM278 ALEX2        TGAAATTTCTTCAAGTCTTTTGA  4218 TTGC       _  A  AI
                    AGTTTCTTCAA TCTT TGA
                    |||||||||| |||| |||
                    TTAAAGAAGTT AGAA ACT
                    CT__        C  A  GI
GAM278 ANKH         TTATAGCCTAAAATAAATTACATAA 4223 A  __        TTI
                    GGTT AAATAAATTGC
                    |||| |||||||||||
                    TCGG TTTATTTAATG
                    A   AT        |||
GAM278 ANKH         TTATAGCCTAAAATAAATTACATAA 4223 T__  AGGTT      TTAAII
                    TAG  AAATAAATTGC
                    |||  |||||||||||
                    ATC  TTTATTTAATG
                    AAT  GGAT_        TATTII
GAM278 AREG         TTAAATATTAAATAAATTATTTA   4227  G       C  AI
                    TTAGA GTTAAATAAATTG TTA
                    ||||| ||||||||||| |||
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                         AATTT TAATTTATTTAAT AAT
                           A        A  II
GAM278 AREG        TTAAATATTAAATAAATTATTTA  4227  G      CTTI
                     TAGA GTTAAATAAATTG
                     |||| |||||||||||||
                     ATTT TAATTTATTTAAT
                       A         AAAI
GAM278 ATRX        GTTTCTTCAGATTCTTCTGA   4214 TTG  T    AATCTT
                     CAG TTCTTC    ATGA
                     ||| ||||||    ||||
                     GTC AAGAAG    TACT
                     AA_  T    AC____
GAM278 CCR2        TTGCAGTTTTCAGCTTTAATTTTAT  4229      CT  ATCTTATGAAII
                     TTGCAGTTT TCA
                     ||||||||| |||
                     AACGTCAAA AGT
                          __  CGAAATTAAAAT
GAM278 CTBP2       TGTACTGTCTTCAATCCTATG   4220 TTGCAGTT        AA
                     TCTTCAATCTTATG
                     ||||||||||||||
                     AGAAGTTAGGATAC
                     CATGAC__           GI
GAM278 DIO3        TTGCAGTTTACCTCAAGCCTTTAT  4230      _  _  ATGAAI
                     TTGCAGTTT CTTCAA TCTT
                     ||||||||| |||||| ||||
                     AACGTCAAA GGAGTT GGAA
                           T   C  ATAIII
GAM278 F2R         TTAGGAGGTTAAA-AAA-TGCTT  4222 TA__       TAAAT  I
                     GAGGTTAAA   TGCT
                     |||||||||   ||||
                     CTCCAATTT   ACGA
                     AATC       TTT__  I
GAM278 F2R         TTAGGAGGTTAAA-AAA-TGCTT  4222 TTA_      TAAAT   AA
                     GAGGTTAAA   TGCTT
                     |||||||||   |||||
                     CTCCAATTT   ACGAA
                     AATC       TTT__  II
GAM278 FLOT1       TTAGGAAGTTAAATAAGTTG   4221 TTA_       A CTTA
                     GAGGTTAAATAA TTG
                     |||||||||||| |||
                     CTTCAATTTATT AAC
                     AATC         C  IIIA
GAM278 FLOT1       TTAGGAAGTTAAATAAGTTG   4221 TTA_       ATTII
                     GAGGTTAAATAA
                     ||||||||||||
                     CTTCAATTTATT
                     AATC        CAACI
GAM278 GCNT2       TGCAGTTTCCCTTCAGTC--ATGA  4215 TT     CAATC   A
                     GCAGTTTCTT  TTATGA
                     ||||||||||  ||||||
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                        CGTCAAAGGG    AGTACT
                          __      AAGTC     C
GAM278  GEMIN5           GCAGTTTCTTCAAGGTGTGTGAA   4213 TTGC          TCTTATGAAI
                          AGTTTCTTCAA
                          |||||||||||
                          TCAAAGAAGTT
                          ____          CCACACACTT
GAM278  GPR48            TTAGAT-TTA--TAAATTGCTTAA   4228 TAG    AA
                          AGGTT ATAAATTGCTTA
                          ||||| |||||||||||
                          TCTAA TATTTAACGAAT
                          AA_   A_
GAM278  GPR48            TTAGAT-TTA--TAAATTGCTTAA   4228 TTAG    AA
                           AGGTT ATAAATTGCTTAA
                           ||||| ||||||||||||
                           TCTAA TATTTAACGAATT
                           AA__   A_
GAM278  HIS1             AGTTTGA-CAATCTTATGAA     4208 TTGCAGTTTCTT
                           CAATCTTATGA
                           |||||||||||
                           GTTAGAATACT
                          ACT_____
GAM278  HNRPDL           CATTTTGTTCAATCTTGTG     4211 TTGCAGTTTC      A A
                           TTCAATCTT TG
                           ||||||||| ||
                           AAGTTAGAA AC
                          AAAC_____       C C
GAM278  IARS             AGAGGTCTCAAATAAATT--TTAA  4204     __       GCTTAI
                           GAGGTT AAATAAATT
                           |||||| |||||||||
                           CTCCAG TTTATTTAA
                           AG      AATIII
GAM278  MYD88            GAGGGTAAAGTATAAATTGCT     4212   T ___       III
                           GAGG TAA  ATAAATTGC
                           |||| |||  |||||||||
                           CTCC ATT  TATTTAACG
                            C  TCA      AII
GAM278  MYD88            GAGGGTAAAGTATAAATTGCT     4212 TTA   TAA      AA
                            GAGGT  ATAAATTGCTT
                            |||||  |||||||||||
                            TTTCA  TATTTAACGAG
                           CCA    ___       AC
GAM278  NARS             TTACAAATTCTTCAATTTCTATG   4232   T     C_   AAI
                            TTGCAG TTCTTCAAT TTATG
                            |||||| ||||||||| |||||
                            AATGTT AAGAAGTTA GATAC
                             T     AA  III
GAM278  NEB              TTAGAGGTTTTATTAGTTGCT     4224         AAATAAA  I
                            TAGAGGTT    TTGC
                            ||||||||    ||||
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                         ATCTCCAA        AACG
                          AATAATC    I
GAM278 NEB               TTAGAGGTTTTATTAGTTGCT    4224       AAATAAA    TAA
                          TTAGAGGTT      TTGCT
                          |||||||||      |||||
                          AATCTCCAA      AACGA
                           AATAATC    III
GAM278 NEDD4             AGAGGTTAAGTAAGCTGCTT     4206      A   A    I
                           GAGGTTAA TAA TTGCT
                          |||||||| ||| |||||
                          CTCCAATT ATT GACGA
                             C   C    I
GAM278 NEDD4             AGAGGTTAAGTAAGCTGCTT      4206 TTAG     A   A    A
                            AGGTTAA TAA TTGCTT
                          ||||||| ||| ||||||
                           TCCAATT ATT GACGAA
                           ____        C   C    G
GAM278 NEDD4             TGAATTGCTTCACATGTCTTATGAA 4216 TTGCA_    TTCAA        II
                            GTTTC   TCTTATGAA
                            |||||   |||||||||
                            CGAAG   AGAATACTT
                          CTTAAA    TGTAC      GI
GAM278 NET1             CAGTCTTTTTCCATCTTATGA     4209 TTGCAG    TCA       A
                            TTTCT  ATCTTATGA
                            |||||  |||||||||
                            AAAGG  TAGAATACT
                          AGAA__      ___        G
GAM278 PEX3             AGATGCCAAATAAATTGATT      4207 AGAG         CI
                            GTTAAATAAATTG
                            |||||||||||||
                            CGGTTTATTTAAC
                          TA__        TA
GAM278 PEX3             AGATGCCAAATAAATTGATT      4207 TTAGAG        C  A
                            GTTAAATAAATTG TT
                            ||||||||||||| ||
                            CGGTTTATTTAAC AA
                          TA____          T A
GAM278 PPP1R3A           TTGCAGATTCAAAGTCAATCTTAT  4231      T  T___       GAAI
                           TTGCAG TTC   TCAATCTTAT
                           |||||| |||   ||||||||||
                           AACGTC AAG   AGTTAGAATA
                            T  TTTC       IIIA
GAM278 PRKRA            TGCAGTTTCTT-TCTCTGATG     4219 TT      CAA   T  A
                           GCAGTTTCTT  TCT ATG
                          |||||||||| ||| |||
                           CGTCAAAGAA  AGA TAC
                           __       AG_  C  A
GAM278 PTGES            TTGCAGTTTC--CAAACCT-TGAA   4233       TC   ATGAA
                           TTGCAGTTTCT AATCTT
                           |||||||||| ||||||
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                        AACGTCAAAGG TTGGAA
                         T_     CTTII
GAM278 SDPR             CAGTTTCTTCTTCAATCTT    4210 TTGCAG        ATGA
                        TTTCTTCAATCTT
                        |||||||||||||
                        GAAGAAGTTAGAA
                        AAA___           CCTI
GAM278 SERPINB6        TGCAGTTTCCTCAGATATT    4217 TT        ATCTTATGA
                        GCAGTTTCTTCA
                        ||||||||||||
                        CGTCAAAGGAGT
                         __         CTATAAGII
GAM278 SHANK2         AGAGGTAGCAAAATAAATTACTT   4205 GA  T        I
                        GGT AAATAAATTGCT
                        ||| |||||||||||
                        TCG TTTATTTAATGA
                        CA  T         I
GAM278 SHANK2         AGAGGTAGCAAAATAAATTACTT   4205 TTAGA  T        AAI
                        GGT AAATAAATTGCTT
                        ||| ||||||||||||
                        TCG TTTATTTAATGAA
                        TCCA_  T        CTI
GAM278 TCF2          TTAGTGATAAAATAAATTGTTT    4226   A  T        CTTAA
                        TTAG GGT AAATAAATTG
                        |||| ||| ||||||||||
                        AATC CTA TTTATTTAAC
                          A  T        AAAII
GAM278 TCF2          TTAGTGATAAAATAAATTGTTT    4226   A  T        CTI
                        TAG GGT AAATAAATTG
                        ||| ||| ||||||||||
                        ATC CTA TTTATTTAAC
                          A  T        AAI
GAM278 UBE2H        TTAGTAATAAAAAAAATTGCTT    4225   AG T  T     AA
                        TTAG  GT AAA AAATTGCTT
                        ||||  || ||| |||||||||
                        AATC  TA TTT TTTAACGAA
                         AT  T  T        II
GAM278 UBE2H        TTAGTAATAAAAAAAATTGCTT    4225   AG T  T      I
                        TAG  GT AAA AAATTGCT
                        |||  || ||| ||||||||
                        ATC  TA TTT TTTAACGA
                         AT  T  T        I
GAM279 ADCY8         GCAGCCGGAG---GAGGGGT     4241        TCA  TGI
                        GCAGCCGGAG  GAG
                        ||||||||||  |||
                        CGTCGGCCTC  CTC
                          ___    CCC
GAM279 ADCY8         GCAGCCGGAG---GAGGGGT     4241 TAGC       TCA  T
                        AGCCGGAG  GAG GGT
                        ||||||||  ||| |||
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                              TCGGCCTC  CTC CCA
                              ____      ___  C
GAM279  ADCY8        GCAGCCGGATGCAG-GTGGAGG  4242 _      GT  A  TGI
                         CAGCCGGA  CAG GTGG
                         |||||||| ||| ||||
                         GTCGGCCT  GTC CACC
                         C     AC  _   TCI
GAM279  ADCY8        GCAGCCGGATGCAG-GTGGAGG  4242 TAGC    GT  A  T
                          AGCCGGA  CAG GTGG GG
                          ||||||| ||| |||| ||
                          TCGGCCT  GTC CACC CC
                          ____       AC  _  T
GAM279  ARSF        TAACAGAAGG-GCCAGGAGTGGTGG  4244    CC  A   _    I
                         TAGCAG  GG GTCAG AGTGGTGG
                         ||||||  || ||||| ||||||||
                         ATTGTC  CC CGGTC TCACCACC
                          TT _   C       I
GAM279  ARSF        TAACAGAAGG-GCCAGGAGTGGTGG  4244    CC  A   _    I
                          AGCAG  GG GTCAG AGTGGTG
                          |||||  || ||||| |||||||
                          TTGTC  CC CGGTC TCACCAC
                          TT _   C       I
GAM279  BMP4        CAGCCGGAG-CAGCAGCGG       4237      T  _  II
                         CAGCCGGAG CAG AGTG
                         ||||||||| ||| ||||
                         GTCGGCCTC GTC TCGC
                          _  G   CI
GAM279  BMP4        CAGCCGGAG-CAGCAGCGG       4237 TAGCAG   T  _
                          CCGGAG CAG AGTGGT
                          |||||| ||| ||||||
                          GGCCTC GTC TCGCCG
                          _____    _  G
GAM279  DMRT1       GCAGCCGGAGGCGCAGCTGG      4240       T__  AGTGII
                         GCAGCCGGAG  CAG
                         ||||||||||  |||
                         CGTCGGCCTC  GTC
                          CGC  GACCII
GAM279  DMRT1       GCAGCCGGAGGCGCAGCTGG      4240 TAGC     T__  AG  TG
                          AGCCGGAG  CAG TGG
                          ||||||||  ||| |||
                          TCGGCCTC  GTC ACC
                          ____       CGC  G_  TC
GAM279  GNG2        CAGCTAGAATCAGAGTGGTGG     4238  CG         I
                         AGC  GAGTCAGAGTGGTG
                         |||  ||||||||||||||
                         TCG  CTTAGTCTCACCAC
                          AT        I
GAM279  GNG2        CAGCTAGAATCAGAGTGGTGG     4238 TAGCAGCC
                            GGAGTCAGAGTGGTGG
                            ||||||||||||||||
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                              TCTTAGTCTCACCACC
                         GA_____
GAM279 LZTR1             AGACGACGGCCGAGTGGTGG    4236 ___ C  AGTCA        I
                           G CGG    GAGTGGTG
                           I III   IIIIIIII
                           C GCC    CTCACCAC
                         CTG T  GG___        I
GAM279 LZTR1             AGACGACGGCCGAGTGGTGG    4236 TAGCAGC  AGTCA
                             CGG    GAGTGGTG
                             III   IIIIIIII
                             GCC    CTCACCAC
                         CT_____  GG___
GAM279 NPY2R             GCAGCCGGAGCAGTCAGAGCGGCTGG 4239 AGC      ___         GI
                           CGGAGT  CAGAGTGGT
                           IIIIII  IIIIIIIII
                           GCCTCG  GTCTCGCCG
                         ___      TCA       AI
GAM279 NPY2R             GCAGCCGGAGCAGTCAGAGCGGCTGG 4239 TAGC        ___    _ II
                           AGCCGGAGT  CAGAGTGG TGG
                           IIIIIIIII  IIIIIIII III
                           TCGGCCTCG  GTCTCGCC ACC
                         ____         TCA      G CG
GAM279 SLC1A2            GCGGGAGCAGAGAGTGGTGG    4243 C   C_       II
                           GC GGAGT  AGAGTGGTG
                           II IIIII  IIIIIIIII
                           CG CCTCG  TCTCACCAC
                          C   TC     CI
GAM279 SLC1A2            GCGGGAGCAGAGAGTGGTGG    4243 T    CCGGAGTC
                           AGCAG      AGAGTGGTG
                           IIIII      IIIIIIIII
                           TCGTC      TCTCACCAC

                         _    _____
GAM280 BCL2L2            GCAGCTCCTCTTGGCTAAAGGTC  4250 CAGG   __       I
                           CCTC  GGCTAAAGGT
                           IIII  IIIIIIIIII
                           GGAG  CCGATTTCCA
                         GA__   AA       I
GAM280 BCL2L2            GCAGCTCCTCTTGGCTAAAGGTC  4250 T AGG  __        GI
                           GGC  CCTC GGCTAAAGGTCT
                           III  IIII IIIIIIIIIIII
                           TCG  GGAG CCGATTTCCAGG
                         _  A__  AA       GI
GAM280 COMT             GCAGGCCTCGGC-CGAGGTGTG   4253 _        AA  CTI
                           CAGGCCTCGGCT AGGT
                           IIIIIIIIIIII IIII
                           GTCCGGAGCCGG TCCA
                         C        C_  CAI
GAM280 COMT             GCAGGCCTCGGC-CGAGGTGTG   4253 TGGC       AA  CTG
                           AGGCCTCGGCT AGGT
                           IIIIIIIIIII IIII
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                              TCCGGAGCCGG  TCCA
                              ____          C_    CAC
GAM280  CXorf6      GGCAGGCCT-GGCCAGAAGGT    4255       C   _   I
                        GCAGGCCT GGCTA AAGG
                        ||||||||| ||||| ||||
                        CGTCCGGA CCGGT TTCC
                              _    C   I
GAM280  CXorf6      GGCAGGCCT-GGCCAGAAGGT    4255 TG    C   _   CT
                          GCAGGCCT GGCTA AAGGT
                          ||||||||| ||||| |||||
                          CGTCCGGA CCGGT TTCCA
                          __    _    C   CI
GAM280  CYP1A1        GCAGGCCTCCTGGCTCAAG      4251       __  AAAIII
                        GCAGGCCTC GGCT
                        ||||||||| ||||
                        CGTCCGGAG CCGA
                          GA  GTTCII
GAM280  CYP1A1        GCAGGCCTCCTGGCTCAAG      4251 TGGC    __  A  GTCT
                          AGGCCTC GGCT AAG
                          ||||||| |||| |||
                          TCCGGAG CCGA TTC
                          ____      GA  G  GTII
GAM280  EPHB2       AGGCC-CAGC-AAAGGTCTG       4248 _  T   T    I
                          GGCC CGGC AAAGGTCT
                          |||| |||| ||||||||
                          CCGG GTCG TTTCCAGA
                          T  _   _    I
GAM280  GNPI      GGCAGGCCTGTGCAAGAAGGACT    4256 G     CG  TA_  TCI
                        CAGGCCT GC  AAGG
                        ||||||| || ||||
                        GTCCGGA CG  TTCC
                          _    CA  TTC   TGI
GAM280  GNPI      GGCAGGCCTGTGCAAGAAGGACT    4256 TG    CG  TA_  T GI
                        GCAGGCCT GC  AAGG CT
                        |||||||| || |||| ||
                        CGTCCGGA CG  TTCC GA
                          __     CA  TTC  T GI
GAM280  ITPKB       GCAGGCCTCCGC---AGGT       4252       G TAA
                        GCAGGCCTC GC  AGG
                        ||||||||| || |||
                        CGTCCGGAG CG  TCC
                          G ___
GAM280  ITPKB       GCAGGCCTCCGC---AGGT       4252 TGGC    G TAA
                        AGGCCTC GC  AGGT
                        ||||||| || ||||
                        TCCGGAG CG  TCCA
                        ____       G ___
GAM280  NAGA      GGCAGGCCTGGGAT-GAGGT       4257 _    C CTAA  I
                        GCAGGCCT GG   AGG
                        |||||||| ||   |||
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                         CGTCCGGA CC   TCC
                         C      C TAC_  I
GAM280 NAGA              GGCAGGCCTGGGAT-GAGGT    4257 TG      C CTAA  CT
                          GCAGGCCT GG   AGGT
                          IIIIIIII II   IIII
                          CGTCCGGA CC   TCCA
                          __       C TAC_   TI
GAM280 NPTX1             GGCAGGAGGGAGCTAAAGGTC   4258      CCTC       I
                          GCAGG   GGCTAAAGGT
                          IIIII   IIIIIIIIII
                          CGTCC   TCGATTTCCA
                           TCCC        I
GAM280 NPTX1             GGCAGGAGGGAGCTAAAGGTC   4258 TG   CCTC      TG
                          GCAGG   GGCTAAAGGTC
                          IIIII   IIIIIIIIII
                          CGTCC   TCGATTTCCAG
                          __   TCCC       TI
GAM280 RERE             CAGGCCTCGGTCCAAGCCTCTG   4249 A      _  AA   I
                         GGCCTCGG CTA  GGTCT
                         IIIIIIII III  IIIII
                         CCGGAGCC GGT  TCGGA
                         _      A __    G
GAM280 RERE             CAGGCCTCGGTCCAAGCCTCTG   4249 TGGCAG   _  AA   G
                          GCCTCGG CTA  GGTCT
                          IIIIIII III  IIIII
                          CGGAGCC GGT  TCGGA
                          _____      A __    G
GAM280 RNPEPL1          TGGCAGGCCTGGCCCACAG     4260       C  AA_  GTCT
                         TGGCAGGCCT GGCT  AG
                         IIIIIIIIII IIII   II
                         ACCGTCCGGA CCGG   TC
                         _     GTG   IIIG
GAM280 RNPEPL1          TGGCAGGCCTGGCCCACAG     4260       C  AAAII
                         TGGCAGGCCT GGCT
                         IIIIIIIIII IIII
                         ACCGTCCGGA CCGG
                         _     GTGTC
GAM280 SLC2A3           AGGGTTTGGCTAAAGGGTCTG    4247 GGCCTC      _  I
                          GGCTAAAGG TCT
                          IIIIIIIII III
                          CCGATTTCC AGA
                         CCAAA_        C  I
GAM280 SLC7A5           GGCAGGGGT-GAATAAAGGTCT   4259 _   CCTC GC      I
                          GCAGG  G TAAAGGTC
                          IIIII  I IIIIIIII
                          CGTCC   C ATTTCCAG
                          C   CCA_ TT     I
GAM280 SLC7A5           GGCAGGGGT-GAATAAAGGTCT   4259 TG   CCTC GC      G
                          GCAGG   G TAAAGGTCT
                          IIIII   I IIIIIIII
```

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                         CGTCC   C ATTTCCAGA
                          __    CCA_ TT      A
GAM280 ZNF278        GCAGGGCTCAG--AAAGGTCTG   4254    C    CT      I
                         GCAGG CTCGG  AAAGGTC
                         ||||| |||||  ||||||||
                         CGTCC GAGTC  TTTCCAG
                             C     __       A
GAM280 ZNF278        GCAGGGCTCAG--AAAGGTCTG   4254 TGGC  C    CT
                          AGG CTCGG  AAAGGTCT
                          ||| |||||  ||||||||
                          TCC GAGTC  TTTCCAGA
                          ___       C  __
GAM281 CD79B         TCACTGAGGCCAGGGAGCCT     4270      __       TGGCG
                         TCACTGAGG AGGGGCCT
                         ||||||||| |||||||||
                         AGTGACTCC TCCCTCGGA
                              GG      IIIGG
GAM281 CD79B         TCACTGAGGCCAGGGAGCCT     4270      __       III
                         TCACTGAGG AGGGGCC
                         ||||||||| ||||||||
                         AGTGACTCC TCCCTCGG
                              GG      AII
GAM281 CYP46         CACAGAGGAGGGGCCCCTGCCGG  4265  T       G   G I
                         AC GAGGAGGGG CCTTG CG
                         || ||||||||| ||||| ||
                         TG CTCCTCCCC GGGAC GC
                          T       G   G I
GAM281 CYP46         CACAGAGGAGGGGCCCCTGCCGG  4265 TC T       G   G I
                         AC GAGGAGGGG CCTTG CGG
                         || ||||||||| ||||| |||
                         TG CTCCTCCCC GGGAC GCC
                          __ T      G    G G
GAM281 DDX11         CTGACTGAGGCTGCCTTGGCGG   4266 TC      AGGGG
                          ACTGAGG   GCCTTGGCGG
                          ||||||    ||||||||||
                          TGACTCC   CGGAACCGCC
                          __     GA___
GAM281 DDX11         CTGACTGAGGCTGCCTTGGCGG   4266 TGAG   GG      I
                          GAGG GCCTTGGCG
                          |||| ||||||||||
                          CTCC CGGAACCGC
                          CTGA  GA      I
GAM281 EPHB6         TGAGGAGGGGGC--TGGTGG     4275          CT CI
                         TGAGGAGGGGGC TGG
                         |||||||||||| |||
                         ACTCCTCCCCCG ACC
                             __   AC
GAM281 GALE          TGAGGTAGGGGAGGCCTTGGC    4274    _  __       III
                         TGAGG AGGGG GCCTTGG
                         ||||| ||||| ||||||||
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                              ACTCC TCCCC  CGGAACC
                                 A    TC      GII
GAM281 GALE            TGAGGTAGGGGAGGCCTTGGC    4274 TCACTG  A         GG
                         AGG GGGGGCCTTGGC
                         ||| ||||||||||||
                         TCC CCTCCGGAACCG
                         CA____  _         AA
GAM281 ITGA11        CACAGAGCCTGAGGGAGGCCTTGGCG 4264 A__      AG         I
                         CTGAGG GGGGCCTTGGC
                         |||||| |||||||||||
                         GACTCC CTCCGGAACCG
                         TCG        __         I
GAM281 ITGA11        CACAGAGCCTGAGGGAGGCCTTGGCG 4264 TCA____      AG         GII
                         CTGAGG GGGGCCTTGGCG
                         |||||| ||||||||||||
                         GACTCC CTCCGGAACCGC
                         TGTCTCG    __         AII
GAM281 KIFC3         CTAAGGAGGGGGC--TGGC       4268          CT   I
                         CTGAGGAGGGGGC TGG
                         ||||||||||||| |||
                         GATTCCTCCCCCG ACC
                                __   G
GAM281 KIFC3         CTAAGGAGGGGGC--TGGC       4268 TCACTG        CT
                         AGGAGGGGGC TGGC
                         |||||||||| ||||
                         TCCTCCCCCG ACCG

                         _____    __
GAM281 MAPRE3        CTGGGGCAGGGGGCCTTGG        4267 A _         II
                         CTG GG AGGGGGCCTTG
                         ||| || |||||||||||
                         GAC CC TCCCCCGGAAC
                          C G      CI
GAM281 MAPRE3        CTGGGGCAGGGGGCCTTGG       4267 TCACTGA _       CG
                         GG AGGGGGCCTTGG
                         || |||||||||||
                         CC TCCCCCGGAACC
                         C_____ G       CA
GAM281 OAS3          TCAGGGAGGAGGGGGCATT       4272  CT        CTII
                         TCA GAGGAGGGGGC
                         ||| ||||||||||
                         AGT CTCCTCCCCCG
                           CC        TAAI
GAM281 OAS3          TCAGGGAGGAGGGGGCATT       4272  CT        CTTGGCG
                         TCA GAGGAGGGGGC
                         ||| |||||||||
                         AGT CTCCTCCCCCG
                           CC        TAAIIIG
GAM281 PLA2G2D         TCACTCAGGGAGAGGGGCCTTGG  4271  G _ _        CGGI
                         TCACT AGG AG GGGGCCTTGG
                         ||||| ||| || |||||||||
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                              AGTGA TCC TC CCCCGGAACC
                                G   C   T        IIIG
GAM281  PLA2G2D        TCACTCAGGGAGAGGGGCCTTGG   4271 CA  G  _ _       I
                              CT AGG AG GGGGCCTTG
                              II III II IIIIIIIII
                              GA TCC TC CCCCGGAAC
                              __  G   C   T      I
GAM281  PRODH         TCACAGAGGTGGGGGCCTTGG   4273   T   A       CGG
                             TCAC GAGG GGGGGCCTTGG
                             IIII IIII IIIIIIIIIII
                             AGTG CTCC CCCCCGGAACC
                               T   A        III
GAM281  PRODH         TCACAGAGGTGGGGGCCTTGG   4273   T   A       I
                             CAC GAGG GGGGGCCTTG
                             III IIII IIIIIIIIII
                             GTG CTCC CCCCCGGAAC
                              T   A       I
GAM281  RAD23A        ACTGGGGAGGGGGCCTTGG     4263 TCAC  A        _ G
                            TG GGAGGGGGCCTTGG C
                            II IIIIIIIIIIIIII I
                            AC CCTCCCCCGGAACC G
                            ____  C         C I
GAM281  RAD23A        ACTGGGGAGGGGGCCTTGG     4263   A        II
                            ACTG GGAGGGGGCCTTG
                            IIII IIIIIIIIIIII
                            TGAC CCTCCCCCGGAAC
                              C        CI
GAM281  SOST       CTGAGG--GGGGCCTTGCCGG    4269 _   AG     G I
                          TGAGG  GGGGCCTTG CG
                          IIIII IIIIIIIII II
                          ACTCC  CCCCGGAAC GC
                            G   __    G I
GAM281  SOST       CTGAGG--GGGGCCTTGCCGG    4269 TCACTGA  A     G
                          GG GGGGGCCTTG CG
                          II IIIIIIIII II
                          TC CCCCCGGAAC GC
                          _____ _      G
GAM282  ARHA       TGCCACCCATGAGAACTGGTG    4289 G    _ AG   TTI
                          CCACCCA GA  ACTG
                          IIIIIII II  IIII
                          GGTGGGT CT  TGAC
                          _      A  CT   CAI
GAM282  ARHA       TGCCACCCATGAGAACTGGTG    4289 TCACTGCC   _ AG   T
                          ACCCA GA  ACTG TG
                          IIIII II  IIII II
                          TGGGT CT  TGAC AC
                          _____     A  CT   C
GAM282  CCBL1      CTCCCACCCAGAACATTCTGT    4282 G        GA__ III
                          CT CCACCCAGAA  CTG
                          II IIIIIIIIII   III
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                    GA GGTGGGTCTT   GAC
                     G       GTAA  AII
GAM282 CCBL1        CTCCCACCCAGAACATTCTGT    4282 TCACTG      GA__  TG
                    CCACCCAGAA   CTGT
                    IIIIIIIIII  IIII
                    GGTGGGTCTT   GACA
                    _____      GTAA   CA
GAM282 CPE          CACTGGGGCCACCCAGAGGA    4279  ___       AGIII
                    CACT  GCCACCCAGA
                    IIII  IIIIIIIIII
                    GTGA  CGGTGGGTCT
                     CCC        CCTII
GAM282 CPE          CACTGGGGCCACCCAGAGGA    4279 TCACT_      A CTGTT
                    GCCACCCAGA GA
                    IIIIIIIIII II
                    CGGTGGGTCT CT
                    TGACCC        C CIIIG
GAM282 FMR2         TCACTGCCATCCACATGTCT    4286     C GAAGACTGTT
                    TCACTGCCA CCA
                    IIIIIIIII III
                    AGTGACGGT GGT
                     A  GTACAGAIII
GAM282 FMR2         TCACTGCCATCCACATGTCT    4286    C GAAGACI
                    CACTGCCA CCA
                    IIIIIIII III
                    GTGACGGT GGT
                     A  GTACAGI
GAM282 HOXD3        TCACTGCCACCTCCAATGTCTGCTG 4284       CA_ AGA   II
                    TCACTGCCACC GA CTGTTG
                    IIIIIIIIII II IIIIII
                    AGTGACGGTGG TT GACGAC
                     AGG ACA     II
GAM282 HOXD3        TCACTGCCACCTCCAATGTCTGCTG 4284 C      CA_ AGA   I
                    ACTGCCACC GA CTGTT
                    IIIIIIII II IIIII
                    TGACGGTGG TT GACGA
                    _     AGG ACA    I
GAM282 KRT19        TCCCT-CTACCCAGAAGAC    4285 A GCC      TGT
                    TC CT  ACCCAGAAGAC
                    II II  IIIIIIIIIII
                    AG GG  TGGGTCTTCTG
                    _ AGA        III
GAM282 KRT19        TCCCT-CTACCCAGAAGAC    4285 A GCC      I
                    TC CT  ACCCAGAAGA
                    II II  IIIIIIIIII
                    AG GG  TGGGTCTTCT
                    _ AGA        G
GAM282 MAGEA9       CACTGCCACTGAGAACACTGATTG 4281 A    CC  G  TTI
                    CTGCCAC  AGAA ACTG
                    IIIIIII  IIII IIII
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                    GACGGTG  TCTT TGAC
                    _    AC   G   TAA
GAM282 MAGEA9        CACTGCCACTGAGAACACTGATTG  4281 TC      CC   G   _   I
                    ACTGCCAC  AGAA ACTG TTG
                    |||||||| |||| |||| |||
                    TGACGGTG  TCTT TGAC AAC
                      __      AC   G   T  G
GAM282 MBNL          TCAGCTGC-AGTGAAAAGACTGTTG  4283  _    CACCC         I
                    TCA CTGC   AGAAGACTGTTG
                    ||| ||||   |||||||||||
                    AGT GACG   TTTTCTGACAAC
                     C   TCAC_        I
GAM282 MBNL          TCAGCTGC-AGTGAAAAGACTGTTG 4283 CA_   CACCC         I
                    CTGC    AGAAGACTGTT
                    ||||    |||||||||||
                    GACG    TTTTCTGACAA
                    GTC   TCAC_        I
GAM282 MECP2         TGCCACCCAACAGAAGATTGT    4288          ___    C  III
                    TGCCACCCA  GAAGA TG
                    |||||||||  ||||| ||
                    ACGGTGGGT  CTTCT AC
                     TGT    A  AII
GAM282 MECP2         TGCCACCCAACAGAAGATTGT    4288 TCACT  ACC     C   G
                      GCC  CAGAAGA TGTT
                      |||  ||||||| ||||
                      TGG  GTCTTCT ACAG
                    _____   GTT     A   A
GAM282 PPP2R2C       CACTGCCACCTCTGCAG-CTGT    4280        CAGA_ A I
                    ACTGCCACC   AG CTG
                    |||||||||   || |||
                    TGACGGTGG   TC GAC
                     AGACG _  I
GAM282 PPP2R2C       CACTGCCACCTCTGCAG-CTGT    4280 TC      CAGA_ A   G
                    ACTGCCACC   AG CTGTT
                    |||||||||   || |||||
                    TGACGGTGG   TC GACAG
                     __     AGACG _   I
GAM282 STMN1         TCACTGCCACCAACAGCACTGT    4287        CAGA _  TG
                    TCACTGCCACC   AG ACTGT
                    |||||||||||   || |||||
                    AGTGACGGTGG   TC TGACA
                     TTG_ G    II
GAM282 STMN1         TCACTGCCACCAACAGCACTGT    4287        CAGA _   I
                    CACTGCCACC   AG ACTG
                    ||||||||||   || ||||
                    GTGACGGTGG   TC TGAC
                     TTG_ G   I
GAM282 TM7SF3        ACTTGCACC-AGA-GACTGTTG    4278 C__  CAC   A    I
                    TGC  CCAGA GACTGTT
                    |||  ||||| |||||||
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                              ACG  GGTCT CTGACAA
                              TGA  T__    _    I
GAM282 TM7SF3         ACTTGCACC-AGA-GACTGTTG   4278 TCAC  CAC   A
                              TGC  CCAGA GACTGTT
                              |||  ||||| |||||||
                              ACG  GGTCT CTGACAA
                              A___    T__    _
GAM283 CDK10         GGCGGCCC-GC-TTGTTGCGG    4297 TG    A AG      C
                              GCGGCC TG  TTGTTGCGG
                              |||||| ||  |||||||||
                              CGCCGG GC  AACAACGCC
                              __    _ G_      A
GAM283 FBXL7         GGCGGCCAC---TTGTTGCGG    4294 TG     GAG
                              GCGGCCAT  TTGTTGCGG
                              ||||||||  |||||||||
                              CGCCGGTG  AACAACGCC

                              __      ___
GAM283 IFRD2         TGGTGGAGACCAGTTGTTGC    4299 ___  C   TGA     GGC
                              TGG GGCCA  GTTGTTGC
                              ||| |||||  ||||||||
                              ACC CTGGT  CAACAACG
                              ACC  T    ___        |||
GAM283 LASS1         GCGGCCATGAGGCGTTGCG     4292 TGGC      T     C
                              GGCCATGAG TGTTGCGG
                              ||||||||| ||||||||
                              CCGGTACTC GCAACGCT
                              ____         C      C
GAM283 MUCDHL        GGCGGCCAT-AGTGCTTGTGG   4295 TG     G  TG C C
                              GCGGCCAT AGT  TTG GG
                              |||||||| |||  ||| ||
                              CGCCGGTA TCA  AAC CC
                              __      _  CG  A T
GAM283 PDAP1         GGCCATGAGGGGCTGTTGCAGCG  4293 T___  C  CATGA    T   I
                              GG GGC   GTTGT GCGGCG
                              || |||   ||||| ||||||
                              CC CCG   CAACG CGCCGC
                              TACT _  A____    T   G
GAM283 SMARCD2       TGGCGGCCA-GAGCCGCTTGC   4298      T   _ GGC
                              TGGCGGCCA GAGTTGTT GC
                              ||||||||| |||||||| ||
                              ACCGCCGGT CTCGGCGA CG
                              _      A |||
GAM283 SOLH          TGGCGGCCAGGAGGTCTGGCCAGGCG 4300     T TT GC GII
                              TGGCGGCCA GAG GTT GGC
                              ||||||||| ||| ||| |||
                              ACCGCCGGT CTC CAG CCG
                              C __ A_ GTC
GAM283 TBX6          GGCGGCCATTTGGTGTGGGGG    4296 TG    GAG T C CG
                              GCGGCCAT  TTG TG GG
                              ||||||||  ||| || ||
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                    CGCCGGTA  AAC AC CC
                    __      ___  C A CC
GAM284 ARG2         GCTCGCCATCCTGGGAGGCCTG  4306 TG  _ A        AAGG
                    GCTG CC TGGGAGGCCTG
                    |||| || |||||||||||
                    CGGT GG ACCCTCCGGAC
                    AG  A _        CAII
GAM284 B3GNT3       TGGCAGACACTG-AGGCCTGAAG  4314   TGC GG      G
                    TGGC  CAT GAGGCCTGAAG
                    ||||  ||| ||||||||||
                    ACCG  GTG CTCCGGACTTC
                    TCT  A_       I
GAM284 BMP1         CTGCCATGGGGAAGGGCTGA      4304 TGGCTG    __ C AG
                    CCATGGG AGG CTGA
                    ||||||| ||| ||||
                    GGTACCC TCC GACT
                    _____     CT  C  CT
GAM284 BTG4         CTGCCATGGAAGCCC--AAGG     4305 TGGCTG   G   G
                    CCATGG AGGCCT AAG
                    |||||| |||||| |||
                    GGTACC TTCGGG TTC
                    _____    _   _
GAM284 ELMO1        GCAGCCATGGGAAGTGACCTGAAG  4308 TGGCT      ___       GI
                    GCCATGGGA GGCCTGAAG
                    ||||||||| |||||||||
                    CGGTACCCT CTGGACTTC
                    T____        TCA      GT
GAM284 GCN5L2       GCTGCACGCTTGGGGGTGCCTGAAGG 4307 TG _ CAT AG      II
                    GC TGC GGG GCCTGAAGG
                    || ||| ||| |||||||||
                    CG GCG CCC CGGACTTCC
                    A_ T AAC CA      AG
GAM284 HAP1         GGCTGCCATGTGGCCCAGGCCTG   4310 TG       _ ___       AAGGI
                    GCTGCCATG GG AGGCCTG
                    ||||||||| || |||||||
                    CGACGGTAC CC  TCCGGAC
                    __       A GGG    CIIIG
GAM284 IGFBP6       CCATGGGGCGGGGCCTGAAGG     4303 T  TGCCATG A
                    GGC    GG GGCCTGAAGG
                    |||     || |||||||||
                    CCG     CC CCGGACTTCC
                    _  _____  _
GAM284 LENG4        TGGAAGCCATGGGACGGCC       4311   CT     _ TGAAG
                    TGG  GCCATGGGA GGCC
                    |||  ||||||||| ||||
                    ACC  CGGTACCCT CCGG
                    TT   G  IIIGG
GAM284 LIF          TGTCTTCCTTCCCAGGCCTGAAGG  4317  G G ATGGG         I
                    TG CT CC   AGGCCTGAAGG
                    || || ||   ||||||||||
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                              AC GA GG    TCCGGACTTCC
                               A  A AAGGG          I
GAM284 MASP1          TGCCTGCCATGGGTGAGCCT    4312 G      A_    GAAG
                      TG CTGCCATGGG GGCCT
                      II IIIIIIIIII IIIII
                      AC GACGGTACCC TCGGA
                       G      AC   IIIG
GAM284 MUC4              GCAGCCCTTGGAGGCCTGA    4309 TGGCT  ATG      AG
                        GCC  GGAGGCCTGA
                        III  IIIIIIIIII
                        CGG  CCTCCGGACT
                        T___  GAA      CA
GAM284 SLC7A8         TGGCTCTGATCTCAGGCCTGAAGG  4316     GCCATGGG          I
                      TGGCT    AGGCCTGAAGG
                      IIIII    IIIIIIIIIII
                      ACCGA    TCCGGACTTCC
                       GACTAGAG        I
GAM284 SOX15          TGGCTATCATGGGAGGACTGCAGG  4315    C    C A I
                      TGGCTG CATGGGAGG CTG AGG
                      IIIIII IIIIIIIII III III
                      ACCGAT GTACCCTCC GAC TCC
                           A     T G  I
GAM284 STIM1          TGGATCCC-TGG-AGGCCTGA    4313   CTG ATG      AG
                      TGG  CC GGAGGCCTGA
                      III  II IIIIIIIIII
                      ACC  GG CCTCCGGACT
                       TA_ GA_      II
GAM285 CNP           TACCTAGTT-ATGGTGTGAAGG    4324       CCA _    CI
                     TACCTAGTT  GGT TGAGGG
                     IIIIIIIII  III IIIIII
                     ATGGATCAA  CCA ACTTCC
                          TA_ C  II
GAM285 CNP           TACCTAGTT-ATGGTGTGAAGG    4324       CCA _    I
                      ACCTAGTT  GGT TGAGG
                      IIIIIIII  III IIIII
                      TGGATCAA  CCA ACTTC
                          TA_ C  I
GAM285 DRD3          TAGATCACAGGGTTGAGGGC    4327  T _  _    III
                     TAG TC CAGG TTGAGGG
                     III II IIII IIIIIIII
                     ATC AG GTCC AACTCCC
                      T T  C   GII
GAM285 HOXC11        ACCTAACACCAGGTTGAAGG    4321    TT      I
                     CCTAG CCAGGTTGAGG
                     IIIII IIIIIIIIIII
                     GGATT GGTCCAACTTC
                      GT      I
GAM285 HOXC11        ACCTAACACCAGGTTGAAGG    4321 TA  TT       C
                     CCTAG CCAGGTTGAGGG
                     IIIII IIIIIIIIIII
```

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                         GGATT  GGTCCAACTTCC
                          __     GT           A
GAM285  KCNK6            ACCTAGTTCCA-GTTCCGGG    4322 _          GTTGA  I
                          CCTAGTTCCAG    GG
                          |||||||||||    ||
                          GGATCAAGGTC    CC
                          T          AAGG_  I
GAM285  KCNK6            ACCTAGTTCCA-GTTCCGGG    4322 TA         GTTGA  C
                          CCTAGTTCCAG    GGG
                          |||||||||||    |||
                          GGATCAAGGTC    CCC
                          __          AAGG_  T
GAM285  MYO5A            TACCTAGTT---GGTTAAGG    4325         CCA      G
                          TACCTAGTT  GGTTGAGG
                          |||||||||  ||||||||
                          ATGGATCAA  CCAATTCC
                            ___          I
GAM285  MYO5A            TACCTAGTT---GGTTAAGG    4325 _       CCA
                          ACCTAGTT  GGTTGAG
                          ||||||||  |||||||
                          TGGATCAA  CCAATTC
                          A          ___
GAM285  PIP5K1A          CTTGTTCCAGGTCTTCTGAGG    4323 CTA       ____    IIIC
                          GTTCCAGGT  TGAG
                          |||||||||  ||||
                          CAAGGTCCA  ACTC
                          GAA        GAAG  CIII
GAM285  SIGLEC11          ACCTGG---CAGGTTGAGG    4320    A TTC
                          ACCT G  CAGGTTGAG
                          |||| |  |||||||||
                          TGGA C  GTCCAACTC
                            C ___
GAM285  SIGLEC11          ACCTGG---CAGGTTGAGG    4320 TA   A TTC
                          CCT G  CAGGTTGAGG
                          ||| |  ||||||||||
                          GGA C  GTCCAACTCC
                          __   C ___
GAM285  SIGLEC9          TAGCTCATCACGTTGAGGGC    4326    __ G      III
                          TAGTTC  CA GTTGAGGG
                          ||||||  || |||||||||
                          ATCGAG  GT CAACTCCC
                          TA  G      GII
GAM285  SIGLEC9          TAGCTCATCACGTTGAGGGC    4326 TACCTAGTTC  G
                             CA GTTGAGGGC
                             || |||||||||
                             GT CAACTCCCG
                          AGTA_____  G
GAM286  AAT1             CCTCCTGGAATCCTGATGC    4331 G _        AGII
                          CC CC GGAATCCTGA
                          || || ||||||||||
```

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                           GG GG CCTTAGGACT
                            A  A       ACGI
GAM286  AAT1          CCTCCTGGAATCCTGATGC     4331 TGCCG _      A  CCA
                           CC GGAATCCTGA GC
                           || |||||||||| ||
                           GG CCTTAGGACT CG
                           A____ A    A  AAI
GAM286  ARSA          GCCGCC----TCCTGAAGCTCCA  4335    GGAA      CI
                           GCCGCC  TCCTGAAGC
                           ||||||  |||||||||
                           CGGCGG  AGGACTTCG
                             ____        AG
GAM286  ARSA          GCCGCC----TCCTGAAGCTCCA  4335 TG   GGAA       _
                           CCGCC  TCCTGAAGC CCA
                           |||||  ||||||||| |||
                           GGCGG  AGGACTTCG GGT
                           __  ____        A
GAM286  ATRX          TGCAGCTCACAATCCCATGAAGCCCA 4341  C _ G   __     AII
                           TGC GC CG AATCCT GAAGCCCA
                           ||| || || |||||| ||||||||
                           ACG CG GT TTAGGG CTTCGGGT
                            T  A  G   TA      III
GAM286  ATRX          TGCAGCTCACAATCCCATGAAGCCCA 4341 GCC _ G   __    I
                           GC CG AATCCT GAAGCCC
                           || || |||||| |||||||
                           CG GT TTAGGG CTTCGGG
                           ___  A G  TA    I
GAM286  CASP2         CCGTGCATCCTGAAGATCAA    4330  GA_    CC II
                           CCG ATCCTGAAG CA
                           ||| |||||||| ||
                           GGC TAGGACTTC GT
                           ACG       TA TI
GAM286  CASP2         CCGTGCATCCTGAAGATCAA     4330 TGCCGCCGGA    CC
                           ATCCTGAAG CA
                           ||||||||| ||
                           TAGGACTTC GT
                           G_____     TA
GAM286  CDKN2B        GCCGCCGGGGACTTACTGAAGCCCA 4333  CC ATC_     I
                           CCG GGA  CTGAAGCCC
                           ||| |||  |||||||||
                           GGC CCT  GACTTCGGG
                           C_ GAAT      I
GAM286  CDKN2B        GCCGCCGGGGACTTACTGAAGCCCA 4333 TG    AATC___     AII
                           CCGCCGG   CTGAAGCCCA
                           |||||||   ||||||||||
                           GGCGGCC   GACTTCGGGT
                           __    CCTGAAT     GII
GAM286  CHIC2         TGCCGCCGG-CTCC-GAGGCC   4342    AA T A CA
                           TGCCGCCGG TCC GA GCC
                           ||||||||| ||| || |||
```

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                        ACGGCGGCC  AGG CT CGG
                          G_  _ C  II
GAM286  CHIC2           TGCCGCCGG-CTCC-GAGGCC    4342 _      AA  T A  I
                          GCCGCCGG  TCC GA GC
                          |||||||| ||| || ||
                          CGGCGGCC  AGG CT CG
                          A    G_  _ C  I
GAM286  EBAF            TGCCCCCAG---CCTGAAGCCC    4343   G   AAT      A
                          TGCC CCGG  CCTGAAGCCC
                          |||| ||||  ||||||||||
                          ACGG GGTC  GGACTTCGGG
                           G   ___       I
GAM286  EBAF            TGCCCCCAG---CCTGAAGCCC    4343 _  G   AAT
                          GCC CCGG  CCTGAAGCC
                          ||| ||||  |||||||||
                          CGG GGTC  GGACTTCGG
                          A  G   ___
GAM286  LANCL1          GCCTCCCGCGTCCTGAAGCCC    4339 ____   CGGAA      I
                          CCGC   TCCTGAAGCC
                          ||||   ||||||||||
                          GGCG   AGGACTTCGG
                          GGAG   C____      I
GAM286  LANCL1          GCCTCCCGCGTCCTGAAGCCC    4339 TG__   CGGAA     AA
                          CCGC   TCCTGAAGCCC
                          ||||   |||||||||||
                          GGCG   AGGACTTCGGG
                          GGAG   C____      AI
GAM286  PAX7            GCGGCCGGAATC--GAGGCC     4338  C      CTGAAGI
                          GC GCCGGAATC
                          || |||||||||
                          CG CGGCCTTAG
                           C      CTCCGGI
GAM286  PAX7            GCGGCCGGAATC--GAGGCC     4338 TGCC     CT A  C
                          GCCGGAATC  GA GCC
                          |||||||||  || |||
                          CGGCCTTAG  CT CGG
                          GC__      __ C  C
GAM286  PTPRE           GCCGTGGGT-TCCTGAAGCC     4337 CC   GAA__       I
                          GCCG    TCCTGAAGC
                          ||||    ||||||||||
                          CGGC    AGGACTTCG
                          __  ACCCA      I
GAM286  PTPRE           GCCGTGGGT-TCCTGAAGCC     4337 TG  CC AA      CA
                          CCG GG  TCCTGAAGCC
                          ||| ||  ||||||||||
                          GGC CC  AGGACTTCGG
                          __  A_ CA      CI
GAM286  ROCK2           GCC-CCGGGAGGCTGAAGCCCA   4340 _  G   AATC      I
                          CC CCGG   CTGAAGCCC
                          || ||||   |||||||||
```

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                        GG GGCC   GACTTCGGG
                        C  _  CTCC        I
GAM286 ROCK2        GCC-CCGGGAGGCTGAAGCCCA   4340 TG  G   AATC        A
                        CC CCGG   CTGAAGCCCA
                        || ||||  ||||||||||
                        GG GGCC   GACTTCGGGT
                        __ _  CTCC        C
GAM286 RPS6KA2      GCCAGCGGGCACCTCCTGAAGCCC  4332 CC  C AA__        I
                        GC GG   TCCTGAAGCC
                        || ||   ||||||||||
                        CG CC   AGGACTTCGG
                        __ C GTGG         I
GAM286 RPS6KA2      GCCAGCGGGCACCTCCTGAAGCCC  4332 TG _  C AA__        AAI
                        CC GC GG   TCCTGAAGCCC
                        || || ||  |||||||||
                        GG CG CC   AGGACTTCGGG
                        __ T C GTGG         AII
GAM286 SMARCA3       GCC-CCGCAGCCCTGAAGCC      4336 ___  C AA      I
                        CCGC GG  TCCTGAAGC
                        |||| ||  |||||||||
                        GGCG TC  GGGACTTCG
                        CGG  _ __         I
GAM286 SMARCA3       GCC-CCGCAGCCCTGAAGCC      4336 TG  C AA      CA
                        CCGC GG  TCCTGAAGCC
                        |||| ||  ||||||||||
                        GGCG TC  GGGACTTCGG
                        GG  _ __         CI
GAM286 TNFSF10     GCAGCCGG--TCACTGAAGCCC     4334 CC_   AA _    I
                        GCCGG  TC CTGAAGCC
                        ||||| || |||||||||
                        CGGCC  AG GACTTCGG
                        CGT   __ T    I
GAM286 TNFSF10     GCAGCCGG--TCACTGAAGCCC     4334 TGCC   AA _    A
                        GCCGG  TC CTGAAGCCC
                        ||||| || ||||||||||
                        CGGCC  AG GACTTCGGG
                        GT__   __ T    A
GAM287 CRAT       GGGAACCAAGGAGCTGAGCCCTG    4348 T_ G    _ GTI
                        AT AAGGAGCTG GCC
                        || |||||||||| |||
                        TG TTCCTCGAC CGG
                        CT G    T III
GAM287 CRAT       GGGAACCAAGGAGCTGAGCCCTG    4348 TCGGGT G      _ G I
                        AT AAGGAGCTG GCC TG
                        || ||||||||| ||| ||
                        TG TTCCTCGAC CGG AC
                        CT____ G    T G C
GAM287 ISG20      TCAGGGCTGACGGAGCTGGC       4352 TA A     CGT
                        TCGGG TGA GGAGCTGGC
                        ||||| ||| |||||||||
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                          AGTCC  ACT CCTCGACCG
                            CG  G       III
GAM287  ISG20        TCAGGGCTGACGGAGCTGGC      4352 C_    A   A      I
                          GGGT TGA GGAGCTGG
                          |||| ||| |||||||||
                          CCCG ACT CCTCGACC
                            GT  _  G          I
GAM287  MBD3         CGGGCATGGGGAGGAGCTGGCC    4346 ____   TAT A      I
                          GGG  GA GGAGCTGGC
                          |||  || |||||||||
                          CCC  CT CCTCGACCG
                          CGTA ___  _        I
GAM287  MBD3         CGGGCATGGGGAGGAGCTGGCC    4346 TC     A__        GTG
                          GGGTATG AGGAGCTGGCC
                          ||||||| |||||||||||
                          CCCGTAC TCCTCGACCGG
                          __    CCC        AII
GAM287  NAGA       GGGCAT--AGAACCTGGCCGTG     4350     GA  G      I
                          GGGTAT AGGA CTGGCCG
                          |||||| |||| |||||||
                          CCCGTA TCTT GACCGGC
                           __   G     A
GAM287  NAGA       GGGCAT--AGAACCTGGCCGTG     4350 TCGG   GA  G
                          GTAT AGGA CTGGCCGT
                          |||| |||| |||||||||
                          CGTA TCTT GACCGGCA
                          ____  __   G
GAM287  PCDH1        GGGCATTTGGGAGCTGGCCG      4349     GAA        I
                          GGTAT GGAGCTGGCC
                          ||||| ||||||||||
                          CCGTA CCTCGACCGG
                           AAC        I
GAM287  PCDH1        GGGCATTTGGGAGCTGGCCG      4349 TCGG   GAA        T
                          GTAT GGAGCTGGCCG
                          |||| |||||||||||
                          CGTA CCTCGACCGGC
                          ____   AAC       C
GAM287  PCDHGB7     CGGGTCTC--GGAGCTGGC       4347     ATGAA      I
                          CGGGT  GGAGCTGG
                          |||||  |||||||||
                          GCCCA  CCTCGACC
                          GAG__      G
GAM287  PCDHGB7     CGGGTCTC--GGAGCTGGC       4347 TC   ATGAA        CG
                          GGGT  GGAGCTGGC
                          ||||  ||||||||||
                          CCCA  CCTCGACCG
                          __  GAG__       TI
GAM287  TLL2        GGTATGAAGAAGCATAGCCG      4351           _    II
                          GGTATGAAGGAGC TGGCC
                          ||||||||||| |||||
```

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                        CCATACTTCTTCG ATCGG
                             T    CI
GAM287  TLL2        GGTATGAAGAAGCATAGCCG    4351 TCGGGT      _     T
                        ATGAAGGAGC TGGCCG
                        ||||||||| |||||
                        TACTTCTTCG ATCGGC
                        _____        T    C
GAM288  BCAT1        GGTAAGGTAAGTTACTACTACCA  4362 TGGC  _   C_      AI
                        AAGG AAGT  CTACTACCAG
                        |||| ||||  ||||||||||
                        TTCC TTCA  GATGATGGTT
                        CA__   A   AT       II
GAM288  BUB3        GGAAAGGTCCAAGTCCTACT--CAGA 4361 TGGC   ___      AC   I
                        AAGG  AAGTCCTACT CAGA
                        ||||  |||||||||| ||||
                        TTCC  TTCAGGATGA GTCT
                        CT__  AGG        __    C
GAM288  EIF2B5      GCAAGGAAG--CTGCCACC    4358 TGGC    CCTA   A
                        AAGGAAGT  CTACC
                        ||||||||  |||||
                        TTCCTTCG  GGTGG
                        ____      AC__    C
GAM288  NOTCH2      CAAGGAAGTAACCATAGTACCA  4355 TGGCAA    __ _ C    GA
                        GGAAGT CC TA TACCA
                        |||||| || || |||||
                        CCTTCA GG AT ATGGT
                        _____      TT  T  C   GA
GAM288  OVOL1       TGGGTAGGAAGTCCTGCTGCCAG  4367   CA     A A  AI
                        TGG AGGAAGTCCT CT CCAG
                        ||| |||||||||| || ||||
                        ACC TCCTTCAGGA GA GGTC
                        CA        C  C  II
GAM288  PAEP        GGCAGGAGGAAGTCCCACT    4360 TG  __       ACCAG
                        GCA AGGAAGTCCTACT
                        ||| ||||||||||||
                        CGT TCCTTCAGGGTGA
                        __  CC       CIIIA
GAM288  PPP1R12B    TGGCAAGGAACT-CTATTGCCAGA 4368    G C CTA   I
                        TGGCAAGGAA TC TA  CCAGA
                        ||||||||| || || |||||
                        ACCGTTCCTT AG AT  GGTCT
                        G _ AAC   I
GAM288  RAD52       GCAAGGAAGTCTTTCT-CCAG   4359 TGGC    CTA A
                        AAGGAAGTC CT CCAG
                        ||||||||| || ||||
                        TTCCTTCAG GA GGTC
                        ____      AAA  _
GAM288  RBBP9       GCATATGAAGTCCTAATAC    4357 TGGCAAG     C  CAG
                        GAAGTCCTA TAC
                        ||||||||| |||
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                                   CTTCAGGAT ATG
                        TATA___        T  AAI
GAM288  RNMT            TGTCAAGGAAGAGTCCTACTA    4365  G   __        CCAGA
                        TG CAAGGA  AGTCCTACTA
                        || |||||| |||||||||||
                        AC GTTCCT  TCAGGATGAT
                         A    TC        IIIAG
GAM288  RRM2            TGGCAAA-AGGTGATACTACCAG   4366      AA CC     A
                        TGGCAAGG GT TACTACCAG
                        |||||||| || |||||||||
                        ACCGTTTT CA ATGATGGTC
                            C_ CT       I
GAM288  SULT2B1         TGGCAAGGAACTTCCTCCT--CAGA  4364      G_  A AC  I
                        TGGCAAGGAA TCCT CT CAGA
                        |||||||||| |||| || ||||
                        ACCGTTCCTT AGGA GG GTCT
                           GA  _ A_  I
GAM288  TEM5            GGCAAGGAAGTGCT-CTTCC    4363 TG      C A A AG
                         GCAAGGAAGT CT CT CC
                         |||||||||| || || ||
                         CGTTCCTTCA GA GA GG
                          __        C _ A AI
GAM288  TNFRSF17         CAAGGAAGT--TTCTACCA    4356 TGGCAA    CCTA
                            GGAAGT  CTACCA
                            ||||||  ||||||
                            CCTTCA  GATGGT
                         _____     AA__
GAM289  CTBP1           CAGCGCTGCCCCCTCCCGC     4372 TGTCAG     CG  A
                          CGCTGCTCTC CCGC
                          |||||||||| ||||
                          GCGACGGGGG GGCG
                         _____      AG   G
GAM289  EGFL4           TGCCGGCGCTGCTC-CTGCCGC  4377  A      CC   AG
                         TGTC GCGCTGCTCT GCCGC
                         |||| |||||||||| |||||
                         ACGG CGCGACGAGG CGGCG
                           C      A_   II
GAM289  KPNB1           CAGCGCTGCTGTTGGCGGC     4373 TGTCAG    CTCC C A
                          CGCTGCT  GC GC
                          |||||||   || ||
                          GCGACGA   CG CG
                         _____      CAAC C A
GAM289  NEDD4L          TGCCTGCAGCTGCTCTCTGCC   4374   A _     C GCAG
                         TGTC GC GCTGCTCTC GCC
                         |||| || ||||||||| |||
                         ACGG CG CGACGAGAG CGG
                           A T    A IIIG
GAM289  PER2            TGGCAGTGGCTGCTCTCGGCC   4375  T C_     C GCAG
                         TG CAG  GCTGCTCTC GCC
                         || ||| ||||||||| |||
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                         AC GTC  CGACGAGAG CGG
                          C  AC      C  IIIG
GAM289  PVR              CAGCGCTGC-CTCCCCCTGCA   4371 TGTCAG     T   G _
                         CGCTGC CTCC CC GCA
                         ||||||| |||| || |||
                         GCGACG GAGG GG CGT
                         _____     _  G  A
GAM289  RELA             TGCCAGC-CTGCTCTCCCCC    4376        G     G GCA
                         TGTCAGC CTGCTCTCC CC
                         ||||||| ||||||||| ||
                         ACGGTCG GACGAGAGG GG
                              _      G III
GAM290  ARHGAP6          CGCTCAGACAGCACTGGGGA    4386        C _    AGGT
                         CGCTCAGACA CA TGGGGA
                         |||||||||| || ||||||
                         GCGAGTCTGT GT ACCCCT
                               C  G    IIIG
GAM290  ARHGAP6          CGCTCAGACAGCACTGGGGA    4386        C _   II
                         CGCTCAGACA CA TGGGG
                         |||||||||| || |||||
                         GCGAGTCTGT GT ACCCC
                               C  G   TI
GAM290  ARHGEF12         CTCA-ATACCAGTGGGGAAGG   4391  AC  _      I
                         TCAG  ACCA TGGGGAAG
                         ||||  |||| |||||||||
                         AGTT  TGGT ACCCCTTC
                               A_   C        I
GAM290  ARHGEF12         CTCA-ATACCAGTGGGGAAGG   4391 CGCTCAGAC  _
                         ACCA TGGGGAAGGT
                         |||| ||||||||||
                         TGGT ACCCCTTCCG
                         GTTA_____   C
GAM290  C18orf2          AGTCTCCATGGG-AAGGTG     4382 AGACA     G   I
                         CCATGGG AAGGT
                         ||||||| |||||
                         GGTACCC TTCCA
                         TCAGA     _    C
GAM290  COLQ             CAGACACCA-GGTGATGGT     4385       T G A I
                         CAGACACCA GG GA GG
                         ||||||||| || || ||
                         GTCTGTGGT CC CT CC
                          _  A  A  A
GAM290  COLQ             CAGACACCA-GGTGATGGT     4385 CGCTCAGA   T G A
                         CACCA GG GA GG
                         ||||| || || ||
                         GTGGT CC CT CC
                         _____  _ A A
GAM290  CST              CTCAGACACCA-GGCG-TGGTG  4395         T GGAAGGI
                         CTCAGACACCA GG
                         |||||||||| ||
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                         GAGTCTGTGGT CC
                         _ GCACCAC
GAM290 CST          CTCAGACACCA-GGCG-TGGTG   4395 CGCT      T GGAA
                         CAGACACCA GG   GGT
                         |||||||| ||   |||
                         GTCTGTGGT CC   CCA
                         ____      _ GCA_
GAM290 HBQ1         CTCAAACAC---GGGGAAGGT   4394 _      CAT
                         TCAGACAC  GGGGAAGG
                         |||||||  ||||||||
                         AGTTTGTG  CCCCTTCC
                         G      ___
GAM290 HBQ1         CTCAAACAC---GGGGAAGGT   4394 CGCT     CAT
                         CAGACAC  GGGGAAGG
                         |||||||  ||||||||
                         GTTTGTG  CCCCTTCC

                         ____      ___
GAM290 IER5        CTCTTAAACCCTGGGGAAGG    4393 CG  C   A A      T
                         CT AGAC CC TGGGGAAGG
                         || |||| || |||||||||
                         GA TTTG GG ACCCCTTCC
                         __ A  _ _      T
GAM290 IER5        CTCTTAAACCCTGGGGAAGG    4393 TC__   A A     I
                         AGAC CC TGGGGAAG
                         |||| || |||||||||
                         TTTG GG ACCCCTTC
                         AGAA  _ _     I
GAM290 ILK        AGACACCATGTGGCAAGTG    4381        _ G  GTII
                         AGACACCATG GG AAG
                         |||||||||| || |||
                         TCTGTGGTAC CC TTC
                         A  G  ACII
GAM290 KIF5C     CGCTCCGAGCCC---GGGAAGGTG  4389   A CA ATG
                         CGCTC GA CC  GGGAAGGTG
                         ||||| || || |||||||||
                         GCGAG CT GG  CCCTTCCAC
                         G  CG ___
GAM290 KIF5C     CGCTCCGAGCCC---GGGAAGGTG  4389 _  A CA ATG
                         GCTC GA CC  GGGAAGGT
                         |||| || ||  ||||||||
                         CGAG CT GG  CCCTTCCA
                         G   G CG ___
GAM290 MMP15       CGCTCAGGG-CCATGGGGAAG   4387     ACA      GT
                         CGCTCAG  CCATGGGGAAG
                         |||||||  |||||||||||
                         GCGAGTC  GGTACCCCTTC
                         CC_       ||
GAM290 MMP15       CGCTCAGGG-CCATGGGGAAG   4387 _   ACA      I
                         GCTCAG  CCATGGGGAA
                         ||||||  ||||||||||
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                        CGAGTC  GGTACCCCTT
                        G     CC_        I
GAM290 NEK6            GCTCAGACA--AT-TGGAAGGT   4397       CCATGG    I
                        GCTCAGACA    GGAAG
                        IIIIIIIII    IIIII
                        CGAGTCTGT    CCTTC
                            TAA___     C
GAM290 NEK6            GCTCAGACA--AT-TGGAAGGT   4397 CG      CCATGG
                         CTCAGACA     GGAAGGT
                         IIIIIIII     IIIIIII
                         GAGTCTGT     CCTTCCA
                        __      TAA___
GAM290 PCDHGA1         TCAGT-ACCATGGGGATGGTG   4399 _ AC      A  I
                        CAG  ACCATGGGGA GGT
                        III IIIIIIIIII III
                        GTC  TGGTACCCCT CCA
                        A  A_      A  I
GAM290 PCDHGA1         TCAGT-ACCATGGGGATGGTG   4399 CGCTCAGAC      A
                            ACCATGGGGA GGT
                            IIIIIIIIII III
                            TGGTACCCCT CCA
                        CA_____       A
GAM290 PCDHGA10        TCAGT-ACCATGGGGATGGTG   4399 _ AC      A  I
                        CAG  ACCATGGGGA GGT
                        III IIIIIIIIII III
                        GTC  TGGTACCCCT CCA
                        A  A_      A  I
GAM290 PCDHGA10        TCAGT-ACCATGGGGATGGTG   4399 CGCTCAGAC      A
                            ACCATGGGGA GGT
                            IIIIIIIIII III
                            TGGTACCCCT CCA
                        CA_____       A
GAM290 PCDHGA11        TCAGT-ACCATGGGGATGGTG   4399 _ AC      A  I
                        CAG  ACCATGGGGA GGT
                        III IIIIIIIIII III
                        GTC  TGGTACCCCT CCA
                        A  A_      A  I
GAM290 PCDHGA11        TCAGT-ACCATGGGGATGGTG   4399 CGCTCAGAC      A
                            ACCATGGGGA GGT
                            IIIIIIIIII III
                            TGGTACCCCT CCA
                        CA_____       A
GAM290 PCDHGA12        TCAGT-ACCATGGGGATGGTG   4399 _ AC      A  I
                        CAG  ACCATGGGGA GGT
                        III IIIIIIIIII III
                        GTC  TGGTACCCCT CCA
                        A  A_      A  I
GAM290 PCDHGA12        TCAGT-ACCATGGGGATGGTG   4399 CGCTCAGAC      A
                            ACCATGGGGA GGT
                            IIIIIIIIII III
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                                  TGGTACCCCT CCA
                          CA_____          A
GAM290  PCDHGA2        TCAGT-ACCATGGGGATGGTG   4399 _ AC      A  I
                          CAG  ACCATGGGGA GGT
                          ||| ||||||||||| |||
                          GTC  TGGTACCCCT CCA
                          A A_        A  I
GAM290  PCDHGA2        TCAGT-ACCATGGGGATGGTG   4399 CGCTCAGAC      A
                              ACCATGGGGA GGT
                              |||||||||| |||
                              TGGTACCCCT CCA
                          CA_____          A
GAM290  PCDHGA3        TCAGT-ACCATGGGGATGGTG   4399 _ AC      A  I
                          CAG  ACCATGGGGA GGT
                          ||| ||||||||||| |||
                          GTC  TGGTACCCCT CCA
                          A A_      A  I
GAM290  PCDHGA3        TCAGT-ACCATGGGGATGGTG   4399 CGCTCAGAC      A
                              ACCATGGGGA GGT
                              |||||||||| |||
                              TGGTACCCCT CCA
                          CA_____          A
GAM290  PCDHGA4        TCAGT-ACCATGGGGATGGTG   4399 _ AC      A  I
                          CAG  ACCATGGGGA GGT
                          ||| ||||||||||| |||
                          GTC  TGGTACCCCT CCA
                          A A_       A  I
GAM290  PCDHGA4        TCAGT-ACCATGGGGATGGTG   4399 CGCTCAGAC      A
                              ACCATGGGGA GGT
                              |||||||||| |||
                              TGGTACCCCT CCA
                          CA_____          A
GAM290  PCDHGA5        TCAGT-ACCATGGGGATGGTG   4399 _ AC      A  I
                          CAG  ACCATGGGGA GGT
                          ||| ||||||||||| |||
                          GTC  TGGTACCCCT CCA
                          A A_        A  I
GAM290  PCDHGA5        TCAGT-ACCATGGGGATGGTG   4399 CGCTCAGAC      A
                              ACCATGGGGA GGT
                              |||||||||| |||
                              TGGTACCCCT CCA
                          CA_____          A
GAM290  PCDHGA6        TCAGT-ACCATGGGGATGGTG   4399 _ AC      A  I
                          CAG  ACCATGGGGA GGT
                          ||| ||||||||||| |||
                          GTC  TGGTACCCCT CCA
                          A A_       A  I
GAM290  PCDHGA6        TCAGT-ACCATGGGGATGGTG   4399 CGCTCAGAC      A
                              ACCATGGGGA GGT
                              |||||||||| |||
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                              TGGTACCCCT CCA
                        CA_____        A
GAM290  PCDHGA7         TCAGT-ACCATGGGGATGGTG   4399 _ AC      A  I
                          CAG  ACCATGGGGA GGT
                          |||  |||||||||| |||
                          GTC  TGGTACCCCT CCA
                          A A_       A  I
GAM290  PCDHGA7         TCAGT-ACCATGGGGATGGTG   4399 CGCTCAGAC      A
                            ACCATGGGGA GGT
                            |||||||||| |||
                            TGGTACCCCT CCA
                        CA_____        A
GAM290  PCDHGA8         TCAGT-ACCATGGGGATGGTG   4399 _ AC      A  I
                          CAG  ACCATGGGGA GGT
                          |||  |||||||||| |||
                          GTC  TGGTACCCCT CCA
                          A A_       A  I
GAM290  PCDHGA8         TCAGT-ACCATGGGGATGGTG   4399 CGCTCAGAC      A
                            ACCATGGGGA GGT
                            |||||||||| |||
                            TGGTACCCCT CCA
                        CA_____        A
GAM290  PCDHGA9         TCAGT-ACCATGGGGATGGTG   4399 _ AC      A  I
                          CAG  ACCATGGGGA GGT
                          |||  |||||||||| |||
                          GTC  TGGTACCCCT CCA
                          A A_       A  I
GAM290  PCDHGA9         TCAGT-ACCATGGGGATGGTG   4399 CGCTCAGAC      A
                            ACCATGGGGA GGT
                            |||||||||| |||
                            TGGTACCCCT CCA
                        CA_____        A
GAM290  PCDHGB1         TCAGT-ACCATGGGGATGGTG   4399 _ AC      A  I
                          CAG  ACCATGGGGA GGT
                          |||  |||||||||| |||
                          GTC  TGGTACCCCT CCA
                          A A_       A  I
GAM290  PCDHGB1         TCAGT-ACCATGGGGATGGTG   4399 CGCTCAGAC      A
                            ACCATGGGGA GGT
                            |||||||||| |||
                            TGGTACCCCT CCA
                        CA_____        A
GAM290  PCDHGB2         TCAGT-ACCATGGGGATGGTG   4399 _ AC      A  I
                          CAG  ACCATGGGGA GGT
                          |||  |||||||||| |||
                          GTC  TGGTACCCCT CCA
                          A A_       A  I
GAM290  PCDHGB2         TCAGT-ACCATGGGGATGGTG   4399 CGCTCAGAC      A
                            ACCATGGGGA GGT
                            |||||||||| |||
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                              TGGTACCCCT CCA
                     CA_____           A
GAM290  PCDHGB3      TCAGT-ACCATGGGGATGGTG    4399 _ AC       A  I
                        CAG  ACCATGGGGA GGT
                        ||| |||||||||| |||
                        GTC  TGGTACCCCT CCA
                        A A_       A  I
GAM290  PCDHGB3      TCAGT-ACCATGGGGATGGTG    4399 CGCTCAGAC        A
                             ACCATGGGGA GGT
                             |||||||||| |||
                             TGGTACCCCT CCA
                     CA_____           A
GAM290  PCDHGB4      TCAGT-ACCATGGGGATGGTG    4399 _ AC       A  I
                        CAG  ACCATGGGGA GGT
                        ||| |||||||||| |||
                        GTC  TGGTACCCCT CCA
                        A A_       A  I
GAM290  PCDHGB4      TCAGT-ACCATGGGGATGGTG    4399 CGCTCAGAC        A
                             ACCATGGGGA GGT
                             |||||||||| |||
                             TGGTACCCCT CCA
                     CA_____           A
GAM290  PCDHGB5      TCAGT-ACCATGGGGATGGTG    4399 _ AC       A  I
                        CAG  ACCATGGGGA GGT
                        ||| |||||||||| |||
                        GTC  TGGTACCCCT CCA
                        A A_       A  I
GAM290  PCDHGB5      TCAGT-ACCATGGGGATGGTG    4399 CGCTCAGAC        A
                             ACCATGGGGA GGT
                             |||||||||| |||
                             TGGTACCCCT CCA
                     CA_____           A
GAM290  PCDHGB6      TCAGT-ACCATGGGGATGGTG    4399 _ AC       A  I
                        CAG  ACCATGGGGA GGT
                        ||| |||||||||| |||
                        GTC  TGGTACCCCT CCA
                        A A_       A  I
GAM290  PCDHGB6      TCAGT-ACCATGGGGATGGTG    4399 CGCTCAGAC        A
                             ACCATGGGGA GGT
                             |||||||||| |||
                             TGGTACCCCT CCA
                     CA_____           A
GAM290  PCDHGB7      TCAGT-ACCATGGGGATGGTG    4399 _ AC       A  I
                        CAG  ACCATGGGGA GGT
                        ||| |||||||||| |||
                        GTC  TGGTACCCCT CCA
                        A A_       A  I
GAM290  PCDHGB7      TCAGT-ACCATGGGGATGGTG    4399 CGCTCAGAC        A
                             ACCATGGGGA GGT
                             |||||||||| |||
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                              TGGTACCCCT CCA
                          CA_____        A
GAM290  PCDHGC3           TCAGT-ACCATGGGGATGGTG   4399 _ AC        A  I
                              CAG  ACCATGGGGA GGT
                              ||| |||||||||| |||
                              GTC  TGGTACCCCT CCA
                              A A_       A  I
GAM290  PCDHGC3           TCAGT-ACCATGGGGATGGTG   4399 CGCTCAGAC       A
                                  ACCATGGGGA GGT
                                  |||||||||| |||
                                  TGGTACCCCT CCA
                          CA_____        A
GAM290  PCDHGC4           TCAGT-ACCATGGGGATGGTG   4399 _ AC        A  I
                              CAG  ACCATGGGGA GGT
                              ||| |||||||||| |||
                              GTC  TGGTACCCCT CCA
                              A A_       A  I
GAM290  PCDHGC4           TCAGT-ACCATGGGGATGGTG   4399 CGCTCAGAC       A
                                  ACCATGGGGA GGT
                                  |||||||||| |||
                                  TGGTACCCCT CCA
                          CA_____        A
GAM290  PCDHGC5           TCAGT-ACCATGGGGATGGTG   4399 _ AC        A  I
                              CAG  ACCATGGGGA GGT
                              ||| |||||||||| |||
                              GTC  TGGTACCCCT CCA
                              A A_       A  I
GAM290  PCDHGC5           TCAGT-ACCATGGGGATGGTG   4399 CGCTCAGAC       A
                                  ACCATGGGGA GGT
                                  |||||||||| |||
                                  TGGTACCCCT CCA
                          CA_____        A
GAM290  PRDM2             CAGAGCTCACCATGGGCTGCAGGTG 4383 AGA        GA__  I
                              CACCATGGG    AGGT
                              ||||||||    ||||
                              GTGGTACCC   TCCA
                              A__        GACG   I
GAM290  PRDM2             CAGAGCTCACCATGGGCTGCAGGTG 4383 C   AGAC       GA__  II
                              GCTC   ACCATGGG   AGGTG
                              ||||   |||||||||   |||||
                              CGAG   TGGTACCC   TCCAC
                              _  ____       GACG    TG
GAM290  PRDM2             CTCAGACACCTTAGGCAAGG      4392        A  G  I
                              TCAGACACC TGGG AAG
                              ||||||||| |||| |||
                              AGTCTGTGG ATCC TTC
                                 A   G  I
GAM290  PRDM2             CTCAGACACCTTAGGCAAGG      4392 CGCT    A  G  T
                              CAGACACC TGGG AAGG
                              ||||||||| |||| ||||
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                        GTCTGTGG ATCC TTCC
                        ____      A  G  T
GAM290 PXN          CAGACACCATCAGTGAAGG     4384        G _   II
                        CAGACACCAT GG GAAG
                        IIIIIIIII II IIII
                        GTCTGTGGTA TC CTTC
                            G  A   CI
GAM290 PXN          CAGACACCATCAGTGAAGG     4384 CGCTCAGA   G _
                          CACCAT GG GAAGGT
                          IIIIII II IIIIII
                          GTGGTA TC CTTCCG
                        _____     G A
GAM290 RAI14        AGACACCATGGCTGAAAGT     4380        G_   II
                        AGACACCATGG GAAGG
                        IIIIIIIIII IIIII
                        TCTGTGGTACC CTTTC
                            GA    AI
GAM290 RARB       CTCAAACAGCTCGCATGGGGAA  4390      C____      IIIT
                        CTCAGACA   CATGGGGA
                        IIIIIIII   IIIIIIII
                        GAGTTTGT   GTACCCCT
                            CGAGC     TIII
GAM290 SLA        TCAGACACCA--GGGAGGG     4398      T   AAGI
                        TCAGACACCA GGGG
                        IIIIIIIIII IIII
                        AGTCTGTGGT CCCT
                          _    CCCI
GAM290 SLA        TCAGACACCA--GGGAGGG     4398 CGCTCA    T  AA
                        GACACCA GGGG GG
                        IIIIIII IIII II
                        CTGTGGT CCCT CC
                        _____    _    CC
GAM290 SPG3A     CGCTCAGACTC--TGAGGATGTTG 4388      ACCA    AG G
                        CGCTCAGAC  TGGGGA GT
                        IIIIIIIII  IIIIII II
                        GCGAGTCTG  ACTCCT CA
                           AG__    A_ A
GAM290 SPG3A     CGCTCAGACTC--TGAGGATGTTG 4388      ACCA    AGGI
                        CGCTCAGAC  TGGGGA
                        IIIIIIIII  IIIIII
                        GCGAGTCTG  ACTCCT
                           AG__   ACAA
GAM290 ZNF24      GCTCAGACA--A-GGGGAAG    4396      CCAT  I
                        GCTCAGACA  GGGGA
                        IIIIIIIII  IIIII
                        CGAGTCTGT  CCCCT
                            T___  T
GAM290 ZNF24      GCTCAGACA--A-GGGGAAG    4396 CG      CCAT
                        CTCAGACA  GGGGAAGG
                        IIIIIIII  IIIIIIII
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                    GAGTCTGT   CCCCTTCT
                    __        T___
GAM291 ANXA9        TCTGGCCAGGGTACAGGAGG    4425   A        C I
                    CTG CCAGGGTACGG AG
                    ||| |||||||||| ||
                    GAC GGTCCCATGTC TC
                        C        C I
GAM291 ANXA9        TCTGGCCAGGGTACAGGAGG    4425 AGTC  A      C   C
                      TG CCAGGGTACGG AGG
                      || |||||||||| |||
                      AC GGTCCCATGTC TCC
                    ___    C      C  C
GAM291 AQP6         TGACCAGGGCTTGCTCCAGGC   4426        ACGG__   III
                    TGACCAGGGT   CAGG
                    |||||||||    ||||
                    ACTGGTCCCG   GTCC
                       AACGAG   GII
GAM291 ARHGDIA      AGGCGGACCAGGGT--GGGAGG   4405 AGTCT     AC C  C
                      GACCAGGGT GG AGG
                      ||||||||| || |||
                      CTGGTCCCA CC TCC
                    TCCGC      __  C  I
GAM291 ARHGDIA      GACCAGGGT--GGGAGGGGC    4419       AC C  CI
                    GACCAGGGT GG AGG
                    ||||||||| || |||
                    CTGGTCCCA CC TCC
                          __ C  CC
GAM291 ATP11A       TGAGCAGGGTACGGC-GGTGC   4427 _ C      A CGI
                    GA CAGGGTACGGC GG
                    || ||||||||||| ||
                    CT GTCCCATGCCG CC
                    A C        _ ACI
GAM291 BACE         TCTG-CCAGGGTACCACAGG    4423 _ A      G  I
                    CTG CCAGGGTAC GCAG
                    ||| |||||||||| ||||
                    GAC GGTCCCATG TGTC
                      A _      G  I
GAM291 BACE         TCTG-CCAGGGTACCACAGG    4423 AGTC  A     G    C
                      TG CCAGGGTAC GCAGG
                      || |||||||||| |||||
                      AC GGTCCCATG TGTCC
                    ___  _    G   C
GAM291 BIRC7        TCTGACCAGGTTTGCAGCAG    4422       GTA_   II
                    TCTGACCAGG   CGGCA
                    |||||||||    |||||
                    AGACTGGTCC   GTCGT
                       AAAC   CI
GAM291 BIRC7        TCTGACCAGGTTTGCAGCAG    4422 AGTC     GTA_    C
                    TGACCAGG   CGGCAGG
                    ||||||||   |||||||
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                        ACTGGTCC   GTCGTCT
                    ____        AAAC     T
GAM291 GNAZ         GTTTCACCA---TA-GGCAGGCGC  4421 TCTG_   GGGTAC
                        ACCA     GGCAGGCG
                        ||||     |||||||||
                        TGGT     CCGTCCGC
                    CAAAG   AT____
GAM291 HRASLS       ACCCGGG-A-GGCAGGCGC   4402  A  TAC      I
                        ACC GGG   GGCAGGCG
                        ||| |||   ||||||||
                        TGG CCC   CCGTCCGC
                         G  T__      G
GAM291 MAPT         CTGAGGCCGGCGGGCGGCAGGCGC  4409 TGACCA__  TA      I
                        GGG CGGCAGGCG
                        ||| |||||||||
                        CCC GCCGTCCGC
                    TCCGGCCG  __      I
GAM291 MEN1         TGCCCAGCGGAGGGCAGGCGC   4428 GA   _ TAC      I
                        CCAG GG  GGCAGGCG
                        |||| ||  |||||||||
                        GGTC CC  CCGTCCGC
                     CG  G  TC_      I
GAM291 MUC1         GAACAGATTCAGGCAGGCGC   4418 AC   GTAC      I
                        CAGG   GGCAGGCG
                        ||||   |||||||||
                        GTCT   CCGTCCGC
                    TT  AAGT      I
GAM291 MUS81        CTGACCAGGGAATTCCAGGTGC   4415       TACGG   CGI
                        TGACCAGGG   CAGG
                        |||||||||   ||||
                        ACTGGTCCC   GTCC
                        TTAAG   ACI
GAM291 MUS81        CTGACCAGGGAATTCCAGG   4411 AGTCTG    TACGG   C
                        ACCAGGG   CAGG
                        |||||||   ||||
                        TGGTCCC   GTCC
                    _____      TTAAG   A
GAM291 NEO1         CTGACCAGGGGAAGGCAGG   4412        TAC   II
                        CTGACCAGGG  GGCAG
                        ||||||||||  |||||
                        GACTGGTCCC  CCGTC
                         CTT   CI
GAM291 NEO1         AGGCTGACCAGGGGAAGGCAGG  4406  T      TAC   CG
                        AG CTGACCAGGG  GGCAGG
                        || |||||||||  ||||||
                        TC GACTGGTCCC  CCGTCC
                         C      CTT   II
GAM291 NR1I2        AGGCTGACCAGGAGT-GGGGAGG  4404  T      _ AC C  CG
                        AG CTGACCAGG GT GG AGG
                        || ||||||||| || || |||
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                    TC GACTGGTCC CA  CC TCC
                        C    T CC _  II
GAM291 OPHN1         CTGACCAGGG-CCCGCTGGC    4413 AGTCTG      ACG A
                        ACCAGGGT  GC GGC
                        IIIIIIII  II III
                        TGGTCCCG  CG CCG
                        _____     GG_ A
GAM291 OPHN1         CTGACCAGGG-CCCGCTGGC    4413 C       AC___   AGI
                        TGACCAGGGT   GGC
                        IIIIIIIII   III
                        ACTGGTCCG   CCG
                        _       GGCGA  III
GAM291 OPTN         CTGACCAGGGAACCTGCCGGCG   4410 T     T G_ A  I
                        GACCAGGG AC  GC GGC
                        IIIIIIII II  II III
                        CTGGTCCC TG  CG CCG
                        _     T GA G  I
GAM291 PES1         TCTGACCAGGCACCAGCAGG     4424        GTA   I
                        CTGACCAGG  CGGCAG
                        IIIIIIIII  IIIIII
                        GACTGGTCC  GTCGTC
                            GTG     I
GAM291 PES1         TCTGACCAGGCACCAGCAGG     4424 AGTC       GTA     _
                        TGACCAGG  CGGCAGG C
                        IIIIIIII  IIIIIII I
                        ACTGGTCC  GTCGTCC G
                        ____        GTG     C
GAM291 PIGR         CCAGGCGTGCTGGCAGGCGC     4408    _ AC_      III
                        CCAGG GT  GGCAGGCG
                        IIIII II  IIIIIIII
                        GGTCC CA  CCGTCCGC
                         G CGA      GII
GAM291 PLGL         AGTCTGACCTAGGT-CTGCGGG   4407      A  ACG A  CG
                        AGTCTGACC GGGT  GC GG
                        IIIIIIIII IIII  II II
                        TCAGACTGG TCCA  CG CC
                         A  GA_ C  II
GAM291 PRKCABP       GAGCAGGG-A-GGCAGGCGC    4420 AC_   TAC    I
                        CAGGG  GGCAGGCG
                        IIIII  IIIIIIII
                        GTCCC  CCGTCCGC
                        CTC    T__    I
GAM291 SLC21A2       GACCAGGGTTAGTTGCAGG     4417       ACG__  III
                        GACCAGGGT   GCAG
                        IIIIIIIII   IIII
                        CTGGTCCCA   CGTC
                        ATCAA   CII
GAM291 SLC8A2       GACCAGGGTCCAAGAGCAGGTGC  4416 ACC   AC___     CGI
                        AGGGT   GGCAGG
                        IIIII    IIIIII
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                              TCCCA    TCGTCC
                        ___       GGTTC    ACI
GAM291  SSX3      AGCCTGACCAGGACGCATGGCA  4403          TACG  _
                        AGTCTGACCAGGG   GCA GGCG
                        |||||||||||   ||| ||||
                        TCGGACTGGTCCT   CGT CCGT
                              G___    A
GAM291  USP11     CTGACCAGGTAATGCCAAGC    4414      GTACG  AGGI
                        TGACCAGG    GC
                        ||||||||    ||
                        ACTGGTCC    CG
                         ATTA_ GTTC
GAM291  USP11     CTGACCAGGTAATGCCAAGC    4414 AGTCTG    GTACG  _
                        ACCAGG    GC AGGC
                        ||||||    || ||||
                        TGGTCC    CG TTCG
                        _____     ATTA_ G
GAM292  ABCC3     CACCTG-CTTCAGGAAGCTGGG   4436 _    T       CGI
                        ACTTG CTTCAGGAAGCT
                        ||||| |||||||||||
                        TGGAC GAAGTCCTTCGA
                        G    _        CCI
GAM292  ACCN2     TCACTTGTCTCTCATTAAGATAGG  4442      _  GG  CTCGI
                        ACTTGTCT TCA  AAG
                        |||||||| ||| |||
                        TGAACAGA AGT  TTC
                         G  AA  TATII
GAM292  APM1      CACTT-TCTCTGAGGAAGCTC    4433  G  C_       I
                        ACTT TCTT AGGAAGCT
                        |||| |||| ||||||||
                        TGAA AGAG TCCTTCGA
                         _   AC     I
GAM292  AQP1      CTTGGTCCCCAGGAAGCTCTGA   4438 TT        GI
                        GTCTTCAGGAAGCTC
                        |||||||||||||||
                        CAGGGGTCCTTCGAG
                        C_          AC
GAM292  ASL       CTCGTCGTCCGGAAGCTTCGG    4439 TT  T A   _  I
                        GTC TC GGAAGCT CG
                        ||| || |||||| ||
                        CAG AG CCTTCGA GC
                        G_   C  G    A I
GAM292  CABC1     TGGCTGCAGGAAGCTGGGA    4446  T  T     C  II
                        TG CT CAGGAAGCT GG
                        || || |||||||| ||
                        AC GA GTCCTTCGA CC
                         C  C      C TI
GAM292  CDR1      TGTCTTCCAACTAAGCTCGGA    4444       AGG__      III
                        TGTCTTC   AAGCTCGG
                        |||||||   |||||||
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                        ACAGAAG   TTCGAGCC
                          GTTGA     TII
GAM292 DAAM2            CACTTGTCTTGCAGTGGGAGCTC  4434 ACT    _  GA__   I
                        TGTCTT CAG   AGCT
                        ||||||  |||    ||||
                        ACAGAA GTC   TCGA
                              C  ACCC   I
GAM292 GBP1            TTGTCTTCACTAAGAAGCTAGG  4447       ___      CGIII
                        TTGTCTTCA  GGAAGCT
                        ||||||||| |||||||
                        AACAGAAGT  TCTTCGA
                            GAT      TCCII
GAM292 IRF2          TTGTCTTCA--AATCTGGGA    4448 _       GAAG  C  I
                        TGTCTTCAG   CT GG
                        |||||||||    || ||
                        ACAGAAGTT   GA CC
                        A     TA__  C  I
GAM292 NFRKB        CACT-GTCTTCAGGAAACTGGG   4437 C           CI
                        TTGTCTTCAGGAAGCT
                        ||||||||||||||||
                        GACAGAAGTCCTTTGA
                            T       CI
GAM292 NUCB1        ACTGGTCTTCAGG-GGCTC     4432  T     AA  I
                        ACT GTCTTCAGG GCT
                        ||| ||||||||| |||
                        TGA CAGAAGTCC CGA
                          C     C_  G
GAM292 PHEMX        TGTCCTCAGGAAGCTCCGGA    4445           _  II
                        TGTCTTCAGGAAGCTC GG
                        |||||||||||||||| ||
                        ACAGGAGTCCTTCGAG CC
                            G  TI
GAM292 RAB27A       TCACATGTCCTCTTCAGGAAG   4441  T   ___     III
                        TCAC TGTCT  TCAGGAA
                        |||| |||||  |||||||
                        AGTG ACAGG  AGTCCTT
                          T    AGA    CII
GAM292 SCAP1       CACTTGTCTTACTGGTAGCT    4435        CA_ A  II
                        CACTTGTCTT  GG AGC
                        ||||||||||  || |||
                        GTGAACAGAA  CC TCG
                          TGA A  AI
GAM292 SELPLG       TCACTTGTCACTAGATGGAAGCTC  4440 CAC    TTCA___     I
                        TTGTC    GGAAGCT
                        |||||    |||||||
                        AACAG    CCTTCGA
                          ___       TGATCTA    I
GAM292 SLC4A4       TCA-TTGTCTTCAGGTTCAAGTTC  4443 AC       AAGCTI
                        TTGTCTTCAGG
                        |||||||||||
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                          AACAGAAGTCC
                          __        AAGTTC
GAM292  USP14          ACATGTCTTCAGCCAAGCTC     4431  T       G_    II
                          AC TGTCTTCAG  AAGCT
                          II IIIIIIIII  IIIII
                          TG ACAGAAGTC  TTCGA
                          T       GG   GI
GAM293  CYP26A1        GGGGTGCGGGGCTAGGAGCTGC    4453      CCTCC      I
                          GGGTGTG   AGGAGCTG
                          IIIIIIII  IIIIIIIII
                          CCCACGC   TCCTCGAC
                            CCCGA       I
GAM293  LPL           GGGCGCGTCCCTCTGGAGGAGCTGC 4451 GGG   G   C__      I
                          GTGT CCTC  AGGAGCTG
                          IIII IIII  IIIIIIIII
                          CGCA GGAG  TCCTCGAC
                          G__  G  ACC       I
GAM293  LPL           GGGCGCGTCCCTCTGGAGGAGCTGC 4451 TG G   G   C__       II
                          GG GTGT CCTC  AGGAGCTGC
                          II IIII IIII  IIIIIIIII
                          CC CGCA GGAG  TCCTCGACG
                          __  G   G  ACC      TI
GAM293  MAGEA2        GGAGTGCGGGCAGGAGCTG      4455  T  CTC      II
                          GG GTGC  CAGGAGCT
                          II IIII  IIIIIIII
                          CC CACG  GTCCTCGA
                          T  CCC      CI
GAM293  NCF4          GGGAGT-CC-CCAGGAGCTGC     4454   T  G  T      I
                          GGG GT CC CCAGGAGCT
                          III II II IIIIIIIII
                          CCC CA GG GGTCCTCGA
                          T  _  _       C
GAM293  NCF4          GGGAGT-CC-CCAGGAGCTGC     4454 TGGGGGTGTGC
                             CTCCAGGAGCTG
                             IIIIIIIIIIII
                             GGGGTCCTCGAC
                          TCA_____
GAM293  NDN           GGGCCTCTGCGTCCAGGAGCT     4452 GG  G__  C      I
                          GGT  TGC TCCAGGAGC
                          III  III IIIIIIIII
                          CCG  ACG AGGTCCTCG
                          __  GAG  C      I
GAM293  NDN           GGGCCTCTGCGTCCAGGAGCT     4452 TGGG  G__  C      GC
                          GGT  TGC TCCAGGAGCT
                          III  III IIIIIIIII
                          CCG  ACG AGGTCCTCGA
                          ____  GAG  C     GI
GAM293  TJP1          TGGGGGTGTCCTTCCCTG-GCTGC  4457        G _ AGGA  I
                          TGGGGGTGT CCT CC  GCTGC
                          IIIIIIIII III II   IIIII
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                          ACCCCCACA GGA GG   CGACG
                            _  A  GAC_    I
GAM293  TJP1          TGGGGGTGTCCTTCCCTG-GCTGC  4457 _      G  _ AGGA   I
                          GGGGGTGT CCT CC   GCTG
                          |||||||| ||| ||   ||||
                          CCCCCACA GGA GG   CGAC
                          A      _  A  GAC_    I
GAM293  TMC1          TGGGGGTGT-CCTGTCAGAAG   4456       G  C_     CTG
                          TGGGGGTGT CCT CAGGAG
                          ||||||||| ||| ||||||
                          ACCCCCACA GGA  GTCTTC
                             _  CA      III
GAM293  TMC1          TGGGGGTGT-CCTGTCAGAAG   4456       G  C_    I
                          GGGGGTGT CCT CAGGA
                          |||||||| ||| |||||
                          CCCCCACA GGA  GTCTT
                             _  CA    I
GAM294  NXF1          GCTTCTGA-GGCATGACTAC   4460 A _  C       II
                          GC TC GA GGCATGACTA
                          || || || ||||||||||
                          CG AG CT CCGTACTGAT
                          A  A  _       GI
GAM294  NXF1          GCTTCTGA-GGCATGACTAC   4460 TGGCATC  C       TG
                             GA GGCATGACTAC
                             || |||||||||||
                             CT CCGTACTGATG
                        AAGA___  _        CT
GAM294  SPON1       TGGCATCCAC---AAGACTACTGG  4461     G   CAT
                          TGGCATC ACGG  GACTACTGG
                          ||||||| ||||  |||||||||
                          ACCGTAG TGTT  CTGATGACC
                             G  ___
GAM294  SPON1       TGGCATCCAC---AAGACTACTGG  4461 _    G   CAT
                          GGCATC ACGG  GACTACTG
                          |||||| ||||  ||||||||
                          CCGTAG TGTT  CTGATGAC
                          A    G  ___
GAM295  CTH        TATAACCAGTCGAA---GCCGGGT  4472 TAA  G    AGA
                          AA CGGTCGA  AGCCGGGT
                          || |||||||  ||||||||
                          TT GTCAGCT  TCGGCCCA
                        ATA  G     ___
GAM295  MAP3K5        TACAAGGGGTGGG-GAAGCCGGGT  4471 TAA  C  CGAA        I
                          AAG GGT  GAAGCCGGGT
                          ||| |||  ||||||||||
                          TTC CCA  CTTCGGCCCA
                        ATG  C  CCC_      I
GAM295  PITX2        GCGGTCGAACAGGAGCCGGGG    4467 TAAAAG  TCGA A
                          CGG  AG AGCCGGG
                          |||   || |||||||
```

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                           GCT   TC TCGGCCC
                    _____     TG__  C
GAM295 STUB1        AAGCGGTCGGGGTGGCCAGG    4466 TAAAAG     AAGAA
                        CGGTCG   GCCGGG
                        ||||||   ||||||
                        GCCAGC   CGGTCC
                    _____     CCCAC
GAM295 SUOX         TAAATG-GGT-GAAGAAGCC    4468 TAAAAGC  C      GG
                        GGT GAAGAAGCC
                        ||| |||||||||
                        CCA CTTCTTCGG
                    ATTTAC_  _       II
GAM295 SWAP70       TAAAAGCAG-C--A-AAGCCGGGT  4469        CGAA
                        TAAAAGCGGT   GAAGCCGGG
                        |||||||||   |||||||||
                        ATTTTCGTCG   TTTCGGCCC

                       _____
GAM295 TAF6         AAGCAGGTCGAAGATCCCCGG    4465 TAAAAGC      AG_
                        GGTCGAAGA  CCGGGT
                        |||||||||  ||||||
                        CCAGCTTCT  GGCCCG
                    GT_____        AGG
GAM295 TNFAIP2      TAAAAGCGGTAGAGCAGGCCGGGT  4470        C A AA_    I
                        TAAAAGCGGT GA G  GCCGGGT
                        |||||||||| || |  |||||||
                        ATTTTCGCCA CT C  CGGCCCA
                        T _ GTC    I
GAM295 ZFHX1B       AAAAGCA-T-GAAGAAGCCG    4464 TA   GTC      G
                        AAAGCG  GAAGAAGCCG
                        ||||||  ||||||||||
                        TTTCGT  CTTCTTCGGC
                    __    A__        G
GAM296 DLG5         CAGAGGGGACAGGGGCTGGGCACCGGCA4478 TCAGA_ CGA   __       III
                        GAC  GGCT GCACCGGCA
                        |||  |||| |||||||||
                        CTG  CCGA CGTGGCCGT
                    TCTCCC  TCC  CC      TII
GAM296 EXTL1        CAGACGGCCGAGGCTGAGCCG    4477 TC  GA_     CA  GCA
                        AGA  CCGAGGCTG CCG
                        |||  |||||||||| |||
                        TCT  GGCTCCGAC GGC
                    __   GCC      TC GII
GAM296 GJB1         CAGCAGGCAGAGGCCTGTGCACCGGCA4476 TCAGAGACC     ___       III
                        GAGGCT  GCACCGGCA
                        ||||||  |||||||||
                        CTCCGG  CGTGGCCGT
                    TCGTCCGT_   ACA      CII
GAM296 GLUD1        CACAGAGCAAGGCTGCACAGCCA  4483 T   AC       C AI
                        CAGAG CGAGGCTGCAC GGC
                        ||||| ||||||||||| |||
```

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                         GTCTC  GTTCCGACGTG TCG
                         T   __        _ GT
GAM296 HS2ST1        CAGAGACCGTATGGGCTGCA   4480 TC     A___      CCGGC
                         AGAGACCG   GGCTGCA
                         |||||||| |||||||
                         TCTCTGGC   CCGACGT
                           __      ATAC    TIIIA
GAM296 MAN2A2       TCAGATACCGTCGGGGCTGCACC  4484    G  A___      GGCAI
                         TCAGA ACCG   GGCTGCACC
                         ||||| |||| |||||||||
                         AGTCT TGGC   CCGACGTGG
                          A   AGCC     IIIAC
GAM296 MYOM2        CAGAGACCGCCACATGCTGCAC    4479 TC     AG____    CGGCA
                         AGAGACCG    GCTGCAC
                         ||||||||    |||||||
                         TCTCTGGC    CGACGTG
                           __      GGTGTA   TIIIA
GAM296 NTSR1        CAGGGATAGGGGCTGCACCG    4481 TC A CCGA       C
                          AG GA   GGCTGCACCGG
                          || ||   |||||||||||
                          TC CT   CCGACGTGGCT
                          __  C ATCC          I
GAM296 NTSR1        TCAGAGACC-AGGCACCATCG    4487      G  TGC  GC
                         TCAGAGACC AGGC  ACCG
                         ||||||||| |||| ||||
                         AGTCTCTGG TCCG  TGGT
                          _   ___     AG
GAM296 PRKAB1       TCACAGACCGAGGCGCTGCA    4485  G      __  CCGGC
                         TCA AGACCGAGGC  TGCA
                         ||| |||||||||| ||||
                         AGT TCTGGCTCCG  ACGT
                          G      CG   IIIAC
GAM296 SEPX1        TCAGAGACC-A-GCTGCACC    4486     GA     GG
                         TCAGAGACC  GGCTGCACC
                         |||||||||  |||||||||
                         AGTCTCTGG  TCGACGTGG
                           __          ||
GAM296 TCOF1        CAGAGACCGA-GCGGCACGGG   4482 TC     G T  C C
                          AGAGACCGAG C GCAC GG
                          |||||||||| | |||| ||
                          TCTCTGGCTC G CGTG CC
                           __      _C   C T
GAM296 XRCC2        AGAGGCAGAGGCTGCAGCGG    4475 TCAGAGACC      C  _
                              GAGGCTGCA CGG C
                              ||||||||| ||| |
                              CTCCGACGT GCC G
                          TCCGT____        C C
GAM297 BMPR1A       GCATATTTTCATAAGTCCGG     4504 _       C  II
                         GCA ATTTTCATAA TCTG
                         ||| |||||||||| ||||
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                          CGT TAAAAGTATT AGGC
                           A       C   CI
GAM297  BMPR1A        GCATATTTTCATAAGTCCGG    4504 AGCA      C    TGA
                          ATTTTCATAA TCTGG
                          |||||||||| |||||
                          TAAAAGTATT AGGCC
                          GTA_        C   TII
GAM297  C7orf2        ATTTTCATA--TCAGGTGAA    4498 _      AC  T    I
                          TTTTCATA  TC GGTGA
                          ||||||||  || |||||
                          AAAAGTAT  AG CCACT
                           T      _  T    I
GAM297  CDH10         AGCATCACTTT--TAACTCTGG   4491    __    CA      TGA
                          AGCA  ATTTT  TAACTCTGG
                          ||||  |||||  |||||||||
                          TCGT  TGAAA  ATTGAGACC
                              AG     __      III
GAM297  CDH10         AGCATCACTTT--TAACTCTGG   4491   __   CA     I
                          GCA  ATTTT  TAACTCTG
                          |||  |||||  ||||||||
                          CGT  TGAAA  ATTGAGAC
                            AG      __       I
GAM297  FBXW1B        TTCATAACTCAGCTGTGAA    4506      TG__   III
                          TTCATAACTC  GTGA
                          ||||||||||  ||||
                          AAGTATTGAG  CACT
                               TCGA   TII
GAM297  FGG           CAATTTTTAAATAACTCTG    4502     C__      III
                          CAATTTT  ATAACTCT
                          |||||||  ||||||||
                          GTTAAAA  TATTGAGA
                              ATT       CII
GAM297  FGG           CAATTTTTAAATAACTCTG    4502 AGCAA  TC       GA
                          TTT  ATAACTCTGGT
                          |||  ||||||||||||
                          AAA  TATTGAGACTA
                          TAA__   TT       II
GAM297  GATA6         ATTTTTAAAACTCTGGTGAA    4500 _   CAT        I
                          TTTT  AACTCTGGTGA
                          ||||  |||||||||||
                          AAAA  TTGAGACCACT
                            A  TT_         I
GAM297  GATA6         ATTTTTAAAACTCTGGTGAA    4500 AGCAATTTTCAT
                             AACTCTGGTGA
                             |||||||||||
                             TTGAGACCACT
                          AATT_____
GAM297  IL4R          AGCAATTTTCATGTCCTCTGTTG   4493       _  AA_   G  AAI
                          AGCAATTTT CAT  CTCTG TG
                          ||||||||| |||  ||||| ||
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                              TCGTTAAAA GTA   GAGAC AC
                                   A  CAG    A  III
GAM297 IL4R            AGCAATTTTTCATGTCCTCTGTTG  4493 CAA     AA_     GI
                              TTTTCAT   CTCTG
                              ||||||| |||||
                              AAAAGTA  GAGAC
                               TA_      CAG    AI
GAM297 LLT1           AGCATATTTTCATATAC-CTGTTG  4492   _      _ T  G  AAI
                             AGCA ATTTTCATA AC CTG TG
                             |||| ||||||||| || ||| ||
                             TCGT TAAAAGTAT TG GAC AC
                                 A    A _   A III
GAM297 LLT1          AGCATATTTTCATATAC-CTGTTG  4492 CA       _ T  GI
                              ATTTTCATA AC CTG
                              ||||||||| || |||
                              TAAAAGTAT TG GAC
                               TA    A _  AI
GAM297 MADH4           AGCAATTTTGAT-CCTTTGG    4495     CATAA  C  TGA
                             AGCAATTTT   CT TGG
                             |||||||||   || |||
                             TCGTTAAAA   GA ACC
                               CTAG_  A  III
GAM297 MBNL          AGCAATTTTTAGAA--CTGCTGAA  4497     CAT   _   TGAA
                             AGCAATTTT  AACT CTGG
                             |||||||||  |||| ||||
                             TCGTTAAAA  TTGA GACT
                               ATC   C   TIII
GAM297 MBNL          AGCAATTTTTAGAA--CTGCTGAA  4497     CAT   _   TGI
                             AGCAATTTT  AACT CTGG
                             |||||||||  |||| ||||
                             TCGTTAAAA  TTGA GACT
                               ATC   C   TII
GAM297 MBNL          AGCAATTTTGCTCAGTCTG       4494      CATAAC  GTGA
                             AGCAATTTT   TCTG
                             |||||||||   ||||
                             TCGTTAAAA   AGAC
                              CGAGTC  IIIA
GAM297 MS4A6A         ATTTTCATA--TCCAGTGAA     4499 _      AC TG   I
                             TTTTCATA TC GTGA
                             |||||||| || ||||
                             AAAAGTAT AG CACT
                               T    __ GT  I
GAM297 NBS1         TTTCCAT---TCTGGTGAA        4507      AAC
                             TTTTCAT TCTGGTGA
                             ||||||| ||||||||
                             AAAGGTA AGACCACT
                                ___
GAM297 NFIA          GCATATTTTCATATATCTGG      4505 _      AC  II
                             GCA ATTTTCATA TCTG
                             ||| ||||||||| ||||
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                             CGT TAAAAGTAT AGAC
                              A      AT  CI
GAM297 NFIA            GCATATTTTCATATATCTGG   4505 AGCA      AC    TGA
                          ATTTTCATA TCTGG
                          |||||||| |||||
                          TAAAAGTAT AGACC
                            GTA_     AT   CII
GAM297 PPP1R12B         CAATTTTCAACAAACAGGTG   4503 AGCA     TAACTCT  A
                          ATTTTCA    GGTG
                          ||||||    ||||
                          TAAAAGT    CCAC
                          ____      TGTTTGT  C
GAM297 SLC10A2         CAATTTTCACTTTAACTCT      4501          ___   III
                          CAATTTTCAT  AACTC
                          ||||||||| |||||
                          GTTAAAAGTG TTGAG
                            AAA    AII
GAM297 SLC10A2         CAATTTTCACTTTAACTCT      4501 AGCA    ___    GGTGA
                          ATTTTCAT  AACTCT
                          ||||||||  ||||||
                          TAAAAGTG  TTGAGA
                           ____       AAA    AAIII
GAM297 VDAC1           AGCTATTT-CATA-CTCTGGTG   4496  AAT    A     A
                          AGC   TTTCATA CTCTGGTG
                          |||  ||||||| ||||||||
                          TCG   AAAGTAT GAGACCAC
                          AT_    _     I
GAM297 VDAC1           AGCTATTT-CATA-CTCTGGTG   4496 _ AAT    A    I
                           GC   TTTCATA CTCTGGT
                           ||  ||||||| |||||||
                           CG   AAAGTAT GAGACCA
                          T AT_    _    I
GAM297 ZNF192          AATTTCTCAATTCCAACTCTGGTGAA 4490 AG___   TCA        II
                          CAATTT  TAACTCTGGTGAA
                          ||||||  |||||||||||||
                          GTTAAG  GTTGAGACCACTT
                          AAGA    ___        AT
GAM297 ZNF192          AATTTCTCAATTCCAACTCTGGTGAA 4490 ATT_  A         I
                           TTC TAACTCTGGTGA
                           ||| |||||||||||||
                           AAG GTTGAGACCACT
                          AGTT  _        I
GAM298 ASH1            TGAGTTATACCTGGGTATA     4518 TATGA     _    ACTA
                           TTATAC TGGGTATA
                           |||||| |||||||||
                           AATATG ACCCATAT
                          TC___   G    CCII
GAM298 C4orf1          ATG-TTATAGTCAATATAACTAT   4511 TA A    CTG
                           TG TTATA  GGTATAACTAT
                           || |||||  |||||||||||
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                          AC AATAT   TTATATTGATA
                          __  _      CAG
GAM298  FBXL2        TGATTATACTACAGATAACT      4520 TATG      _  T    A
                          ATTATACTG GG ATAACT
                          IIIIIIIII II IIIIII
                          TAATATGAT TC TATTGA
                          ____       G  _    A
GAM298  FMR2         TATGTTCTTTTCTGGGTATAA     4513 TATGATTATA_      CTAT
                             CTGGGTATAA
                             IIIIIIIIII
                             GACCCATATT
                          ATACAAGAAAA       IIIT
GAM298  IREB2        TGAGTATACTGGGACTATCT      4519 TATGAT      TATA
                             TATACTGGG  ACTA
                             IIIIIIIII  IIII
                             ATATGACCC  TGAT
                          TC____        ____
GAM298  MAP3K7IP2      ATTATACTGAGGTATTATTA    4512 TATGATTA   _  AACTA
                             TACTG GGTAT
                             IIIII IIIII
                             ATGAC CCATA
                          _____        T   ATAAT
GAM298  PRKAR2B       TATGATTATCAGTCTGAATAAGTA 4514      A___      TAACTATI
                          TATGATTAT  CTGGGTA
                          IIIIIIIII  IIIIIII
                          ATACTAATA  GACTTAT
                          GTCA       TCATIIIT
GAM298  RB1CC1        TATGATTATTCTAGAGTCATAA   4515     A  _ ATAACTAT
                          TATGATTAT CTGG GT
                          IIIIIIIII IIII II
                          ATACTAATA GATC CA
                             A  T GTATTIII
GAM298  SCN3A          ATGGTTA----GGGTATAAC    4510 TATGATTATACT
                             GGGTATAAC
                             IIIIIIIII
                             CCCATATTG
                          ACCAAT_____
GAM298  TSG          TATGATTATACT-TGTTTAA      4516      GG ATAACTA
                          TATGATTATACT GT
                          IIIIIIIIIIII II
                          ATACTAATATGA CA
                             A_ AATTIII
GAM298  USP6         TATGATTAT--T-GGTA-AACT    4517      ACTG  T
                          TATGATTAT  GGTA AACT
                          IIIIIIIII  IIII IIII
                          ATACTAATA  CCAT TTGA
                             A___  _
GAM299  ACTN4        TTGCATAGATACA-GAGTGGAGGAAT 4536 TCCA  _  T  A     I
                          AGA ACA GA TGGAGGAA
                          III III II IIIIIIII
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                         TCT TGT CT ACCTCCTT
                     CGTA   A  _  C        I
GAM299 ACTN4         TTGCATAGATACA-GAGTGGAGGAAT 4536 TTCCA_ _   T A       II
                         AGA ACA GA TGGAGGAAT
                         ||| ||| || ||||||||||
                         TCT TGT CT ACCTCCTTA
                     AACGTA   A  _  C         II
GAM299 ALPPL2        TTCCCAGAA---GAATGGAGG    4543    A  CAT      A
                         TTCC AGAA  GAATGGAGG
                         |||| ||||  |||||||||
                         AAGG TCTT  CTTACCTCC
                           G  ___        I
GAM299 ALPPL2        TTCCCAGAA---GAATGGAGG    4543 _  A  CAT
                          TCC AGAA  GAATGGAG
                          ||| ||||  |||||||||
                          AGG TCTT  CTTACCTC
                           A  G  ___
GAM299 ATP10C        TTCCAAGAACA-GA--GGAGG    4541      T AT   A
                        TTCCAAGAACA GA  GGAGG
                        ||||||||||| || |||||
                        AAGGTTCTTGT CT  CCTCC
                             _  __      I
GAM299 ATP10C        TTCCAAGAACA-GA--GGAGG    4541 _       T AT
                         TCCAAGAACA GA  GGAG
                         |||||||||| || ||||
                         AGGTTCTTGT CT  CCTC
                        A            _  __
GAM299 ATRX          AAGAACATGATGATGAGAGAAA    4523           __ _    III
                        AAGAACATGA ATG GAGGA
                        |||||||||| ||| |||||
                        TTCTTGTACT TAC CTCTT
                          AC   T    TII
GAM299 BSG           AGAATCCTGAATGGAGAAA       4525   CA_        II
                        AGAA  TGAATGGAGGA
                        ||||  |||||||||||
                        TCTT  ACTTACCTCTT
                          AGG       TI
GAM299 BSG           AGAATCCTGAATGGAGAAA       4525 TTCCAAGAACA
                            TGAATGGAGGAA
                            ||||||||||||
                            ACTTACCTCTTT
                        GG_____
GAM299 DEDD          TTTCAAGC-CATGGAATGGAGGAA 4540 TC   AA   _      I
                         CAAG CATG AATGGAGGA
                         |||| |||| |||||||||
                         GTTC GTAC TTACCTCCT
                         AA   G_   C     I
GAM299 DEDD          TTTCAAGC-CATGGAATGGAGGAA 4540 TTC   AA   _      TI
                         CAAG CATG AATGGAGGAA
                         |||| |||| ||||||||||
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                          GTTC  GTAC TTACCTCCTT
                          AAA   G_   C        II
GAM299 DSC1         TTCCAAGAACCTTAGAAGTTGGAG  4539       AT__ __    GAATI
                      TTCCAAGAAC  GAA TGGAG
                      |||||||||   |||  |||||
                      AAGGTTCTTG  CTT ACCTC
                           GAAT  CA   IIITA
GAM299 ESRRG       CAGGAACCT--ATGGAGGAAT   4530 AA_  ATGA      I
                      GAAC  ATGGAGGAA
                      ||||  |||||||||
                      CTTG  TACCTCCTT
                       GTC  GA__       I
GAM299 ESRRG       CAGGAACCT--ATGGAGGAAT    4530 TTCCAA  ATGA
                       GAAC  ATGGAGGAA
                       ||||  |||||||||
                       CTTG  TACCTCCTT
                      _____  GA__
GAM299 FZD8        TCCCCGCACATCAATGGAGGAA   4535 _ AAGA  G      I
                      CC  ACAT AATGGAGGA
                      ||  |||| |||||||||
                      GG  TGTA TTACCTCCT
                       G GCG_  G      I
GAM299 FZD8        TCCCCGCACATCAATGGAGGAA   4535 TT AAGA  G      T
                       CC  ACAT AATGGAGGAA
                       ||  |||| ||||||||||
                       GG  TGTA TTACCTCCTT
                       G_ GCG_  G        T
GAM299 HNF3B       CAACAACAGCAATGGAGGA     4528  G  TG      II
                       CAA AACA  AATGGAGG
                       ||| ||||  |||||||||
                       GTT TTGT  TTACCTCC
                        G  CG     TI
GAM299 HNF3B       CAACAACAGCAATGGAGGA     4528 TTCCAAG  TG      A
                        AACA  AATGGAGGA
                        ||||  |||||||||
                        TTGT  TTACCTCCT
                        G_____  CG     C
GAM299 ITGAV       AAGTACATGAATGGAGGAA     4524  A          II
                       AAG ACATGAATGGAGGA
                       ||| ||||||||||||||
                       TTC TGTACTTACCTCCT
                        A          TI
GAM299 ITGAV       AAGTACATGAATGGAGGAA     4524 TTCCAAGA
                          ACATGAATGGAGGAA
                          |||||||||||||||
                          TGTACTTACCTCCTT
                      _____
GAM299 LILRB4      TTCCAAGAACAAGA---GAGG   4542      T AT AI
                      TTCCAAGAACA GA GG
                      |||||||||| || ||
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                              AAGGTTCTTGT CT  CC
                                 T  CT  II
GAM299  LILRB4        TTCCAAGAACAAGA---GAGG    4542          TGAAT    A
                      TTCCAAGAACA   GGAGG
                      ||||||||||   |||||
                      AAGGTTCTTGT    TCTCC
                              TC___     I
GAM299  MEN1          CAATAACAGGAAAAATGGAGGA    4527  G  T___        III
                      CAA AACA   GAATGGAGG
                      ||| ||||   |||||||||
                      GTT TTGT   TTTACCTCC
                        A  CCTT        TII
GAM299  MEN1          CAATAACAGGAAAAATGGAGGA    4527 TTCCAAG   T___        AT
                           AACA   GAATGGAGGA
                           ||||   ||||||||||
                           TTGT   TTTACCTCCT
                        A_____   CCTT        AT
GAM299  OXR1          CAAGAACATGATTTGAAAAAT    4529         ATG    I
                      AAGAACATGA  GAGGAA
                      ||||||||||  ||||||
                      TTCTTGTACT  CTTTTT
                             AAA     I
GAM299  OXR1          CAAGAACATGATTTGAAAAAT    4529 TTCCAA       ATG
                           GAACATGA  GAGGAAT
                           ||||||||  |||||||
                           CTTGTACT  CTTTTTA
                          _____        AAA
GAM299  RPA1          CAAAATACATGAATGCAGGAAT    4526 AAGA       G   I
                           ACATGAATG AGGAA
                           ||||||||| |||||
                           TGTACTTAC TCCTT
                           TTTA       G   I
GAM299  RPA1          CAAAATACATGAATGCAGGAAT    4526 TTCCAAGA      G
                           ACATGAATG AGGAAT
                           ||||||||| ||||||
                           TGTACTTAC TCCTTA
                           TTA_____       G
GAM299  SLC19A2       CCAAGAACATTCATATGATGAAT   4531 C      GA  _ G  I
                        AAGAACAT ATG GA GAA
                        |||||||| ||| || |||
                        TTCTTGTA TAT CT CTT
                         _      AG  A  A  I
GAM299  SLC19A2       CCAAGAACATTCATATGATGAAT   4531 TTCC      GA  _ G  I
                        AAGAACAT ATG GA GAAT
                        |||||||| ||| || ||||
                        TTCTTGTA TAT CT CTTA
                         ____      AG  A  A
GAM299  SPON1         TCCAAGAAC---AAGGGAGCAA    4534         TGAAT  GI
                      TCCAAGAACA   GGAG
                      ||||||||||   ||||
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                              AGGTTCTTGT   CCTC
                                 TC___   GT
GAM299 SPON1          TCCAAGAAC---AAGGGAGCAA   4534 TT      TGAAT   G
                         CCAAGAACA   GGAG AA
                         |||||||||   |||| ||
                         GGTTCTTGT   CCTC TT
                          __      TC___   G
GAM299 TRPS1          CCAAGAACATGTTTGTGAG   4532      AA GAII
                         CCAAGAACATG  TG
                         |||||||||| ||
                         GGTTCTTGTAC AC
                          AA  ACTC
GAM299 TRPS1          CCAAGAACATGTTTGTGAG   4532 TTCC      AA _ GAA
                          AAGAACATG  TG GAG
                          ||||||||| || |||
                          TTCTTGTAC AC CTC
                          ____      AA A ATI
GAM299 TRPS1          TTTCAAGAGAACACATGAATG   4537 TTC  ____      GAGGAAT
                         CAAGA   ACATGAATG
                         |||||   |||||||||
                         GTTCT   TGTACTTAC
                          AAA    CTTG    IIITAAG
GAM299 TRPS1          TTTCAAGAGAACACATGAATG   4537 TTC  ____      IIIC
                         CAAGA   ACATGAAT
                         |||||   ||||||||
                         GTTCT   TGTACTTA
                          AAA    CTTG    CIII
GAM299 TRPS1          TTCCAAGAATAGTGATATG   4538     CA_ _ GAGGAA
                         TTCCAAGAA  TGA ATG
                         |||||||||  ||| |||
                         AAGGTTCTT  ACT TAC
                          ATC  A  IIITAA
GAM299 TRPS1          TTCCAAGAATAGTGATATG   4538     CA_ ATIII
                          TTCCAAGAA  TGA
                          |||||||||  |||
                          AAGGTTCTT  ACT
                          ATC  ATACI
GAM299 VPS26          CCATGCATATGAATGGATGA   4533 CCAAGAAC    GI
                            ATGAATGGA
                            |||||||||
                            TACTTACCT
                         TACGTA__      AC
GAM299 VPS26          CCATGCATATGAATGGATGA   4533 TTCCAAGAAC   G A
                            ATGAATGGA GA
                            ||||||||| ||
                            TACTTACCT CT
                         TACGTA____      A G
GAM300 BACE           TGGGTGGGGAGGGTCCTGAG   4555 TC   TACTTAC      T
                            TGGG   GGTCCTGAG
                            ||||   |||||||||
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                          ACCC     CCAGGACTC
                        CC  CTC____         C
GAM300  GOLGA4          TCTGGGTACAATTAATGTTTCTGA  4548       TTACG__ C_  GTCI
                        TCTGGGTAC     GT CTGA
                        |||||||||     ||  ||||
                        AGACCCATG     CA GACT
                          TTAATTA AA  IIIC
GAM300  GPR30           TCTGGGTACCTGCCGTCCAGA  4549       ACG  T GTC
                        TCTGGGTACTT  GTCC GA
                        ||||||||||  |||| ||
                        AGACCCATGGA  CAGG CT
                          CGG  T III
GAM300  IFNW1           TCTGGGTAC-TAAAGTCATAAGT  4552       TAC  C  C
                        TCTGGGTACT  GGTC TGAGT
                        ||||||||||  |||| |||||
                        AGACCCATGA  TCAG ATTCA
                          TT_  T  I
GAM300  JAM3            TCTGGGTACAGACTGTCCT-AGTC  4553      TT G  G  I
                        TCTGGGTAC AC GTCCT AGTC
                        ||||||||| || ||||| ||||
                        AGACCCATG TG CAGGA TCAG
                          TC  A   _   I
GAM300  KIF3B           TCAGGATGCT-ACGGTCCTGAG  4550 T  A T      TC
                        TC GGGT CT ACGGTCCTGAG
                        || |||| || |||||||||||
                        AG CCTA GA TGCCAGGACTC
                          T  C  _        II
GAM300  MAT1A           GGGTATGTCACAGGCTCCTGAGTC  4546 TCTGGGTAC  _ _      I
                        TTAC GG TCCTGAGTC
                        |||| || |||||||||
                        AGTG CC AGGACTCAG
                        ATAC_____  T G     T
GAM300  MEOX2           GGATAATCCCGGTCCTGAG      4547 TCTGGGTACTTA
                             CGGTCCTGAGT
                             |||||||||||
                             GCCAGGACTCG
                        ATTAGG_____
GAM300  SORCS2          TGGGCACTG--GGTCCTGAG  4554 TCTG    TAC
                           GGTACT  GGTCCTGAG
                           ||||||  |||||||||
                           CCGTGA  CCAGGACTC
                              ____     C__
GAM300  SP110           TCTGGGT--TTG-GGTCCTGAG  4551       ACTTAC    T
                        TCTGGGT   GGTCCTGAG
                        |||||||   |||||||||
                        AGACCCA   CCAGGACTC
                          AAC___      I
GAM301  ANXA4           GACATTAACTATAATAATATGG  4567 TG     C  __    AA
                         ACATTAACTA AAT TATGGG
                         |||||||||| ||| ||||||
```

```
                        TGTAATTGAT TTA  ATACCT
                          __        A  TT    II
GAM301 CDH5         CAATTACTACAATTATAGAAA   4564 ATTA         I
                        ACTACAATTATGGGA
                        IIIIIIIIIIIIII
                        TGATGTTAATATCTT
                        TTAA          I
GAM301 CDH5         CAATTACTACAATTATAGAAA    4564 TGACATTA
                        ACTACAATTATGGGAA
                        IIIIIIIIIIIIIII
                        TGATGTTAATATCTTT
                   AA_____
GAM301 CHD2        GACTTTGACTCTTCAATTATGGG  4566 ____  ATTAA  A      AAI
                        TGAC   CT CAATTATGGG
                        IIII   II IIIIIIIII
                        ACTG   GA GTTAATACCC
                   TGAA  A____  A     GII
GAM301 CHD2        GACTTTGACTCTTCAATTATGGG  4566 ACATTAA  A     I
                        CT CAATTATGG
                        II IIIIIIIII
                        GA GTTAATACC
                   AAACTGA  A      I
GAM301 DCX       ATTAACTACAAAATGTTNTGGGA   4561 TG     C _  G AA
                        ACATTAACTA AA TTAT GG
                        IIIIIIIIII II IIII II
                        TGTAATTGAT TT AATG CC
                          __        T C  A AI
GAM301 ENC1       TGACATTAATCCACAATTA     4571        _      TGGGA
                        TGACATTAA CTACAATTA
                        IIIIIIIII IIIIIIIII
                        ACTGTAATT GGTGTTAAT
                          A     IIIAA
GAM301 ENC1       TGACATTAATCCACAATTA     4571        _     II
                        TGACATTAA CTACAATT
                        IIIIIIIII IIIIIIII
                        ACTGTAATT GGTGTTAA
                          A     TI
GAM301 FOXO1A      TGGCTTTA--TACAATTATAGCAA  4577 ACATTAAC      GI
                        TACAATTATGG
                        IIIIIIIIIII
                        ATGTTAATATC
                   ACCGAAAT        GI
GAM301 FOXO1A      TGGCTTTA--TACAATTATAGCAA  4577 TGACATTAAC       G
                        TACAATTATGG AA
                        IIIIIIIIIII II
                        ATGTTAATATC TT
                   ACCGAAAT__        G
GAM301 IRTA1      TGACATTAAC-ATAATTAT      4574      TAC   GGG
                        TGACATTAAC AATTAT
                        IIIIIIIIII IIIIII
```

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                        ACTGTAATTG  TTAATA
                          TA_      III
GAM301  IRTA1          TGACATTAAC-ATAATTAT      4574        TAC    I
                        TGACATTAAC  AATTA
                        |||||||||  |||||
                        ACTGTAATTG  TTAAT
                          TA_      A
GAM301  LEP            GACAAGAACTACAATT-TGG     4568 G  TT        ATI
                          ACA  AACTACAATT
                          |||  ||||||||||
                          TGT  TTGATGTTAA
                          _    TC      ACC
GAM301  LEP            GACAAGAACTACAATT-TGG     4568 TG  TT      A  GA
                          ACA  AACTACAATT TGG
                          |||  |||||||||| |||
                          TGT  TTGATGTTAA ACC
                          __   TC        _  GI
GAM301  LPIN2          ATCAACTACAATGTAATTGGA    4562          TA___   III
                        ATTAACTACAAT    TGGG
                        ||||||||||||    ||||
                        TAGTTGATGTTA    ACCT
                            CATTA    III
GAM301  PCDHA9         ACAT--ACTACAATTCAGGAAA   4560 ATTA        A   I
                              ACTACAATT TGGGA
                              ||||||||| |||||
                              TGATGTTAA GTCCT
                        TGTA        _   I
GAM301  PCDHA9         ACAT--ACTACAATTCAGGAAA   4560 TGACATTA        A
                              ACTACAATT TGGGA
                              ||||||||| |||||
                              TGATGTTAA GTCCT
                        TA_____        _
GAM301  PPP3CA         ACATGTAACTACAAACTTAT     4558 _        TTAIII
                        ACAT TAACTACAA
                        |||| |||||||||
                        TGTA ATTGATGTT
                          C       TGAATA
GAM301  PTPRH          ATTTAATA-AATTATGGGA      4563 TGACATTAACTAC
                              AATTATGGG
                              |||||||||
                              TTAATACCC
                        TTAT_____
GAM301  SEL1L          TGACATTAAGAAC--TTATG     4575        CT AA   GG
                        TGACATTAA AC  TTATG
                        ||||||||| ||  |||||
                        ACTGTAATT TG  AATAC
                          CT __     II
GAM301  SEL1L          TGACATTAAGAAC--TTATG     4575        CT AATTAI
                        TGACATTAA AC
                        ||||||||| ||
```

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                        ACTGTAATT  TG
                        CT  AATACI
GAM301  SGK           ACAATACATACAATTATCAGGAA    4559 TGACATTA _     _   I
                        AC TACAATTAT GGGAA
                        || |||||||||| |||||
                        TG ATGTTAATA TCCTT
                        TTA_____ T     G   A
GAM301  SGK           ACAATACATACAATTATCAGGAA    4559 CATTA _     _   I
                        AC TACAATTAT GGGA
                        || |||||||||| ||||
                        TG ATGTTAATA TCCT
                        TTA__ T     G  I
GAM301  SUFU        TGACATTAAAAACTAATAT      4573       CT  AATTAII
                        TGACATTAA  AC
                        ||||||||| ||
                        ACTGTAATT  TG
                        TT  ATTATAI
GAM301  SUFU        TGACATTAAAAACTAATAT      4573       CT  AATTATGGGA
                        TGACATTAA  AC
                        ||||||||| ||
                        ACTGTAATT  TG
                        TT  ATTATAIIIA
GAM301  TCF3        TGACACGTA-TACAATTAT      4572       TAAC       GGG
                        TGACAT   TACAATTAT
                        ||||||   |||||||||
                        ACTGTG   ATGTTAATA
                        CAT_       III
GAM301  TCF3        TGACACGTA-TACAATTAT      4572       TAAC      I
                        TGACAT   TACAATTA
                        ||||||   ||||||||
                        ACTGTG   ATGTTAAT
                        CAT_       A
GAM301  TFRC        CATGAAGAA-AATTATGGGAA     4565 ATTAACTAC        I
                        AATTATGGGA
                        ||||||||||
                        TTAATACCCT
                        GTACTTCTT        I
GAM301  TFRC        CATGAAGAA-AATTATGGGAA     4565 TGACATTAACTAC
                            AATTATGGGA
                            ||||||||||
                            TTAATACCCT
                        CTTCTT_____
GAM301  TRIM        GAAATTTATTTCAATTATGGG    4569 ACATTAACTA       I
                            CAATTATGG
                            |||||||||
                            GTTAATACC
                        TTTAAATAAA        I
GAM301  TRIM        GAAATTTATTTCAATTATGGG    4569 TGACATTAACTA        AA
                            CAATTATGGG
                            ||||||||||
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                        GTTAATACCC
                        TTTAAATAAA__         GI
GAM301  TRIP15          TGACAGTATGCCACTATAATTATGGG 4570    TTA____   C      AAII
                        TGACA     ACTA AATTATGGG
                        |||||     |||| |||||||||
                        ACTGT     TGAT TTAATACCC
                            CATACGG  A      IIIA
GAM301  TRIP15          TGACAGTATGCCACTATAATTATGGG 4570 GACATTA   C      I
                               ACTA AATTATGG
                               |||| |||||||||
                               TGAT TTAATACC
                            CATACGG  A    I
GAM301  TUFT1           TGACATTAACAAGCCTAATGGGAA 4576          TACAATT    I
                        TGACATTAAC     ATGGGAA
                        ||||||||||     |||||||
                        ACTGTAATTG     TACCCTT
                            TTCGGAT      I
GAM301  TUFT1           TGACATTAACAAGCCTAATGGGAA 4576          TACAATT    I
                        GACATTAAC     ATGGGA
                        |||||||||     ||||||
                        CTGTAATTG     TACCCT
                            TTCGGAT      I
GAM302  ATP5A1          ACAATGACAA-AACTGAACTGG   4580 TGACC  _   C       C
                           ATG CAG AACTGAACTGG
                           ||| ||| |||||||||||
                           TAC GTT TTGACTTGACC
                        T____  T  _       A
GAM302  AVPR1A          TGTCCATGCAGCTCCT--ACTCGGC 4590 TGA      AA  AAC  I
                           CCATGCAGC CTG  TGGC
                           ||||||||| |||  ||||
                           GGTACGTCG GAT  GCCG
                        ACA      AG GA_   I
GAM302  EPHB6           TGACCATGCCGGCACCCTGATCT 4587      A_  A_   A GGCI
                        TGACCATGC GCA CTGA CT
                        ||||||||| ||| |||| ||
                        ACTGGTACG CGT GACT GA
                          GC  GG  A IIIC
GAM302  FUT3            TGGCC-TGAAGCAACTGAAGATCTGG 4589 A A C         ___  CII
                        TG CC TG AGCAACTGAA  CTGG
                        || || || |||||||||||  ||||
                        AC GG AC TCGTTGACTT  GACC
                        C _ T       CTA  III
GAM302  GALNT1          TGACCCAAG-AGCAACTGAA     4586  ATGC      CTGG
                        TGACC   AGCAACTGAA
                        |||||   ||||||||||
                        ACTGG   TCGTTGACTT
                          GTTC      IIIC
GAM302  ITGA4           ACAACGCAACACACCTGAACTGG 4581 TGACC      A__      CI
                        ATGCAGCA CTGAACTGG
                        |||||||| |||||||||
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                          TGCGTTGT  GACTTGACC
                     T____        GTG      CA
GAM302  KCNA7         CATGACCCAACTGAACTGGC    4583 TGACCATGCAG
                                 CAACTGAACTGG

                                 ||||||||||||
                                 GTTGACTTGACC
                     TGG_____
GAM302  LAPTM5          TGACCACAGAGCAACTGAA    4588     C       CTGG
                        TGACCATG AGCAACTGAA

                        ||||||||| ||||||||||
                        ACTGGTGT TCGTTGACTT
                           C      IIIC
GAM302  MAD2L2        CCATGCAGC-ACTGCCCTAGGC    4584 TGACCA     A  AA _
                             TGCAGCA CTG  CT GGC

                             |||||||| ||| || |||
                             ACGTCGT GAC  GA CCG
                     _____        _  GG  T
GAM302  NR1I2          CCCTACAG--ACTGAACTGG    4585 TGACCA   CA
                            TGCAG  ACTGAACTG

                            ||||| |||||||||
                            ATGTC  TGACTTGAC

                     _____       __
GAM302  PBP          CATGCAACA-CTGAACTGG    4582 TGACCATG    A
                            CAGCA CTGAACTG

                            ||||| |||||||||
                            GTTGT GACTTGAC

                     _____       _
GAM302  SLC6A5         TGACACAGGCAACAGACTGAACTGG 25    _ T  _       CII
                        TGAC CA GCAGCA ACTGAACTGG

                        |||| || ||||||| |||||||||||
                        ACTG GT CGTTGT TGACTTGACC
                            T  C    C        III
GAM303  ALDH3B1        CGCAGGCC--GCAGGAGCAGC    4599 TGACGCC   AGGG
                             GGCT  AGGAGCAG

                             ||||   |||||||||
                             CCGG   TCCTCGTC
                     T_____     CG__
GAM303  ALDH3B1        GACCCAGG--AGGGAGGAGGCAG   4605 TG G   CT    _ C
                         AC CCGG  AGGGAGGAG CAG

                         || |||| |||||||||| |||
                         TG GGTC  TCCCTCCTC GTC
                     __ _  C_      C C
GAM303  ARHGAP6       CGGCGGC--GGCAGGAGCAGC    4600 TGACGC  TA G
                            CGGC  GG AGGAGCAG

                            |||| || ||||||||
                            GCCG  CC TCCTCGTC
                     _____   __ G
GAM303  CAPON         GCCGGCTA-GGAGG-GCGGC    4609 TGACGCCG    GA A_
                            GCTAGG  GG  GCA

                            ||||||  ||  |||
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                                CGATCC  CC  CGT
                                _____     TC  GC
GAM303  DAZL            CCGGCTCCAGGAGGAGCAG     4594 TGACGCCGG    G
                             CTAGG AGGAGCAG
                             ||||| |||||||||
                             GGTCC TCCTCGTC
                        A_____     _
GAM303  EN2            CGCCG-CTGGGTGACAGGAGCAGC  4598 TGA  C CTA  G        I
                             CGC GG  GG AGGAGCAGC
                             ||| || || |||||||||
                             GCG CC  CT TCCTCGTCG
                        ___  A CA_ G     G
GAM303  FLT1           CGCCGCTGCCGGGGAGGAGC     4595 TGA  CG TA     AG
                             CGC GC GGGAGGAGC
                             ||| || |||||||||
                             GCG CG CCCTCCTCG
                        ___  A_ GC      GC
GAM303  FXYD6        ACGGGGGC-AGGGAGGAGCAG     4593 TGACGCC  T
                             GGC AGGGAGGAGCAG
                             ||| |||||||||||
                             CCG TCCCTCCTCGTC
                        CCC____  _
GAM303  HMGA2        GACGCCGGC--GGGGCGAGC     4606 TG     TA  AG    A
                             ACGCCGGC GGG GAGC
                             |||||||| ||| ||||
                             TGCGGCCG CCC CTCG
                        __     C_  G_   C
GAM303  IHPK1        TGA-GCC--CT-GGGAGGAGCAGC  4616   C  GG  A
                             TGA GCC  CT GGGAGGAGCAG
                             ||| |||  || |||||||||||
                             ACT CGG  GA CCCTCCTCGTC
                        _  __  _
GAM303  IL2RB       GAGGACGG-TAGGGAGGATTGCAG  4604 TGACGC  C       __  CI
                             CGG TAGGGAGGA  GCAG
                             ||| ||||||||| ||||
                             GCC ATCCCTCCT CGTC
                        TCCT__  _      AA  TI
GAM303  IMMP2L       CGCCGGCTCGGCGGGGAGGAGC   4597 TGAC  _ TA      AGC
                             GC CGGC GGGAGGAGC
                             || |||| |||||||||
                             CG GCCG CCCTCCTCG
                        GC__ A C_      CCC
GAM303  KCNMB4        TGCCTCGGGC--GGGAGGAGCCGC  4617 TGAC  ___ TA      A
                             GCC  GGC GGGAGGAGC GC
                             |||  ||| ||||||||| ||
                             CGG  CCG CCCTCCTCG CG
                        A___  AGC  __     G
GAM303  LASS2         TGACTTGGCGGGTAGGGAGGA   4610  GC__ C      GCAGC
                             TGAC  CGG TAGGGAGGA
                             ||||   || |||||||||
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                        ACTG    GCC ATCCCTCCT
                        AACC   C        IIICG
GAM303 LENG4            GACGCCGGC--GGCATGAAGCAGC  4603 TG      TA  GA_
                        ACGCCGGC  GG  GGAGCAGC
                        IIIIIIII II  IIIIIIII
                        TGCGGCCG  CC  CTTCGTCG
                        __       __  GTA
GAM303 MBD3            GACAGCGGGCATGGGGAGGAGC   4601 TGAC  C  TA_      AGC
                        GC GGC  GGGAGGAGC
                        II III  IIIIIIIII
                        CG CCG  CCCTCCTCG
                        TGT_  C  TAC      AII
GAM303 PAX2           GCAGGCCAGG-AGGAGCAG      4607 TGACGCCG    G
                        GCTAGG AGGAGCA
                        IIIIII IIIIIII
                        CGGTCC TCCTCGT
                        _____   _
GAM303 PPFIA3          TGACGCCGGGCAGCGCGTGGAGCAG 4611     C  GGA__      CII
                        TGACGCCGG TAG   GGAGCAG
                        IIIIIIIII III   IIIIIII
                        ACTGCGGCC GTC   CCTCGTC
                        C  GCGCA      III
GAM303 PPT2           GCCAGATACGGAGGAGCAGC    4608 TGACGCCGGC G
                        TA GGAGGAGCAG
                        II IIIIIIIIII
                        AT CCTCCTCGTC
                        CT_____  G
GAM303 PYCR1         TGACGCCGGCCGCGCAGGA      4613         AGGG   GCAG
                        TGACGCCGGCT  AGGA
                        IIIIIIIIIII  IIII
                        ACTGCGGCCGG  TCCT
                        CGCG   IIIC
GAM303 RIMS1         CGGCGGCAGGAGGAGGAGCAGC   4596 TGACGC  TA_
                        CGGC  GGGAGGAGCAGC
                        IIII  IIIIIIIIIIII
                        GCCG  TCCTCCTCGTCG
                        _____  TCC
GAM303 SLC17A7        TGAGGCAGGACAGAGAGGAGCAG  4615 C  C  C      CI
                        TGA GC GG TAGGGAGGAGCAG
                        III II II IIIIIIIIIIII
                        ACT CG CC GTCTCTCCTCGTC
                        C  T  T        II
GAM303 SLC9A1         TGAGGCAG---AGGGAGGAGC    4614 TGACGCC  T_      A
                        GGC AGGGAGGAGC
                        III IIIIIIIIII
                        CCG TCCCTCCTCG
                        ACT____  TC      I
GAM303 SLC9A1         GAAGCCTGGATCTAGGGAGGGGCAG 4602 TGAC  _ __      A  CII
                        GCC GG CTAGGGAGG GCAG
                        III II IIIIIIIII IIII
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                     CGG CC  GATCCCTCC CGTC
                     TT__  A  TA        C  CII
GAM303 WWP2          TGGCGCCTGCTAGGGAGGCAGGCAG 4612 A  G       A__  CII
                     TG CGCC GCTAGGGAGG  GCAG
                     || |||| |||||||||| ||||
                     AC GCGG CGATCCCTCC  CGTC
                      C  A        GTC  III
GAM304 ATP11A        GAC-TGGGTGTGAATCATGC-AGCAG 4623 ACG      _ __ T  I
                     TGGGTGTGA TC  GC AGCA
                     ||||||||| || || ||||
                     ACCCACACT AG  CG TCGT
                      G__     T TA _  I
GAM304 ATP11A        GAC-TGGGTGTGAATCATGC-AGCAG 4623 TG  G      _ __ T  I
                     AC TGGGTGTGA TC  GC AGCAG
                     || ||||||||| || || |||||
                     TG ACCCACACT AG  CG TCGTC
                     __ _      T TA _  C
GAM304 GARP          CGTGGGTGTGATCCCAACCAG   4621      G  AI
                     GTGGGTGTGATC CTAGC
                     |||||||||||| |||||
                     CACCCACACTAG GGTTG
                      _        GT
GAM304 GARP          CGTGGGTGTGATCCCAACCAG   4621 TGACGT     G  AG
                       GGGTGTGATC CTAGC
                       |||||||||| |||||
                       CCCACACTAG GGTTG
                     _____    _   GT
GAM304 POLR2C        ACCTGGGAATTTGAAGCGCTAGCAG 4620 CGT  TG__ T_     I
                       GGG  TGA CGCTAGCA
                       ||| ||| ||||||||
                       CCC  ACT GCGATCGT
                     ___  TTAA TC      I
GAM304 POLR2C        ACCTGGGAATTTGAAGCGCTAGCAG 4620 TGACG  TG__ T_     II
                      TGGG  TGA CGCTAGCAG
                      |||| ||| |||||||||
                      ACCC  ACT GCGATCGTC
                     G____  TTAA TC    CG
GAM304 PTBP1         GTGGGTGTG-TGGCT-GCAG   4624      ATC A I
                     GTGGGTGTG  GCT GC
                     ||||||||| ||| ||
                     CACCCACAC CGA CG
                      AC_ _ T
GAM304 SSRP1         TGA-GTGGGTGTGCGGAT-GCTCAGCAG4625  C      ATC__ _  II
                     TGA GTGGGTGTG   GCT AGCAG
                     ||| ||||||||| ||| |||||
                     ACT CACCCACAC   CGA TCGTC
                      _       GCCTA G  II
GAM304 SSRP1         TGA-GTGGGTGTGCGGAT-GCTCAGCAG4625 GAC      ATC__ _  I
                      GTGGGTGTG   GCT AGCA
                      ||||||||| ||| ||||
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                           CACCCACAC    CGA TCGT
                           ___       GCCTA  G   I
GAM304  THY1       GACGTGGGTAGATAATCGCATGCAG 4622 AC    __      TA  I
                           GTGGGT GTGATCGC GCA
                           |||||| ||||||||| |||
                           CACCCA TATTAGCG CGT
                           __     TC      TA  I
GAM304  THY1       GACGTGGGTAGATAATCGCATGCAG 4622 TG    __      TA  II
                           ACGTGGGT GTGATCGC GCAG
                           |||||||| ||||||||| ||||
                           TGCACCCA TATTAGCG CGTC
                           __       TC      TA  GI
GAM304  WHSC1        TGACGTGGGCGTGGTGTCGCT  4626         A__    AGCAG
                           TGACGTGGGTGTG  TCGCT
                           ||||||||||||  |||||
                           ACTGCACCCGCAC  AGCGA
                           CAC    IIIGA
GAM304  WHSC1        TGACGTGGGCGTGGTGTCGCT  4626         A__    III
                           TGACGTGGGTGTG  TCGC
                           ||||||||||||  ||||
                           ACTGCACCCGCAC  AGCG
                           CAC    AII
GAM305  ABCC5      TGATGACAGCAGTGACCACGC   4643 ___  GA     _   AGATGC
                           TGA AGCAGTGACC CGC
                           ||| ||||||||||| |||
                           ACT TCGTCACTGG GCG
                           ACT G_    T   IIICGT
GAM305  ABCC5      TGATGACAGCAGTGACCACGC   4643 ___  GA     _   III
                           TGA AGCAGTGACC CG
                           ||| |||||||||| ||
                           ACT TCGTCACTGG GC
                           ACT G_    T  GII
GAM305  APCS      AGAAGCAGTGACCAG--GATG    4635         CGCAGAI
                           AGAAGCAGTGACC
                           |||||||||||||
                           TCTTCGTCACTGG
                           TCCTACI
GAM305  APCS      AGAAGCAGTGACCAG--GATG    4635 TGAG       CGCA
                           AAGCAGTGACC  GATG
                           |||||||||||  ||||
                           TTCGTCACTGG  CTAC
                           ____       TC__
GAM305  CARS     TGGGAATCCCGGACCCGCAGCTGC  4646 A  GCAGT       ATI
                           GAA   GACCCGCAG
                           |||   |||||||||
                           CTT   CTGGGCGTC
                           C  AGGGC     GAI
GAM305  CCKAR      GAAGC-GT--CTCGCAGATGC    4637 AAGC   ACC
                           AGTG  CGCAGATG
                           ||||  ||||||||
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                        TCGC  GCGTCTAC
                      CT__    AGA
GAM305 CCKAR          GAAGC-GT--CTCGCAGATGC    4637 TGAGAAGCA  ACC
                        GTG  CGCAGAT
                        ||| |||||||
                        CGC  GCGTCTA
                      _____  AGA
GAM305 EIF2B1         AAGCAGTGAACCATGCAGA      4630        _ C_  |||
                      AAGCAGTGA CC GCAG
                      ||||||||| || ||||
                      TTCGTCACT GG CGTC
                       T  TA   T||
GAM305 GAMT           TGGGCAGCAGTGACCCTCA      4645 AGA        G GATG
                      TG  AGCAGTGACCC CA
                      ||  |||||||||| ||
                      AC  TCGTCACTGGG GT
                        CCG        A |||C
GAM305 GAMT           TGGGCAGCAGTGACCCTCA      4645 AGA        GC||
                      TG  AGCAGTGACCC
                      ||  ||||||||||
                      AC  TCGTCACTGGG
                        CCG        AGT|
GAM305 GNAI2          GAGAAGCAGGGGCCCCTCCAGACGC 4640 TG    TGA_ G_    ||
                      AGAAGCAG  CCC CAGATGC
                      ||||||||  ||| |||||||
                      TCTTCGTC  GGG GTCTGCG
                      __    CCCG AG    T|
GAM305 GNAI2          GAGAAGCAGGGGCCCCTCCAGACGC 4640 AG    TGA_ G_    |
                      AAGCAG  CCC CAGATG
                      ||||||  ||| ||||||
                      TTCGTC  GGG GTCTGC
                      __   CCCG AG   |
GAM305 KRTHA5         GAGAAGCAGCTCCTTACCC-CAGAT 4638 AGA    G____  G  |
                      AGCAGT  ACCC CAGA
                      ||||||   |||| ||||
                      TCGTCG  TGGG GTCT
                      ___   AGGAA  _  |
GAM305 KRTHA5         GAGAAGCAGCTCCTTACCC-CAGAT 4638 TG     G____  G  GC|
                      AGAAGCAGT  ACCC CAGAT
                      ||||||||   |||| |||||
                      TCTTCGTCG  TGGG GTCTA
                      __    AGGAA  _  A||
GAM305 MAPK8IP1       AGAAGC-----CCCGCAGATG    4634 _  AGTGA
                      GAAGC  CCCGCAGA
                      |||||  ||||||||
                      CTTCG  GGGCGTCT
                      T  _____
GAM305 MAPK8IP1       AGAAGC-----CCCGCAGATG    4634 TGAG  AGTGA
                      AAGC  CCCGCAGA
                      ||||  ||||||||
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```
                              TTCG    GGGCGTCT
                              ____    _____
GAM305  MYO1E        AAGCAGTGACACTCCGTAGTTG   4629        ___  C  ATIII
                     AAGCAGTGAC  CCG AG
                     ||||||||||  ||| ||
                     TTCGTCACTG  GGC TC
                        TGA   A  AACII
GAM305  NRG2         AGCAGAGCCACGCAGATGC     4636    TGA _      II
                     AGCAG  CC CGCAGATG
                     |||||  || ||||||||
                     TCGTC  GG GCGTCTAC
                         TC_  T     GI
GAM305  RBM3         AGAATGAAGGAAGCCGCAGATG   4633 ___   CAGT C     I
                     GAAG   GA CCGCAGAT
                     ||||   || ||||||||
                     CTTC   TT GGCGTCTA
                        TTA   C___  C     I
GAM305  RBM3         AGAATGAAGGAAGCCGCAGATG   4633 TGA   CAGT C      C
                     GAAG   GA CCGCAGATG
                     ||||   || |||||||||
                     CTTC   TT GGCGTCTAC
                        TTA   C___  C      C
GAM305  RERE         TGAGAAGCAGCCCCCACACAGCATGC 4644       GA _  _  II
                     TGAGAAGCAGT CC CGCAG ATGC
                     ||||||||||| || ||||| ||||
                     ACTCTTCGTCG GG GTGTC TACG
                           GG T   G   II
GAM305  RERE         TGAGAAGCAGCCCCCACACAGCATGC 4644 GA       GA _  _  I
                     GAAGCAGT CC CGCAG ATG
                     |||||||| || ||||| |||
                     CTTCGTCG GG GTGTC TAC
                        __     GG T   G   I
GAM305  RU2          AATCAG-GACCCGCAG-TGC    4632 AAG   T     ATI
                     CAG GACCCGCAG
                     ||| |||||||||
                     GTC CTGGCGTC
                        TTA  _     ACG
GAM305  SLC25A1      GAGAAGCAGGGGGCTGCAG      4641        TGACCC  II
                     GAGAAGCAG    GCA
                     |||||||||    |||
                     CTCTTCGTC    CGT
                         CCCCGA  CI
GAM305  SLC25A1      GAGAAGCAGGGGGCTGCAG      4641 TG    TGACCC  ATG
                     AGAAGCAG    GCAG
                     ||||||||    ||||
                     TCTTCGTC    CGTC
                        __      CCCCGA  GII
GAM305  ST3GALVI     AAG-AGTGACCCGCCGAGGC    4631 A  C      A  TI
                     AG AGTGACCCGC GA
                     || |||||||||| ||
```

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                              TC TCACTGGGCG CT
                              _ _        G  CC
GAM305  ST3GALVI       AAG-AGTGACCCGCCGAGGC   4631 TGAGAAGCA       A  T
                              GTGACCCGC GA G
                              |||||||||| || |
                              CACTGGGCG CT C
                              _____      G  C
GAM305  TACC1          GAGAAGCAGCCAAATGCAGAT   4642       GACCC   I
                              AGAAGCAGT   GCAGA
                              ||||||||   |||||
                              TCTTCGTCG   CGTCT
                               GTTTA   I
GAM305  TACC1          GAGAAGCAGCCAAATGCAGAT   4642 TG     GACCC   GC
                              AGAAGCAGT   GCAGAT
                              ||||||||   ||||||
                              TCTTCGTCG   CGTCTA
                              __      GTTTA   GI
GAM305  TREM2          GAGAAGCAGTGTTCAGGCAGA   4639 A     ACCC_   I
                              GAAGCAGTG   GCAG
                              |||||||||   ||||
                              CTTCGTCAC   CGTC
                              _      AAGTC   I
GAM305  TREM2          GAGAAGCAGTGTTCAGGCAGA   4639 TG     ACCC_   TGC
                              AGAAGCAGTG   GCAGA
                              ||||||||||   |||||
                              TCTTCGTCAC   CGTCT
                              __        AAGTC  CII
GAM306  CYBB           AAAGGCTATA--TTCGCACAG   2739 TCAA   AGACT       G
                              AGGT   TTCGCACAG
                              ||||   |||||||||
                              TCCG   AAGCGTGTC
                              ____   ATAT_      G
GAM306  MECP2          TCAAAGGTAGGATTTCCTCCAGG   2743     AC   GCA  TI
                              TCAAAGGTAG TTTC  CAGG
                              |||||||||| |||| ||||
                              AGTTTCCATC AAAG  GTCC
                              CT   GAG  II
GAM306  TCEA1          AAATGTAGACTTT-GCAACAG   2740 TCAAAG    C  _  G
                              GTAGACTTT GCA CAG
                              |||||||||| ||| |||
                              CATCTGAAA CGT GTC
                              TA____       _  T  A
GAM306  TEM8           TCAAAGGTATACATTTGGAAC   2742       G TTTCGCACAGGT
                              TCAAAGGTA AC
                              |||||||||| ||
                              AGTTTCCAT TG
                              A  TAAACCTTGIII
GAM306  TRIM14         CAAAGGTAGACTCAAGTCTCGCAGAG 2741 TC         _____   C  GTII
                              AAAGGTAGACTT   TCGCA AG
                              |||||||||| |||| ||
```

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                        TTTCCATCTGAG   AGCGT TC
                          __      TTCAG   C AIII
GAM307 ADRA2A           TGGAAGGGGAATTAGCCAGG   4665      ___     CGIII
                        TGGAAGGGG  TGGCC
                        IIIIIIIII  IIIII
                        ACCTTCCCC  ATCGG
                          TTA    TCCII
GAM307 CSPG2           ACATAGGAAGCGTGGTGGCCCGG   4656 CCTT   G__      I
                          GGAAG  GGTGGCCCG
                          IIIII  IIIIIIIII
                          CCTTC  CCACCGGGC
                          AT__   GCA     I
GAM307 CSPG2           ACATAGGAAGCGTGGTGGCCCGG   4656 TGACCTT   G__      TI
                          GGAAG  GGTGGCCCGG
                          IIIII  IIIIIIIIII
                          CCTTC  CCACCGGGCC
                          TAT____  GCA       CC
GAM307 DGKG          CTTGGTTGCGCGGTGGCCCGG   4661   AAGG__      III
                          CTTGG   GGTGGCCCG
                          IIIII   IIIIIIIII
                          GAACC   CCACCGGGC
                          AACGCG      CII
GAM307 EGFL4          TGACCTTGGCGAAGGGGCGGC   4662      __       CCGGT
                        TGACCTTGG AAGGGGTGGC
                        IIIIIIIII IIIIIIIIII
                        ACTGGAACC TTCCCCGCCG
                          GC    IIITG
GAM307 EGFL4          TGACCTTGGCGAAGGGGCGGC   4662      __       III
                        TGACCTTGG AAGGGGTGG
                        IIIIIIIII IIIIIIIII
                        ACTGGAACC TTCCCCGCC
                          GC    GII
GAM307 FLNB          TGAACT-GGAAGGGGCTG--CCGGT   4663  C T     G  C
                        TGA CT GGAAGGGGT GCC GGT
                        III II IIIIIIIII III III
                        ACT GA CCTTCCCCG CGG CCA
                          T _    A _
GAM307 FLNB          TGAACT-GGAAGGGGCTG--CCGGT   4663 _ C T    G  C I
                        GA CT GGAAGGGGT GCC GG
                        II II IIIIIIIII III II
                        CT GA CCTTCCCCG CGG CC
                        A T _    A _ I
GAM307 HOXD4           ACCTAGCACAGGGGTGGCC      4655  TGGA_      II
                        ACCT  AGGGGTGGC
                        IIII  IIIIIIIII
                        TGGA  TCCCCACCG
                          TCGTG     GI
GAM307 HOXD4           ACCTAGCACAGGGGTGGCC      4655 TGACCTTGGA      CGG
                          AGGGGTGGCC
                          IIIIIIIIII
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                             TCCCCACCGG
                     GATCGTG___        TTI
GAM307 INHBC         CCATGGAAGGGGGTAGCCAGGT   4657 CT      _   C I
                        TGGAAGGGG TGGCC GG
                        |||||||||| ||||| ||
                        ACCTTCCCC ATCGG CC
                     T_        C   T I
GAM307 INHBC         CCATGGAAGGGGGTAGCCAGGT   4657 TGACCT      _   C
                        TGGAAGGGG TGGCC GGT
                        |||||||||| ||||| |||
                        ACCTTCCCC ATCGG CCA
                     _____        C   T
GAM307 MAGEA12         CCTTGGAAGGTGCACTGGCCC   4658        GG___   III
                        CCTTGGAAGG   TGGCC
                        ||||||||||   |||||
                        GGAACCTTCC   ACCGG
                          ACGTG    GII
GAM307 MAGEA12         CCTTGGAAGGTGCACTGGCCC   4658 TGACCT    GG___     T
                        TGGAAGG   TGGCCCGG
                        |||||||   |||||||||
                        ACCTTCC   ACCGGGTC
                     _____      ACGTG    T
GAM307 MPP2          TGAC-TGGGGAGGGGTGGC   4664   CTT A    CCG
                        TGAC  GG AGGGGTGGC
                        ||||  || |||||||||
                        ACTG  CC TCCCCACCG
                         AC_ C      III
GAM307 MPP2          TGAC-TGGGGAGGGGTGGC   4664   CTT A    I
                        TGAC  GG AGGGGTGG
                        ||||  || ||||||||
                        ACTG  CC TCCCCACC
                         AC_ C      G
GAM307 RAP1GA1        ACCTTCAGAGGGGGTGGCCCGG   4654 CC TG  A       I
                         T GA GGGGTGGCCCG
                         | || |||||||||||
                         A CT CCCCACCGGGC
                        GA GT  C         I
GAM307 SACM2L         TGGAAGGGGTACCCCAGGT   4666        G  II
                        TGGAAGGGGTG CCCGG
                        |||||||||||| |||||
                        ACCTTCCCCAT GGGTC
                          G   CA
GAM307 SLC22A12         CCCTGGAAGGGG-GGCTGGGT   4660 _        T CC I
                        CTTGGAAGGGG GGC GG
                        |||||||||||| ||| ||
                        GGACCTTCCCC CCG  CC
                        G      _ A_ C
GAM307 SLC22A12         CCCTGGAAGGGG-GGCTGGGT   4660 TGACCT      T CC
                        TGGAAGGGG GGC GG
                        |||||||||| ||| ||
```

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                          ACCTTCCCC CCG  CC
                          _____      _   AC
GAM307  WNT3A        CCGTGGAAGGGGCCTTGCCCTGGT  4659 CTT       G__  _ I
                          GGAAGGGGT  GCCC GG
                          |||||||||  |||| ||
                          CCTTCCCCG  CGGG CC
                          ___         GAA  A  I
GAM307  WNT3A        CCGTGGAAGGGGCCTTGCCCTGGT  4659 TGACCT      G__  _ I
                          TGGAAGGGGT  GCCC GGT
                          |||||||||| |||| |||
                          ACCTTCCCCG  CGGG CCA
                          _____      GAA  A  G
GAM308  ADCY8          AGCGGTGG-G-AGCTTAGTG   4672 TA TC  AGC
                          GC TGG  AGCTTAGTGT
                          || ||| ||||||||||
                          CG ACC  TCGAATCACG
                          __  CC  C__
GAM308  ATF5         GCTCTGGAGGATGCTCAG-GTG   4675 TAGC    CA_   T  T
                          TCTGGAG  GCTTAG GTG
                          ||||||| |||||| |||
                          AGACCTC  CGAGTC CAC
                          ____        CTA   _  C
GAM308  CYP4A11        AGCTCTGGAAGTGCAGATTA    4669 TA    ___  C  GTGTG
                          GCTCTGGA  GCAG TTA
                          |||||||| |||| |||
                          CGAGACCT  CGTC AAT
                          __        TCA   T  A|||T
GAM308  DAAM2       AGCTCTGGAACAACGTATTTGTGT  4671 TA        TTAG_  I
                          GCTCTGGAGCAGC   TGTGT
                          |||||||||||||   |||||
                          CGAGACCTTGTTG   ACACA
                          __          CATAA   G
GAM308  GCK         AGCTGTGG-G--GCTTAGTGT     4673 TA  C  AGCA
                          GCT TGG   GCTTAGTGT
                          ||| |||   |||||||||
                          CGA ACC   CGAATCACA
                          __  C  C___
GAM308  JUN         TAGCTCTGG-GCAG-TTAG       4677       A  C  TGT
                          TAGCTCTGG GCAG TTAG
                          ||||||||| |||| ||||
                          ATCGAGACC CGTC AATC
                          _  _  |||
GAM308  LANGERIN      GCTCTGGAGTAACTTTGATGTG   4676 TAGC   C  A_   T
                          TCTGGAG AGCTT GTGTG
                          ||||||| ||||| |||||
                          AGACCTC TTGAA TACAC
                          ____        A  AC  T
GAM308  MASP1       TCTGGAGCAGC-AGGTGTG       4679 TAGCTCTG    TTA
                          GAGCAGC  GTGT
                          ||||||| ||||
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                              CTCGTCG  CACA
                              _____       TC_
GAM308  NDRG2        TAGCTCTGGGGGAGGTGAG    4678      AGCAGCTTAGTGTG
                         TAGCTCTGG
                         |||||||||
                         ATCGAGACC
                              CCCTCCACTCIIIT
GAM308  SALL2        AGCTCTGGAGCCTACAGCTT   4670 TA      ____     AGTGTG
                         GCTCTGGAGC  AGCTT
                         ||||||||||  |||||
                         CGAGACCTCG  TCGAA
                           __     GATG    CIIITG
GAM308  SEPN1        GCTCTGGAGAAGGCTGTGGTGT  4674 TAGC    CA_ TA_  GT
                         TCTGGAG  GCT  GTGT
                         |||||||  |||  ||||
                         AGACCTC  CGA  CACA
                         ____     TTC  CAC  AA
GAM309  ARNT2        TGCAGGGTTTCAACCACCTG    4694      C  G  CAC
                         TGCAGGGTTTC AGCT ACC
                         ||||||||||| |||| |||
                         ACGTCCCAAAG TTGG TGG
                             _  _  ACI
GAM309  BCRP2        TGCCAGGTTTCCA---GACCCACA  4700   A      GCT
                         TGC GGGTTTCCA  GACCCACA
                         ||| |||||||||  ||||||||
                         ACG TCCAAAGGT  CTGGGTGT
                              G       ___
GAM309  DDX11        GCAGAAGATCCCAGCTGA-CCACA  4689 TG   T_       _ CAI
                         CAGGG  TTCCAGCTGACC CA
                         |||||  ||||||||||||| ||
                         GTCTT  AGGGTCGACTGG GT
                           __    CT       T CII
GAM309  EGFL3        CAGGCAGCTTCCAGCTGATCCCA   4683 T  GG       _  CAI
                         GCA  GTTTCCAGCTGA CCCA
                         |||  ||||||||||| ||||
                         CGT  CGAAGGTCGACT GGGT
                         C  __        A  CCI
GAM309  EPS8         TGCAGACTTTCCAGCTGACTCA    4697     G      C CA
                         TGCAGG TTTCCAGCTGAC CA
                         |||||| ||||||||||| ||
                         ACGTCT AAAGGTCGACTG GT
                             G       A II
GAM309  FMN2         TGCA---TTACGAGCTGACCCA   4696    GGGTTCC      C
                         TGCA      AGCTGACCCA
                         ||||      ||||||||||
                         ACGT      TCGACTGGGT
                           AATGC___        I
GAM309  GNAO1        GCAGGGTTTGCAG-TGGCC     4690 TG    C  C A CA
                         CAGGGTTT CAG TG CC
                         |||||||| ||| || ||
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                         GTCCCAAA GTC AC GG
                         __       C  _ C  AI
GAM309  INMT       GCAGTGGTATGTTCCAGCTGACTCCA 4688 TG  _ ___        _ CAII
                         CAG GGT   TTCCAGCTGAC CCA
                         ||| |||   |||||||||| |||
                         GTC CCA   AAGGTCGACTG GGT
                         __  A  TAC         A  TIII
GAM309  MAPT       AGGGTGGCACA-CTGACCCACA   4682 TGCAG  TTCCA
                         GGT   GCTGACCCACA
                         |||   ||||||||||
                         CCG   TGACTGGGTGT
                       CA___   TG___
GAM309  NHP2L1    CAGAGAGTACATCTGACCCACA   4687 TGC   TTC  G
                       AGGGT  CA CTGACCCACA
                       |||||  || ||||||||||
                       TCTCA  GT GACTGGGTGT
                       C__   T__ A
GAM309  PIM1      GCAGGGTT-----CTGACCCAC   4691 TG    TCCAG
                       CAGGGTT   CTGACCCA
                       |||||||   ||||||||
                       GTCCCAA   GACTGGGT
                       __      _____
GAM309  PPAT      CAGGGTT---ATCTGACCCAC   4686 TGCA    TCCAG
                       GGGTT   CTGACCCA
                       |||||   ||||||||
                       CCCAA   GACTGGGT
                       ____     TA___
GAM309  PVT1    TGCAGGGTT--CAGGCCTGACGCA 4695        CCAG   C CA
                       TGCAGGGTTT  CTGAC CA
                       ||||||||||  ||||| ||
                       ACGTCCCAAG  GACTG GT
                         TCCG   C II
GAM309  PYCS    TGCAGCTTGGGTTCCAGCTG      4693  ___ T     ACCCAC
                       TGCAG  GG TTCCAGCTG
                       |||||  || ||||||||||
                       ACGTC  CC AAGGTCGAC
                       GAA  C      IIIACA
GAM309  RAMP3      CAGCCTTTCCAGCTGTCTTCCCAC 4685 TGCAGGG      A___    AI
                       TTTCCAGCTG  CCCAC
                       ||||||||||  |||||
                       AAAGGTCGAC  GGGTG
                       CGG____      AGAA   GT
GAM309  RPL10   TGCAGGGTTT---GCTGCCTCA   4698        CCA  A _ C
                       TGCAGGGTTT  GCTG CC CA
                       ||||||||||  |||| || ||
                       ACGTCCCAAA  CGAC GG GT
                       ___    _ A I
GAM309  SIX2    TGCAGC--TCCCA-CTGACCCACA   4699   GG    G
                       TGCA GTTTCCA CTGACCCACA
                       |||| ||||||| ||||||||||
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                        ACGT  CGAGGGT GACTGGGTGT
                          __   _
GAM309 SLC14A1      CAGGGTTTCACCATGCTG-CCCA   4684 TGCA   __  _   A  CA
                     GGGTTT  CCA GCTG CCCA
                     |||||| ||| |||| ||||
                     CCCAAA  GGT CGAC GGGT
                       ____    GT  A   _   CC
GAM309 SLC7A8       GGGTCTCTCCAGCTGACCC   4692 TGCAGGG        AC
                     TTTCCAGCTGACCC
                     ||||||||||||||
                     AGAGGTCGACTGGG
                     G_____        GA
GAM310 BAALC        CTAATAGGA-TAGTAAGGA     4708     C  _  II
                     CTAATAGGA TAG AAGG
                     ||||||||| ||| ||||
                     GATTATCCT ATC TTCC
                       _  A  TI
GAM310 DNCI1        TAATAGGACTATGCCAGGAG   4718      GA__   III
                     TAATAGGACTA   AGGA
                     ||||||||||    ||||
                     ATTATCCTGAT   TCCT
                       ACGG   CII
GAM310 EIF2AK3      GCTACAAATAGGACTATAA    4711 A T     GAII
                     GC AC AATAGGACTA
                     || || ||||||||||
                     CG TG TTATCCTGAT
                      A T      ATTI
GAM310 GJB5        AATAGGACTCAGCAAGCAG    4705      _ _  GAIII
                     AATAGGACT AG AAG
                     ||||||||| || |||
                     TTATCCTGA TC TTC
                       G G  GTCII
GAM310 HLF         GCAACTTATAAAGGACTAGA   4710     AAT__    III
                     GCAACT   AGGACTAG
                     ||||||   ||||||||
                     CGTTGA   TCCTGATC
                      ATATT     TII
GAM310 HSPA9B       TACTAGGCTAACTAGAAGGA   4717 TAA  ___        III
                     TAGG  ACTAGAAGG
                     ||||  |||||||||
                     ATCC  TGATCTTCC
                     ATG   GAT    TII
GAM310 ISLR        CTAGAAGAGATTAGAAGGAG   4707 AT _ C    II
                     CTA AG GA TAGAAGGA
                     ||| || || ||||||||
                     GAT TC CT ATCTTCCT
                      CT T A    CI
GAM310 ITM2B       GGCAACTAACA--ACTACAA    4715       AG   GI
                     GGCAACTAAT GACTA
                     ||||||||| |||||
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                        CCGTTGATTG TTGAT
                         __        GT
GAM310  MIPOL1       GGCATC--ACAAGA-TAGAAGGAG  4716   ACTA     C     I
                         GGCA   ATAGGA TAGAAGG
                         ||||   |||||| |||||||
                         CCGT   TGTTCT ATCTTCC
                         AG__      _       T
GAM310  MTMR2        GCAAGTATGTTAAGACTAGAAG   4709 CAACTAA          I
                            TAGGACTAGAA
                            |||||||||||
                            ATTCTGATCTT
                         TCATACA          I
GAM310  OA1          GGCAACTA--AGG-CTAGA       4714       AT   A
                         GGCAACTA AGG CTAG
                         |||||||| ||| ||||
                         CCGTTGAT TCC GATC

                              __   _
GAM310  OGT          GGCTACAGAATAGGACT-GAGGGAG 4713  A T_      A A  I
                         GC AC  AATAGGACT GA GGA
                         || ||  ||||||||| || |||
                         CG TG  TTATCCTGA CT CCT
                          A TC       _  C  I
GAM310  SLC21A3      AAGTATTAG---TAGAAGGAG    4704 ACTAA_  GAC
                            TAG  TAGAAGGA
                            |||  ||||||||
                            ATC  ATCTTCCT
                         TTCATA   ___
GAM310  TPT          AATTTATAGGACTAGAATGA     4703 ACTA        GGI
                            ATAGGACTAGAA
                            ||||||||||||
                            TATCCTGATCTT
                         TAAA        ACI
GAM310  VAPB         CAACTAGTA---CTAGAAGGA    4706 AACTAA  G
                            TAG ACTAGAAGG
                            ||| |||||||||
                            ATC TGATCTTCC
                         GTTG__    A
GAM310  XRCC5        GGCAGAGTAATGTGGTAACTAGAAGG 4712 _____   C    AT   ACTAGI
                         GG AACTA  AGG
                         || |||||  |||
                         CC TTGAT  TCC
                         TTACA A    CT   IIIGAT
GAM311  ADRBK1       CAGAGCCCAGGGTGGCACAGC    4728 A    TG T_      I
                          GAGCT G TGGCACAG
                          ||||| | ||||||||
                          CTCGG C ACCGTGTC
                          _    GT CC        I
GAM311  ADRBK1       CAGAGCCCAGGGTGGCACAGC    4728 TC    TG T_      CGG
                          AGAGCT G TGGCACAGC
                          |||||| | |||||||||
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                          TCTCGG C ACCGTGTCG
                          __    GT CC      AII
GAM311 APS            AGAGCTTGGCGTGTCCCACCCGG  4723 G      _ GCA  G   I
                          AGCTTGGT TG  CA CCG
                          IIIIIIII II  II III
                          TCGAACCG AC  GT GGC
                            _     C AGG  G   I
GAM311 APS            AGAGCTTGGCGTGTCCCACCCGG  4723 TCAG     _ GCA  G   I
                          AGCTTGGT TG  CA CCGG
                          IIIIIIII II  II IIII
                          TCGAACCG AC  GT GGCC
                          ____      C AGG  G   C
GAM311 CACNB1           CAGTCCTTG-TTGGCACACTCGG  4733 AG _ G      GC  I
                          AG CTT GTTGGCACA CG
                          II III IIIIIIIII II
                          TC GGA CAACCGTGT GC
                          G_ A  A     GA  I
GAM311 CACNB1           CAGTCCTTG-TTGGCACACTCGG  4733 TCAG _ G      GC
                          AG CTT GTTGGCACA CGG
                          II III IIIIIIIII III
                          TC GGA CAACCGTGT GCC
                          ____ A  A     GA
GAM311 CAPNS1          AGTGCTAGGCTTGGCACAG      4721 AGA  T  _    II
                          GCT GGTT GGCACA
                          III IIII IIIIII
                          CGA CCGA CCGTGT
                          TCA T  A   CI
GAM311 CAPNS1          AGTGCTAGGCTTGGCACAG      4721 TCAGA T  _      CCG
                          GCT GGTT GGCACAG
                          III IIII IIIIIII
                          CGA CCGA CCGTGTC
                          A____  T  A    CAI
GAM311 COL17A1        GAGCT--GATGGCACAGCC       4734   T  T    I
                          GAGCT GGT GGCACAGC
                          IIIIII III IIIIIIII
                          CTCGA CTA CCGTGTCG
                          _ _     G
GAM311 COL17A1        GAGCT--GATGGCACAGCC       4734 TCAGAGCT  T
                          TGGT GGCACAGCC
                          IIII IIIIIIIIII
                          ACTA CCGTGTCGG
                          G_____  _
GAM311 ETV3          AGAGCTTGGTAGTTTCACAG       4725      TGG__  III
                          AGAGCTTGGT   CACA
                          IIIIIIIIII   IIII
                          TCTCGAACCA   GTGT
                          TCAAA  CII
GAM311 ETV3          AGAGCTTGGTAGTTTCACAG       4725 TCAG     TGG__  CCG
                          AGCTTGGT   CACAG
                          IIIIIIII   IIIII
```

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                    TCGAACCA    GTGTC
                         TCAAA    TTI
GAM311 EXTL2        AGAGCT-GGTTGGCAGGGCC    4726 _    T    CA I
                      GAGCT GGTTGGCA  GC
                      ||||| ||||||| ||
                      CTCGA CCAACCGT  CG
                      T    _    CC I
GAM311 EXTL2        AGAGCT-GGTTGGCAGGGCC    4726 TCAG   T    CA
                        AGCT GGTTGGCA  GCCG
                        |||| ||||||||  ||||
                        TCGA CCAACCGT  CGGT
                       ___ _    CC
GAM311 FAT        AGACGTTGGGAAATGGCACAGCCG  4724 GAGC   T___        I
                        TTGG   TGGCACAGCC
                        ||||   ||||||||||
                        AACC   ACCGTGTCGG
                       C___   CTTT       I
GAM311 FAT        AGACGTTGGGAAATGGCACAGCCG  4724 TCAGA _   T___        I
                        GC TTGG   TGGCACAGCCGG
                        || ||||   ||||||||||||
                        TG AACC   ACCGTGTCGGCT
                       _____ C  CTTT       A
GAM311 FCN3        CAGAGGT-GGTTGGCAAAG      4729    CT    CAI
                        CAGAG TGGTTGGCA
                        ||||| |||||||||
                        GTCTC ACCAACCGT
                        C_    TTC
GAM311 FCN3        CAGAGGT-GGTTGGCAAAG      4729 TC   CT    C CC
                        AGAG TGGTTGGCA AG
                        |||| ||||||||| ||
                        TCTC ACCAACCGT TC
                       __  C_    T CI
GAM311 IL2RB       CAGAGCTTGG-TGCCAAACCC    4730 _       T G CAGCI
                        AGAGCTTGGT G CA
                        |||||||||| | ||
                        TCTCGAACCA C GT
                       G     _ G TTGGI
GAM311 IL2RB       CAGAGCTTGG-TGCCAAACCC    4730 TC      T G C  G
                        AGAGCTTGGT G CA AGCC
                        |||||||||| | || ||||
                        TCTCGAACCA C GT TTGG
                       __    _G _  G
GAM311 KCNAB2      GAGCTTGGTAGGCATGGCC      4735       T  CA II
                        GAGCTTGGT GGCA  GC
                        ||||||||| |||| ||
                        CTCGAACCA CCGT  CG
                        T  AC GI
GAM311 KCNAB2      GAGCTTGGTAGGCATGGCC      4735 TCAGAG   T  CA  G
                        CTTGGT GGCA  GCC
                        |||||| |||| |||
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                        GAACCA CCGT CGG
                        _____    T  AC  G
GAM311 MASP1         AGTGCTGGGATTGGCACAG     4722 AGA  T _      II
                        GCT GG TTGGCACA
                        ||| || |||||||||
                        CGA CC AACCGTGT
                        TCA  C  T      CI
GAM311 MASP1         AGTGCTGGGATTGGCACAG     4722 TCAGA  T _      CCG
                        GCT GG TTGGCACAG
                        ||| || ||||||||||
                        CGA CC AACCGTGTC
                        A____   C  T      TCI
GAM311 MVK        CAGAGCTTGGCTGGCATCGCC     4731          CA  I
                        AGAGCTTGGTTGGCA GC
                        |||||||||||||| ||
                        TCTCGAACCGACCGT CG
                               AG  I
GAM311 MVK        CAGAGCTTGGCTGGCATCGCC     4731 TC       CA   G
                        AGAGCTTGGTTGGCA GCCG
                        |||||||||||||| ||||
                        TCTCGAACCGACCGT CGGT
                         __          AG   I
GAM311 OGDH        TCTGACCTGCTTTGGCACAGC    4737 CA  G   G_     I
                        GA CTTG TTGGCACAG
                        || |||| |||||||||
                        CT GGAC AACCGTGTC
                        GA _  GA      I
GAM311 OGDH        TCTGACCTGCTTTGGCACAGC    4737 TCA  G  G_      CGG
                        GA CTTG TTGGCACAGC
                        || |||| ||||||||||
                        CT GGAC AACCGTGTCG
                        AGA _  GA       III
GAM311 PMX1         CAGGGCTATTGTTGGCACA     4727  A TG_     II
                        CAG GCT  GTTGGCAC
                        ||| ||  |||||||||
                        GTC CGA  CAACCGTG
                         C  TAA      TI
GAM311 PMX1         CAGGGCTATTGTTGGCACA     4727 TC A TG_      GCCG
                        AG GCT  GTTGGCACA
                        || ||| |||||||||
                        TC CGA  CAACCGTGT
                        __ C  TAA      AIII
GAM311 RNF14       TCAGAGCTT--TGGGCACA     4736       GGTT   GCC
                        TCAGAGCTT GGCACA
                        ||||||||| ||||||
                        AGTCTCGAA CCGTGT
                              AC__    III
GAM311 RNF14       TCAGAGCTT--TGGGCACA     4736       GGTT  I
                        TCAGAGCTT GGCAC
                        ||||||||| |||||
```

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                        AGTCTCGAA   CCGTG
                          AC__      T
GAM311  SUV39H1      CAGAGCTTGGT---CCCAGCC    4732         __  ACAI
                        CAGAGCTTGGTT GGC
                        |||||||||| |||
                        GTCTCGAACCAG TCG
                          GG  GIII
GAM311  SUV39H1      CAGAGCTTGGT---CCCAGCC    4732 TC        GGCA
                         AGAGCTTGGTT  CAGCC
                         |||||||||| |||||
                         TCTCGAACCAG  GTCGG
                        __         G___
GAM312  ABCA2        CTCCCTGGCCCAGCTCTGG      4754    GCC      II
                        CTCC GCCCAGCTCTG
                        |||| ||||||||||
                        GAGG CGGGTCGAGAC
                          GAC       CI
GAM312  ABCA2        CTCCCTGGCCCAGCTCTGG      4754 GAGCT GCC       T
                         CC GCCCAGCTCTGG
                         || ||||||||||||
                         GG CGGGTCGAGACC
                        _____  AC_       C
GAM312  ABCA2        AGCTCCGCCCACAGCCC-GCTCT  4743 GA       ____  A  GGTG
                        GCTCCGCC  GCCC GCTCT
                        ||||||||  |||| |||||
                        CGAGGCGG  CGGG CGAGA
                        __   GTGT _  GIII
GAM312  ABCA2        AGCTCCGCCCACAGCCC-GCTCT  4743         ____  A  III
                        AGCTCCGCC  GCCC GCTC
                        |||||||||  |||| ||||
                        TCGAGGCGG  CGGG CGAG
                          GTGT _  AII
GAM312  ABCA2        GAG-TCCCTGGCCCAGCTCTGG   4761   CT GCC       TG
                        GAG CC GCCCAGCTCTGG
                        ||| || ||||||||||||
                        CTC GG CGGGTCGAGACC
                         AG AC_       II
GAM312  ABCA2        GAG-TCCCTGGCCCAGCTCTGG   4761 _ CT GCC        I
                         AG CC GCCCAGCTCTG
                         || || |||||||||||
                         TC GG CGGGTCGAGAC
                        C AG AC_        I
GAM312  ACADVL       GAGCTCTGAC--CCAGCTCTGG   4763     CGCC        T
                        GAGCTC GCCCAGCTCTGG
                        |||||| ||||||||||||
                        CTCGAG TGGGTCGAGACC
                          AC__         I
GAM312  ACADVL       GAGCTCTGAC--CCAGCTCTGG   4763     CGCC        I
                        GAGCTC GCCCAGCTCT
                        |||||| ||||||||||
```

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                              CTCGAG   TGGGTCGAGA
                              AC__         C
GAM312 ADA              CTCCGCCGCC--GCTC-GGTG    4755       CA   T  I
                              CTCCGCCGCC GCTC GG
                              IIIIIIIIII IIII II
                              GAGGCGGCGG CGAG CC
                                   __    _ A
GAM312 ADA              CTCCGCCGCC--GCTC-GGTG    4755 GAGCTC    CA   T
                              CGCCGCC GCTC GG
                              IIIIIII IIII II
                              GCGGCGG CGAG CC
                                _____    __  _
GAM312 ALDH1B1           TCCGGCCCTCCCAGCTCTG      4770    _ G_       III
                              TCCG CC CCCAGCTCT
                              IIII II IIIIIIIII
                              AGGC GG GGGTCGAGA
                               C  GA      CII
GAM312 ALDH1B1           TCCGGCCCTCCCAGCTCTG      4770 GAGCTCC  G_      GT
                              GCC CCCAGCTCTG
                              III IIIIIIIIII
                              CGG GGGTCGAGAC
                              _____  GA     AG
GAM312 APOL1            CTCAGCCGCCCAGTTAGCTGG     4752  C      CT__  III
                              CTC GCCGCCCAG  CTG
                              III IIIIIIIII  III
                              GAG CGGCGGGTC  GAC
                               T    AATC CII
GAM312 APOL1            CTCAGCCGCCCAGTTAGCTGG     4752 GAGCTCC     CT__  TG
                              GCCGCCCAG  CTGG
                              IIIIIIIII  IIII
                              CGGCGGGTC  GACC
                              T_____      AATC  TT
GAM312 ARL2            AGCTCCTCCCCGCCCAGCCCT     4744     G__       III
                              AGCTCC  CCGCCCAGCTC
                              IIIIII  IIIIIIIIIII
                              TCGAGG  GGCGGGTCGGG
                                AGG        AII
GAM312 ARL2            AGCTCCTCCCCGCCCAGCCCT     4744 GAG_  G      GGTG
                              CTCC CCGCCCAGCTCT
                              IIII IIIIIIIIIIII
                              GAGG GGCGGGTCGGGA
                              CGAG   _       GIII
GAM312 CDR2          GCGCCGCCGCCCAGACTCCGCTG      4767 GAGCT      _  G I
                              CCGCCGCCCAG CTCTG TG
                              IIIIIIIIIII IIIII II
                              GGCGGCGGGTC GAGGC AC
                              C___       T  G G
GAM312 CDR2          GCGCCGCCGCCCAGACTCCGCTG      4767 T        _  GTI
                              CCGCCGCCCAG CTCTG
                              IIIIIIIIIII IIIII
```

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                          GGCGGCGGGTC GAGGC
                            C     T   GII
GAM312 CEP2           GAGCTCCGCCACCAGCAGC    4759         __    TCTGGT
                         GAGCTCCGCCGCC CAGC
                         IIIIIIIIIIII IIII
                         CTCGAGGCGGTGG GTCG
                            TC   IIIGTG
GAM312 CEP2           GAGCTCCGCCACCAGCAGC    4759         __   III
                         GAGCTCCGCCGCC CAG
                         IIIIIIIIIIII III
                         CTCGAGGCGGTGG GTC
                            TC   GII
GAM312 CNTNAP2          GCTTCGCCTGTGCCCAGCTCT   4766  C  ___       III
                         GCT CGCC  GCCCAGCTC
                         III IIII  IIIIIIIII
                         CGA GCGG  CGGGTCGAG
                          A    ACA      AII
GAM312 CNTNAP2          GCTTCGCCTGTGCCCAGCTCT   4766 GAGCTC  ___      GGTG
                            CGCC  GCCCAGCTCT
                            IIII  IIIIIIIIII
                            GCGG  CGGGTCGAGA
                           AA____   ACA       GTII
GAM312 ESRRA          AGCTCCGC--CCCAGCCCT    4747        GC    I
                         AGCTCCGCC CCAGCTC
                         IIIIIIIII IIIIIII
                         TCGAGGCGG GGTCGGG
                            __        A
GAM312 ESRRA          AGCTCCGC--CCCAGCCCT    4747 GA      GC     GG
                          GCTCCGCC CCAGCTCT
                          IIIIIIII IIIIIIII
                          CGAGGCGG GGTCGGGA
                           __     __    AI
GAM312 GAB2          GCTTGGTCGCCCAGCT-TGGT    4769 CTCCGC_      C  I
                          CGCCCAGCT TGG
                          IIIIIIIII III
                          GCGGGTCGA ACC
                         CGAACCA        _   I
GAM312 GAB2          GCTTGGTCGCCCAGCT-TGGT    4769 GAGCTCCGC       C
                          CGCCCAGCT TGGT
                          IIIIIIIII IIII
                          GCGGGTCGA ACCA
                         AACCA____        _
GAM312 GNA11          CTCCAGCCGCCCAGCCCACGTG   4750 GAGCTCC        TG
                          GCCGCCCAGCTC GTG
                          IIIIIIIIIIII III
                          CGGCGGGTCGGG CAC
                         GT_____          TG
GAM312 GNA11          CTCCAGCCGCCCAGCCCACGTG   4750 T _        _ GTI
                          CC GCCGCCCAGCTC TG
                          II IIIIIIIIIII II
```

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                          GG CGGCGGGTCGGG GC
                          _ T       T AII
GAM312 IKBKG        GAGCT--GCCACCCAGCTCTG   4760    CC          GT
                    GAGCT GCCGCCCAGCTCTG
                    ||||| |||||||||||||
                    CTCGA CGGTGGGTCGAGAC
                          __          II
GAM312 IKBKG        GAGCT--GCCACCCAGCTCTG   4760    CC        I
                    GAGCT GCCGCCCAGCTC
                    ||||| |||||||||||
                    CTCGA CGGTGGGTCGAG
                          __          A
GAM312 KCNJ6        CTCCGCCCGCCCAGCCTCT     4751    _     CIII
                    CTCCGCC GCCCAGCT
                    ||||||| ||||||||
                    GAGGCGG CGGGTCGG
                       G     AGAI
GAM312 KCNJ6        CTCCGCCCGCCCAGCCTCT     4751 GAGCTC  _   _  GGT
                    CGCC GCCCAGC TCT
                    |||| ||||||| |||
                    GCGG CGGGTCG AGA
                    _____    G    G GGT
GAM312 LENG4        CTCC-CTGCACAGCTCTGG     4753    GCC C     I
                    CTCC  GC CAGCTCTG
                    ||||  || ||||||||
                    GAGG  CG GTCGAGAC
                     GA_ T      C
GAM312 LENG4        CTCC-CTGCACAGCTCTGG     4753 GAGCTCCG _ C
                    CC GC CAGCTCTGG
                    || || |||||||||
                    GG CG GTCGAGACC
                    _____ A T
GAM312 LENG4        GCTCCCAGCCGCCCAGGGCTG   4765    __      CT III
                    GCTCC GCCGCCCAG CT
                    ||||| |||||||||| ||
                    CGAGG CGGCGGGTC GA
                       GT        CC CII
GAM312 LENG4        GCTCCCAGCCGCCCAGGGCTG   4765 GAG  C     CT GTG
                    CTC GCCGCCCAG CTG
                    ||| |||||||||| |||
                    GGG CGGCGGGTC GAC
                    A__ T      CC GGI
GAM312 LY94         GAGCTCACGCCGCCCAGGCTC   4756    _     _ TGGTG
                    GAGCTC CGCCGCCCAG CTC
                    |||||| |||||||||| |||
                    CTCGAG GCGGCGGGTC GAG
                        T     C IIIGT
GAM312 LY94         GAGCTCACGCCGCCCAGGCTC   4756    _      _ III
                    GAGCTC CGCCGCCCAG CT
                    |||||| |||||||||| ||
```

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                            CTCGAG GCGGCGGGTC GA
                              T        C  GII
GAM312 MAG            AGCTCAG--GTCCAGCTCTGG    4749 _   CGCCGC        I
                            GCTC    CCAGCTCTG
                            IIII    IIIIIIIII
                            CGAG    GGTCGAGAC
                            T   TCCA__       I
GAM312 MAG            AGCTCAG--GTCCAGCTCTGG    4749 GA  CGCCGC        T
                            GCTC    CCAGCTCTGG
                            IIII    IIIIIIIIII
                            CGAG    GGTCGAGACC
                            __  TCCA__        C
GAM312 MFNG        GAGC-CC-CAGCCCAGCTCAAGTG   4764       CC       T
                        GAGCTCCG GCCCAGCTC GGTG
                        IIIIIIII IIIIIIIII IIII
                        CTCGGGGT CGGGTCGAG TCAC
                            __        T
GAM312 MFNG        GAGC-CC-CAGCCCAGCTCAAGTG   4764       CC       T I
                        GAGCTCCG GCCCAGCTC GG
                        IIIIIIII IIIIIIIII II
                        CTCGGGGT CGGGTCGAG TC
                            __        T A
GAM312 PIG8        AGCTCCGCCGCCGCGGCTCCGG   4746 G      CA_      I
                            CTCCGCCGCC  GCTCTG
                            IIIIIIIIII  IIIIII
                            GAGGCGGCGG  CGAGGC
                            _       CGC    I
GAM312 PIG8        AGCTCCGCCGCCGCGGCTCCGG   4746 GA       CA_     G
                            GCTCCGCCGCC  GCTCTGGT
                            IIIIIIIIIII  IIIIIIII
                            CGAGGCGGCGG  CGAGGCCG
                            __      CGC    I
GAM312 PSMB2        GAGCCACCACACCCAGCTCTGG   4762    _  C        TG
                            GAGCT CCGC GCCCAGCTCTGG
                            IIIII IIII IIIIIIIIIIII
                            CTCGG GGTG TGGGTCGAGACC
                            T   _      II
GAM312 PSMB2        GAGCCACCACACCCAGCTCTGG   4762    _  C        I
                            AGCT CCGC GCCCAGCTCTG
                            IIII IIII IIIIIIIIIII
                            TCGG GGTG TGGGTCGAGAC
                            T   _      I
GAM312 PTBP1        GCGCCGCCGCCC--CTCGGGT   4768 T     AG  TGI
                            GC CCGCCGCCC CTC
                            II IIIIIIIII III
                            CG GGCGGCGGG GAG
                            C       __  CCC
GAM312 PTBP1        GCGCCGCCGCCC--CTCGGGT   4768 GAGCT     AG  T
                            CCGCCGCCC CTC GGT
                            IIIIIIIII III III
```

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                          GGCGGCGGG GAG CCA
                          C____      __  C
GAM312 PTPN1      AGCTACCGCCGCCCTAGCCGCTGCTG 4740 CT     _  _  GTI
                          CCGCCGCCC AGCT CTG
                          ||||||||| |||| |||
                          GGCGGCGGG TCGG GAC
                          T_        A   C  GII
GAM312 PTPN1      AGCTACCGCCGCCCTAGCCGCTGCTG 4740 GA  _     _  _  G II
                          GCT CCGCCGCCC AGCT CTG TG
                          ||| ||||||||| |||| ||| ||
                          CGA GGCGGCGGG TCGG GAC AC
                          __  T     A   C  G  GI
GAM312 RABGGTA       AGCTCCGCC-CACAGCTGTG    4748 _    GCC   CTI
                          GCTCCGCC  CAGCT
                          ||||||||  |||||
                          CGAGGCGG  GTCGA
                          T      GT_   CAI
GAM312 RABGGTA       AGCTCCGCC-CACAGCTGTG    4748 GA    GCC   C GT
                          GCTCCGCC  CAGCT TG
                          ||||||||  ||||| ||
                          CGAGGCGG  GTCGA AC
                          __        GT_  C AI
GAM312 RFP       GAGCTCCGCACTGAGCCCAACTCT  4758       C____       GGTGI
                          GAGCTCCGC   GCCCAGCTCT
                          |||||||||   ||||||||||
                          CTCGAGGCG   CGGGTTGAGA
                          TGACT        IIIGT
GAM312 RFP       GAGCTCCGCACTGAGCCCAACTCT  4758 AGCT  C____      I
                          CCGC   GCCCAGCTC
                          ||||   ||||||||||
                          GGCG   CGGGTTGAG
                          ____   TGACT      I
GAM312 SLC9A1    GAGCCCCCAGCAGCCCTGCTCTGGTG4757     __ C  A_     III
                          GAGCTCC GC GCCC GCTCTGGTG
                          ||||||| || |||| |||||||||
                          CTCGGGG CG CGGG CGAGACCAC
                          GT T  GA        III
GAM312 SLC9A1    GAGCCCCCAGCAGCCCTGCTCTGGTG4757 AG  _ C  A_     I
                          CTCC GC GCCC GCTCTGGT
                          |||| || |||| |||||||||
                          GGGG CG CGGG CGAGACCA
                          __   T T  GA      I
GAM312 SMARCD2       AGCTCCCCAGAGCCAGCTCTG   4745 G  G  C__    I
                          CTCC CCG  CCAGCTCT
                          |||| |||  |||||||||
                          GAGG GGT  GGTCGAGA
                          _  _ CTC       I
GAM312 SMARCD2       AGCTCCCCAGAGCCAGCTCTG   4745 GA   G  C__      TG
                          GCTCC CCG  CCAGCTCTGG
                          ||||| |||  ||||||||||
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                          CGAGG GGT   GGTCGAGACT
                          __    _    CTC      II
GAM312  TCF20     AGCTCACACTGCC-AGCTCTGG   4741   _  C  C    I
                          GCTC CGC GCC AGCTCTG
                          |||| ||| ||| ||||||||
                          CGAG GTG CGG TCGAGAC
                             T   A   _      I
GAM312  TCF20     AGCTCACACTGCC-AGCTCTGG   4741 GA  _  C  C     G
                          GCTC CGC GCC AGCTCTGGT
                          |||| ||| ||| |||||||||
                          CGAG GTG CGG TCGAGACCG
                          __   T   A   _       I
GAM312  TEM6      AGCCCAGCTCGCCCAGCTC        4742    C  _      II
                          AGCTC GC CGCCCAGCT
                          ||||| || |||||||||
                          TCGGG CG GCGGGTCGA
                             T  A      GI
GAM312  TEM6      AGCCCAGCTCGCCCAGCTC        4742 GA  C  _       TGGT
                          GCTC GC CGCCCAGCTC
                          |||| || ||||||||||
                          CGGG CG GCGGGTCGAG
                          __   T  A        CIII
GAM313  ARCN1       GGTCTCCAGTGGCTTGTAAATCT  4779 TGA  GTCACC  G       I
                          CAG    GT TGTAAATCT
                          |||    || |||||||||
                          GTC    CG ACATTTAGA
                          G__  AC____  A       C
GAM313  DIO1     CAAGTCACAGCCGTGTGTA        4776 TG_  GTCA        AATC
                          ACAG   CCGTGTGTA
                          ||||   |||||||||
                          TGTC   GGCACACAT
                          CAG    ____     GAAI
GAM313  E2F3     ACAGGTCACCCTGTAACAAATCT    4773 TGAC     G  TA_  I
                          AGGTCACC TGTG  AATCT
                          |||||||| ||||  |||||
                          TCCAGTGG ACAT  TTAGA
                          ____       G  TGT   T
GAM313  GNA11      CAGGTCACCTTGTG-CAATCT    4777 TGACAG    G    A
                          GTCACC TGTGTAA TC
                          |||||| ||||||| ||
                          CAGTGG ACACGTT AG
                          _____       A    _
GAM313  MUC4     ACAGGTCACACTG-G-AAAT       4775 TGAC    CG TGTAAAT
                          AGGTCAC TG
                          ||||||| ||
                          TCCAGTG AC
                          ____       TG CTTTACC
GAM313  PPM1D    ACAGGTCAC--TATGAAAAT       4774 TGAC    CG T
                          AGGTCAC TGTG AAAT
                          ||||||| |||| ||||
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                              TCCAGTG ATAC TTTA
                              ____        __   T
GAM313  PTEN          GAAAGGT----GTGTGTAAAT   4778 TGAC   CACC
                         AGGT   GTGTGTAAAT
                         ||||   ||||||||||
                         TCCA   CACACATTTA
                      TT__   ____
GAM313  YWHAZ      TGACAAATGGTCTAC-TGTGTAAAT 4780  ___ _ CG    CTI
                      TGACA  GGTC AC TGTGTAAAT
                      |||||  |||| || |||||||||
                      ACTGT  CCAG TG ACACATTTA
                       TTA  A __      |||
GAM314  ARSB         AAAAGAGCCA-GCTGTTCCAGCCT 4784      T  _     TI
                      AAAAGAGCCA GCTGT CTAGTCT
                      |||||||||| ||||| |||||||
                      TTTTCTCGGT CGACA GGTCGGA
                         _   A   ||
GAM314  ARSB         AAAAGAGCCA-GCTGTTCCAGCCT 4784      T  _    I
                      AAAGAGCCA GCTGT CTAGTC
                      ||||||||| ||||| ||||||
                      TTTCTCGGT CGACA GGTCGG
                         _   A   |
GAM314  C14orf1      AGCCATGC--TCTTGTCTT    4796     TG A  I
                      AGCCATGC TCT GTCT
                      |||||||| ||| ||||
                      TCGGTACG AGA CAGA
                          __   A   A
GAM314  CD164        AAGAGCCATGATGT-T-GTCT   4792 AAAA    C  CTA
                        GAGCCATG TGT  GTCT
                        |||||||| ||| ||||
                        CTCGGTAC ACA  CAGA
                       ____     T A__
GAM314  CD164        AAGAGCCATGATGT-T-GTCT   4792       C___   AGTI
                      AAGAGCCATG  TGTCT
                      ||||||||||  |||||
                      TTCTCGGTAC  ACAGA
                       TACA   |||T
GAM314  CDH12        AAAAGAGCCAAGCTGT-TAG    4785     T  C  TCT
                      AAAAGAGCCA GCTGT TAG
                      |||||||||| ||||| |||
                      TTTTCTCGGT CGACA ATC
                       T   _  |||
GAM314  CDH12        AAAAGAGCCAAGCTGT-TAG    4785 A   T  CTI
                       AAAGAGCCA GCTGT
                       ||||||||| |||||
                       TTTCTCGGT CGACA
                       _    T  ATC
GAM314  CLASP1       AGAGACACTATGCTGTCTGAGTTCTT 4794 A C    _  CTI
                        GC ATGCTGTCT AGT
                        || ||||||||| |||
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                        TG TACGACAGA TCA
                        _  A       C  AGI
GAM314 CLASP1        AGAGACACTATGCTGTCTGAGTTCTT 4794 AAAAGA  C        _  _  II
                        GC ATGCTGTCT AGT CTT
                        II IIIIIIIII III III
                        TG TACGACAGA TCA GAA

                        CTG___ A      C  A  GT
GAM314 CTSZ          AGAGCCATGCTGTGCAAGT     4795          CTAGII
                        AGAGCCATGCTGT

                        IIIIIIIIIIII
                        TCTCGGTACGACA

                             CGTTCA
GAM314 CTSZ          AGAGCCATGCTGTGCAAGT     4795 AAAAGA      CT_ CT
                        GCCATGCTGT  AGT

                        IIIIIIIIII III
                        CGGTACGACA  TCA

                        _____       CGT  CA
GAM314 EIF2B5        AAAGAGCCAACTGCTCTCT     4787       __  G III
                        AAAGAGCCA TGCT TC

                        IIIIIIIII IIII II
                        TTTCTCGGT ACGA AG

                           TG   G  AII
GAM314 EIF2B5        AAAGAGCCAACTGCTCTCT     4787 AA      __   G  AGTCT
                        AAGAGCCA TGCT TCT

                        IIIIIIII IIII III
                        TTCTCGGT ACGA AGA

                        __      TG   G  CIIIT
GAM314 GHR          AAAATAGCCATGCT-TGAAGTCT 4786    G      GTCT  T
                        AAAA AGCCATGCT   AGTCT

                        IIII IIIIIIIII   IIIII
                        TTTT TCGGTACGA   TCAGA

                            A    ACT_   I
GAM314 GHR          AAAATAGCCATGCT-TGAAGTCT 4786 AAAG_      GTCT  I
                        AGCCATGCT  AGTC

                        IIIIIIIII   IIII
                        TCGGTACGA   TCAG

                        TTTTA      ACT_  I
GAM314 ITCH         AAAGAGCCAT--TGTCCAATTTT 4791        GC       CI
                        AAAGAGCCAT TGTCTAGT

                        IIIIIIIIII IIIIIIII
                        TTTCTCGGTA ACAGGTTA

                            __      AA
GAM314 ITCH         AAAGAGCCAT--TGTCCAATTTT 4791 AA     GC     CTT
                        AAGAGCCAT TGTCTAGT

                        IIIIIIIII IIIIIIII
                        TTCTCGGTA ACAGGTTA

                        __      __      AAA
GAM314 NR0B2        AAGGAGCCAAGTGCTGTCTA    4788 AAA    __        III
                        GAGCCA TGCTGTCT

                        IIIIII IIIIIIII
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                         CTCGGT ACGACAGA
                         TTC     TC      TII
GAM314 NR0B2        AAGGAGCCAAGTGCTGTCTA    4788 AAAA    __        GTCT
                         GAGCCA TGCTGTCTA
                         |||||| |||||||||
                         CTCGGT ACGACAGAT
                         TC__    TC      AIII
GAM314 PPP1R8       AAAGAGCCAGGGCAGTCTA     4789       T_ T   II
                         AAAGAGCCA GC GTCT
                         ||||||||| || ||||
                         TTTCTCGGT CG CAGA
                             CC T    TI
GAM314 PPP1R8       AAAGAGCCAGGGCAGTCTA     4789 AA    T_ T   GTCT
                         AAGAGCCA GC GTCTA
                         |||||||| || |||||
                         TTCTCGGT CG CAGAT
                         __        CC T   AIII
GAM314 PRKAR2B      AAAAGTGATGCCATGCTGTGTAG  4783 AAAA _      CTI
                         GA GCCATGCTGT
                         || ||||||||||
                         CT CGGTACGACA
                         A___  A       CAT
GAM314 PRKAR2B      AAAAGTGATGCCATGCTGTGTAG  4783 AAAA__ _       C TCTTI
                         GA GCCATGCTGT TAG
                         || |||||||||| |||
                         CT CGGTACGACA ATC
                         TTTTCA A       C  IIITT
GAM314 PTK2B        AGGGCACATGCTGTC-AGTC     4793 A _      T  II
                         AG GC CATGCTGTC AGT
                         || || ||||||||| |||
                         TC CG GTACGACAG TCA
                         C  T        _ GI
GAM314 PTK2B        AGGGCACATGCTGTC-AGTC     4793 AAAAGA _      T
                         GC CATGCTGTC AGTCT
                         || ||||||||| |||||
                         CG GTACGACAG TCAGG
                         _____ T        _
GAM314 RAB6A        AAAGAGCCAT-TTGTTTTAGTC   4790      GC C_  I
                         AAGAGCCAT TGT TAGT
                         ||||||||| ||| ||||
                         TTCTCGGTA ACA ATCA
                         A_  AA   I
GAM314 RAB6A        AAAGAGCCAT-TTGTTTTAGTC   4790 AA      GC C_  TT
                         AAGAGCCAT TGT TAGTC
                         ||||||||| ||| |||||
                         TTCTCGGTA ACA ATCAG
                         __        A_ AA   TI
GAM314 SHANK2       GAGCCATGC-GTCT--TCTT     4797       T AGTCI
                         GAGCCATGC GTCT
                         ||||||||| ||||
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                              CTCGGTACG CAGA
                              _    AGAAI
GAM315 BTG2           AGAGGAGAGTTGTGCTTTTG    4802 TGGC    TAAAT
                              AGAGT   TGTGCTTTT
                              |||||   |||||||||
                              TCTCA   ACACGAAAA
                              C___    _____
GAM315 CASP4         GCAGAACATAAATTGTGATTT    4805 TGGC  GT_     C   G
                              AGA  TAAATTGTG TTTT
                              |||  ||||||||| ||||
                              TCT  ATTTAACAC AAAG
                              ____   TGT     T  A
GAM315 HS3ST2        GCAGAATTA---TGTGCTTTTG    4806 TGGC     AAT
                              AGAGTTA  TGTGCTTTT
                              |||||||  |||||||||
                              TCTTAAT  ACACGAAAA

                              ____      ___
GAM315 MEOX2         CAGAGTTAAAATACACTTTT    4804 TGGCAG    T  TG
                              AGTTAAA TG  CTTTT
                              ||||||| ||  |||||
                              TCAATTT AT  GAAAA
                              _____        T  GT
GAM315 NCOA6         TGACATAGATAG-TTGTGCTTTT   4809    G  TTAAA      G
                              TGGCA AG    TTGTGCTTTT
                              ||||| ||    ||||||||||
                              ACTGT TC    AACACGAAAA
                              A  TATC_       I
GAM315 PIK3CD        TGGCAGAGT---ATT-CGCTTCTG   4811        TAAATTG
                              TGGCAGAGT     TGCTTTT
                              |||||||||     |||||||
                              ACCGTCTCA     GCGAAGA
                              TAA____
GAM315 PIK3CD        GCAGAGTT-AGTTG-GCTTCTG    4807 TGGC     AA  T
                              AGAGTTA TTG GCTTTT
                              ||||||| ||| ||||||
                              TCTCAAT AAC CGAAGA
                              ____      C_  _
GAM315 T             AGA-TTAAGAGTGTGCTTTT    4800 TG C    TAAATT
                              G AGAGT    GTGCTTTT
                              | |||||    ||||||||
                              A TCTCA    CACGAAAA
                              __T     _____
GAM315 TRPC6         TGGCACA---AAATTGTGCT    4808    G GTT      TT
                              TGGCA A  AAATTGTGCT
                              ||||| |  ||||||||||
                              ACCGT T  TTTAACACGA
                              G ___        II
GAM315 TSGA10        AGATTTATTTTGTGCTTTT    4801 TGGCAGAGTTAAA
                              TTGTGCTTTT
                              ||||||||||
```

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                        AACACGAAAA
                    AATAA_____
GAM315  WASF3       TGG-AGAAATGAAATGTGCTTTTG  4810   C   TTAAAT       I
                    TGG AGAG    TGTGCTTTTG
                    ||| ||||    ||||||||||
                    ACC TCTT    ACACGAAAAC
                    _    TACTTT          I
GAM315  ZNF277      CAAATTTAAATTGTTCTTT    4803 TGGCAGAG        G
                             TTAAATTGT CTTTT
                             ||||||||| |||||
                             AATTTAACA GAAAG
                    TA_____          A
GAM316  AEGL1       TAGCCCAGGTTACTGTTGAGG    4816   A   _ _      III
                    TAG CCAG TT CTGTTGAG
                    ||| |||| || ||||||||
                    ATC GGTC AA GACAACTC
                      G   C T    CII
GAM316  EML1        ATATACCAGTTACTTCTGTTGA  4814   G    _____      IIIT
                    ATA ACCAGT   TCTGTTG
                    ||| ||||||   |||||||
                    TAT TGGTCA   AGACAAC
                      A   ATGA       TIII
GAM316  EPB41L2     ATAGACCAGAGCTGGTAAGG    4815    TT  T   I
                    TAGACCAG  CTG TGAG
                    ||||||||  ||| ||||
                    ATCTGGTC  GAC ATTC
                       TC  C   I
GAM316  EPB41L2     ATAGACCAGAGCTGGTAAGG    4815 TCAGATAG   TT  T
                       ACCAG  CTG TGAG
                       |||||  ||| ||||
                       TGGTC  GAC ATTC
                    _____    TC  C
GAM316  HS3ST3B1    TCAGA-ATAC-AGCCCTGTTGAGG 4818    TAGAC
                    TCAGA    CAGTTCTGTTGAGG
                    |||||    ||||||||||||||
                    AGTCT    GTCGGGACAACTCC
                      TAT__
GAM316  HS3ST3B1    TCAGA-ATAC-AGCCCTGTTGAGG 4818 _  TAGAC           I
                     CAGA    CAGTTCTGTTGAG
                     ||||    |||||||||||||
                     GTCT    GTCGGGACAACTC
                    A TAT__          I
GAM316  UBL1        TCAAAAAGAGCAGTGTTCTGTTG  4817    T  C  __    AGGI
                    TCAGA AGA CAGT  TCTGTTG
                    ||||| ||| ||||  |||||||
                    AGTTT TCT GTCA  AGACAAC
                       T  C  CA    IIIG
GAM316  UBL1        TCAAAAAGAGCAGTGTTCTGTTG  4817 CAGAT  C  __    I
                        AGA CAGT  TCTGTT
                        ||| ||||  ||||||
```

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                        TCT GTCA  AGACAA
                        TTT__   C  CA    I
GAM317 ACADVL       TGAGAGCAGGCACAGTGCTGG   4838  C      CTCA  AAT
                        TGA AGCAGGCACA   TGG
                        ||| |||||||||   |||
                        ACT TCGTCCGTGT   ACC
                         C       CACG   |||
GAM317 BCLG         TGACAGCAGTGCAAAC-AATGAAA  4829       _ C TC    TI
                        TGACAGCAG GCA AC  ATGGAA
                        ||||||||| ||| || ||||||
                        ACTGTCGTC CGT TG  TACTTT
                          A  T T_      ||
GAM317 CD2          ACAGAAAACAC-CTCATGGAA    4824 TGAC  C    A
                          AG AGGCAC CTCATGGAA
                          || |||||| |||||||||
                          TC TTTGTG GAGTACCTT
                         ____   T   _
GAM317 CD83         ACAGACAGGCACACCCCTG    4821 TGACA      A  AA
                           GCAGGCACACTC TGG
                           ||||||||||||| |||
                           TGTCCGTGTGGG ACT
                          TC___         G  CI
GAM317 CDC27        TGAAAGT-GGCACACTCATGGTAT  4841  C CA        AATI
                        TGA AG  GGCACACTCATGG
                        ||| ||  ||||||||||||
                        ACT TC  CCGTGTGAGTACC
                         T  A_          ATAI
GAM317 CHS1         TGACAGCAG--AGACT-TTGGAAT  4842       CAC  CA
                        TGACAGCAGG  ACT TGGAAT
                        ||||||||||  ||| ||||||
                        ACTGTCGTCT  TGA ACCTTA
                           C__   A_
GAM317 DRD3         TGACAGCAGACATACCCAAGCAA   4840      C    TGGAATI
                        TGACAGCAGGCA ACTCA
                        |||||||||||| |||||
                        ACTGTCGTCTGT TGGGT
                          A   TCGTTII
GAM317 DRG2         TGACAGCAGCCACAGCCTCCAGGGA  4832     G  __  AT_ ATII
                        TGACAGCAG CACA CTC  GGA
                        ||||||||| |||| ||| |||
                        ACTGTCGTC GTGT GAG  CCT
                          G  CG  GTC  IIIT
GAM317 ENG         TGACAGCAG---CAGTCCTGG    4836      G CAC A  A
                        TGACAGCAG CA  TC TGG
                        ||||||||| ||  || |||
                        ACTGTCGTC GT  AG ACC
                           _  C__   G  I
GAM317 HCFC1        ACAGCAGGC-CCCTCGTGG     4823 TGAC    ACA  A  A
                         AGCAGGC  CTC TGG
                         |||||||  ||| |||
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                    TCGTCCG  GAG ACC
                    ____      GG_  C  G
GAM317 KIF1B        TGACAGCA-GCACAGACAT    4834        G   CT  GGA
                    TGACAGCAG CACA  CAT
                    ||||||||| ||||  |||
                    ACTGTCGTC GTGT  GTA
                          _   CT   |||
GAM317 MASP2        TGACAGCAGCCTCAC-C-TGGA    4839      G A_  CA  A
                    TGACAGCAG C  CACT  TGGA
                    ||||||||| |  ||||  ||||
                    ACTGTCGTC G  GTGG  ACCT
                           _  GA   __   |
GAM317 MFAP4        CAGCAGAGGGAGCACTCATGGA   4826 TGA  C  CA_        AT
                    CAG AGG  CACTCATGGA
                    ||| |||  ||||||||||
                    GTC TCC  GTGAGTACCT
                    ___  _  CTC        CT
GAM317 PDXK         CAGCAGATGCCGGACACTCATGAAA  4825 TGACA  A  C        TII
                    GC GG  ACACTCATGGAA
                    || ||  |||||||||||
                    CG CC  TGTGAGTACTTT
                    GTCTA  G  _        CTT
GAM317 PPARGC1      TGACA-CAGAGCACACACTCATG    4828    G  ___        GAAT
                    TGACA CAG  GCACACTCATG
                    ||||| |||  ||||||||||
                    ACTGT GTC  TGTGTGAGTAC
                        _  TCG       |||T
GAM317 SH3BP4       TGACAGCAGG-GCACGCAGGG    4837        CA  T  T AA
                    TGACAGCAGG CAC CA GG
                    |||||||||| ||| || ||
                    ACTGTCGTCC GTG GT CC
                         C_   C  C II
GAM317 TF           TGAAACCAGGGCAAACTCATGGA   4830 TGA___  CA  C        ATI
                    CAG  GGCA ACTCATGGA
                    |||  |||| |||||||||
                    GTC  CCGT TGAGTACCT
                    ACTTTG  __   T         |||
GAM317 THPO         ACAGCAGGCAGCCCTC-TGG    4822 TGAC      CA_  A  AA
                    AGCAGGCA  CTC TGG
                    ||||||||  ||| |||
                    TCGTCCGT  GAG ACC
                          ____   CGG  _  CC
GAM317 TIRAP        TGACAGCAGTGACA-TCAT    4835        GC  C  GGA
                    TGACAGCAG ACA TCAT
                    ||||||||| ||| ||||
                    ACTGTCGTC TGT AGTA
                         AC  _  III
GAM317 TMPRSS3      TGA-AGCAGGCACA-TCAT    4833  C        C  GGA
                    TGA AGCAGGCACA TCAT
                    ||| |||||||||| ||||
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                              ACT TCGTCCGTGT AGTA
                              _        _    III
GAM317  TPK1          CAG-AGGCACACTTATGGA      4827 TGACAGC      C
                          AGGCACACT ATGGA
                          ||||||||| |||||
                          TCCGTGTGA TACCT
                          _____          A
GAM317  ZNF22        TGACACTTGGCACCATTCTCATGGAA 4831   GCA   A___      TII
                         TGACA GGCAC  CTCATGGAA
                         ||||| |||||  |||||||||
                         ACTGT CCGTG  GAGTACCTT
                           GAA   GTAA      III
GAM318  ARNT2        GAGCCTTACTGTGGCTGCATCTG  4854 A GTA         _  GI
                        AG CC  ATTGTGGCTGCA CTG
                        || ||  |||||||||||| |||
                        TC GG   TGACACCGACGT GAC
                         _ AA_          A  AI
GAM318  ARNT2        GAGCCTTACTGTGGCTGCATCTG  4854 A GTA        CTI
                          CC  ATTGTGGCTGCA
                          ||  ||||||||||||
                          GG  TGACACCGACGT
                        C AA_          AGA
GAM318  CXCL16        GACCTGTGAG-GCGGCTGCACTG  4853   GTAATT         I
                         ACC    GTGGCTGCACT
                         |||    |||||||||||
                         TGG    CGCCGACGTGA
                          ACACTC           I
GAM318  CXCL16        GACCTGTGAG-GCGGCTGCACTG  4853 AG GTAATT          G
                         ACC    GTGGCTGCACTG
                         |||    ||||||||||||
                         TGG    CGCCGACGTGAC
                         __ ACACTC          G
GAM318  DDX5         ACCATAATTACTGCTGCACTG    4845        TG    I
                         CCGTAATTG GCTGCACT
                         ||||||||| |||||||||
                         GGTATTAAT CGACGTGA
                           GA       I
GAM318  DDX5         ACCATAATTACTGCTGCACTG    4845 AGAC     TG      G
                          CGTAATTG GCTGCACTG
                          |||||||| ||||||||||
                          GTATTAAT CGACGTGAC
                           ____     GA      G
GAM318  EPB42        AGATCGTTATC-TGGACTGCACTGG 4847  C A GT        I
                        AGA CGT ATT GGCTGCACTGG
                        ||| ||| ||| ||||||||||
                        TCT GCA TAG CTGACGTGACC
                         A  A  AC       I
GAM318  EPB42        AGATCGTTATC-TGGACTGCACTGG 4847 GAC A  GT        I
                          CGT ATT GGCTGCACTG
                          ||| ||| ||||||||||
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                          GCA TAG  CTGACGTGAC
                          CTA  A  AC         I
GAM318 EPOR           CCATAAGTCTTGAGTCTGCACTGG  4851 AGACCGTAA  TGG       I
                          TTG  CTGCACTGG
                          |||  |||||||||
                          AAC  GACGTGACC
                      ATTCAG___   TCA         A
GAM318 EPOR           CCATAAGTCTTGAGTCTGCACTGG  4851 C_ AA  TGG       I
                       GT TTG  CTGCACTG
                       || |||  |||||||||
                       CA AAC  GACGTGAC
                      TT G_  TCA        I
GAM318 FN1           GACCAGAGAAGTTGTGGCTGCA  4852     TAA___        III
                          GACCG    TTGTGGCTGC
                          |||||    ||||||||||
                          CTGGT    AACACCGACG
                          CTCTTC       TII
GAM318 FN1           GACCAGAGAAGTTGTGGCTGCA  4852 AG  TAA___        CTGG
                          ACCG    TTGTGGCTGCA
                          ||||    |||||||||||
                          TGGT    AACACCGACGT
                          __  CTCTTC       CIII
GAM318 FZD7          AGACCGTAA-TGT--CTGACCCTGG  4848       TG_   GCA
                          AGACCGTAAT TGGCT CTGG
                          |||||||||| ||||| ||||
                          TCTGGCATTA ACTGG GACC
                          CAG     ___
GAM318 FZD7          AGACCGTAA-TGT--CTGACCCTGG  4848       TG_   GCACTI
                          AGACCGTAAT TGGCT
                          |||||||||| |||||
                          TCTGGCATTA ACTGG
                          CAG   GACCII
GAM318 GGPS1         AGACCTACATAACTGTGGCTGC  4846    ___          ACTGG
                          AGACC  GTAATTGTGGCTGC
                          |||||  |||||||||||||
                          TCTGG  TATTGACACCGACG
                          ATG        IIIGG
GAM318 GGPS1         AGACCTACATAACTGTGGCTGC  4846    ___           III
                          AGACC  GTAATTGTGGCTG
                          |||||  ||||||||||||
                          TCTGG  TATTGACACCGAC
                          ATG         GII
GAM318 MAP1A         AGAGC-TGATGCTGTCTGCACTGG  4850 AGACC AAT  GG_       I
                          GT TGT  CTGCACTGG
                          || |||  |||||||||
                          CG ACG  GACGTGACC
                      TCT__ ACT  ACA         I
GAM318 MAP1A         AGAGC-TGATGCTGTCTGCACTGG  4850 GACC AAT  GG_       I
                          GT TGT  CTGCACTG
                          || |||  |||||||||
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                              CG   ACG   GACGTGAC
                            TCT_  ACT  ACA       I
GAM318  NUMB              GTAACAGTGGCTGCACTGG   4857    T        II
                            GTAAT GTGGCTGCACTG
                            ||||| |||||||||||
                            CATTG CACCGACGTGAC
                              T           CI
GAM318  PRIM2A            GTAATTGTGTCACTGCACT    4856 AGACCGTAAT  G
                              TGT GCTGCACTG
                              ||| |||||||||
                              ACA TGACGTGAT
                         AC_____  G
GAM318  PRIM2A            GTAATTGTGTCACTGCACT    4856        __   III
                            GTAATTGTG GCTGCAC
                            ||||||||| |||||||
                            CATTAACAC TGACGTG
                              AG     AII
GAM318  VIM              GTAATATATTGCTGCACTG    4855    _  G    II
                            GTAAT TGT GCTGCACT
                            ||||| ||| |||||||||
                            CATTA ATA CGACGTGA
                              T   A    CI
GAM318  VIM              GTAATATATTGCTGCACTG    4855 AGACCGTAATTGTG
                              GCTGCACTG
                              |||||||||
                              CGACGTGAC
                         TATAA_____
GAM318  WNT8B            AGACC-TAGGTGTGGCTGC    4849    GTAAT      ACT
                            AGACC   TGTGGCTGC
                            |||||   |||||||||
                            TCTGG   ACACCGACG
                              ATCC_        III
GAM318  WNT8B            AGACC-TAGGTGTGGCTGC    4849    GTAAT    I
                            AGACC   TGTGGCTG
                            |||||   ||||||||
                            TCTGG   ACACCGAC
                              ATCC_      G
GAM319  AHSG             GTCA-AGACTTGATATTAATGTA  4861 TG  TA  _      CA
                            TCA  GCTT ATATTAATGTA
                            |||  |||| ||||||||||||
                            AGT  TGAA TATAATTACAT
                            __  TC   C       CI
GAM319  CCNG1            TCATAGCTTAAATCCATTGTA   4862 TGTC     T  AA_  CA
                            ATAGCTTA ATT  TGTA
                            |||||||| |||  ||||
                            TATCGAAT TAG  ACAT
                            ____       T  GTA  TG
GAM319  E2F3            TGTTATGG--TATATTAATGTA   4872 TGTCATAGCT        C
                              TATATTAATGTA
                              ||||||||||||
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                              ATATAATTACAT
                         ACAATACC__          I
GAM319  EIF1A        TGTGCATAGCTTATAGCACTGTA  4865  _        T  A  CAI
                    TGT CATAGCTTATA TA TGTA
                    ||| |||||||||| || ||||
                    ACA GTATCGAATAT GT ACAT
                         C      C  G   |||
GAM319  GPM6A          CAAAGCTATTATATTAATG  4860 TGTCAT  __        TAC
                       AGCT TATATTAATG
                       |||| |||||||||
                       TCGA ATATAATTAC
                    _____    TA       CTT
GAM319  GYPA         TGTAATATTTCATATTAATG   4868  C GC       TAC
                    TGT ATA TTATATTAATG
                    ||| ||| |||||||||||
                    ACA TAT AGTATAATTAC
                      T  AA        |||
GAM319  NFATC1      TCTTTGCACATATTAATGTTCA   4864 TGTCATA T       ACA
                        GC TATATTAATGT
                        || |||||||||||
                        CG GTATAATTACA
                    AAA____ T        AGT
GAM319  PCDHB4      TGTCCATATCTGCAAAGTAATGTACA 4866  _ G _ TAT       II
                   TGTC ATA CT TA  TAATGTACA
                   |||| ||| || ||  |||||||||
                   ACAG TAT GA GT  ATTACATGT
                     G  A C TTC         II
GAM319  SCML2        TCATAGCTTATAAACAT-TACA   4863 TGTC        TTAATG
                     ATAGCTTATA   TACA
                     ||||||||||   ||||
                     TATCGAATAT   ATGT
                    ____        TTGTA_
GAM319  SIM2        TGTCTCTGCATAAATTAATGTA   4871   ATA T T    CA
                    TGTC  GC TA ATTAATGTA
                    ||||  || || |||||||||
                    ACAG  CG AT TAATTACAT
                    AGA  T T       II
GAM319  SUV39H2      TGTCATAGC-AATA-TAATG    4869     TT  T  TA
                    TGTCATAGC ATAT AATG
                    ||||||||| |||| ||||
                    ACAGTATCG TATA TTAC
                      T_   _   II
GAM319  VCAM1        TGTCA--GCAAATATTAATGT   4870   TA TT     AC
                    TGTCA GC ATATTAATGT
                    ||||| || ||||||||||
                    ACAGT CG TATAATTACA
                      __ TT      II
GAM319  VSNL1       TGACATAGCTTATAATTAAGTTACA 4867 T        _  TG  II
                    TG CATAGCTTATA TTAA TACA
                    || |||||||||| |||| ||||
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                    AC GTATCGAATAT AATT ATGT
                    T       T  CA  II
GAM320 ABCD4        GACAACT----GAACTG-GAGGG  4913 TG      GGGA   C
                    ACAACTGA   ACTG GAG
                    |||||||    |||| |||
                    TGTTGACT   TGAC CTC
                    __      ____   _
GAM320 AHR          ACAGCAGATTTTTCACATTGCA  4879 CA      C__  A   GC
                    CAGCAGATT  TGCA TGCAG
                    ||||||||   |||| |||||
                    GTCGTCTAA  GTGT ACGTT
                    __        AAA  A  II
GAM320 AMFR         CACAG--GACTGTTCAATGCAGG  4903   CA CTG     C
                    CACAG GATT  CAATGCAGG
                    ||||| ||||  |||||||||
                    GTGTC CTGA  GTTACGTCC
                    __      CAA       I
GAM320 ANK1         CACAGCAGAGTCT---ATACAG  4900      T GCA    G
                    CACAGCAGA TCT  ATGCAG
                    ||||||||| |||  ||||||
                    GTGTCGTCT AGA  TATGTC
                               C  ___  I
GAM320 AOAH         CAACTGAGGGATGCTG-GAG    4887 TGACAA    A_  C  G
                    CTGAGGGA CTG GAG
                    |||||||| ||| |||
                    GACTCCCT GAC CTC
                    _____       AC _ G
GAM320 ATOX1        GACAACTGAGGG-TCTCCGCAGG  4912 TG      AA_  G
                    ACAACTGAGGG  CTGC AGGG
                    |||||||||||  |||| ||||
                    TGTTGACTCCC  GGCG TCCT
                    __        AGA  _
GAM320 ATP6V1A1     CAGAGCTG-TTCTGCAATATGCAG  4895 C AGA    __    GCI
                    CA AGC  TTCTGCA ATGCAG
                    || |||  ||||||| ||||||
                    GT TCG  AAGACGT TACGTC
                    C  AC_    TA   III
GAM320 B3GALT5      CACCAGATTCTGACAGTGC     4906 CACAG    _ A  AGG
                    CAGATTCTG CA TGC
                    ||||||||| || |||
                    GTCTAAGAC GT ACG
                    G____       T C AGI
GAM320 B3GALT5      CAGCAGATTCTGCACTCCAGG   4908 CACA      ATG  C
                    GCAGATTCTGCA CAGG
                    |||||||||||| ||||
                    CGTCTAAGACGT GTCC
                    ____         GAG  A
GAM320 BCL7A        CACAGCAGAGTTCTTCAGTG    4890      _ G ATGCAGG
                    CACAGCAGA TTCT CA
                    ||||||||| |||| ||
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                        GTGTCGTCT AAGA GT
                          C   A  CACIIIC
GAM320 BTD          GACA-CTGAGGGAATCTGC      4910 TG  A      _    GAG
                        ACA CTGAGGGAA CTGC
                        ||| |||||||| ||||
                        TGT GACTCCCTT GACG
                          __  _       A   GII
GAM320 CASP8        ACAGCAGATGCTCCAGAAATGC    4877 CA      T G ___  AGGC
                        CAGCAGAT CT CA  ATGC
                        |||||||| || ||   ||||
                        GTCGTCTA GA GT  TACG
                          __      C  G CTT  AIII
GAM320 E2F1         CACCAGATTCTGGGA-GCAGGC    4909 CACAG       CAAT
                          CAGATTCTG  GCAGGC
                          ||||||||  ||||||
                          GTCTAAGAC  CGTCCG
                        G____        CCT_
GAM320 GADD45B      CAACAGATTCTGC--TGCTGG     4907 CACA       AA  A
                        GCAGATTCTGC TGC GG
                        ||||||||||| ||| ||
                        TGTCTAAGACG ACG CC
                        ____        __  A
GAM320 GNAI3        AGCACATTCTGCAA---AGGC     4886 CACAGCAG      TGC
                        ATTCTGCAA  AG
                        |||||||| ||
                        TAAGACGTT  TC
                      TG_____        ___
GAM320 GSPT1        ACTGAGGGAAGGCGGCGGGG      4881 TGACAACT   AACT  A
                        GAGGG  GCG GG
                        |||||  ||| ||
                        CTTCC  CGC CC
                      CC_____      GC__  _
GAM320 GSTM5        GCGGATTCTGC-AGACAGGC      4914 CACAGCAG     AT
                        ATTCTGCA GCAGG
                        ||||||| |||||
                        TAAGACGT TGTCC
                        _____      C_
GAM320 HLCS         GACAACTGAGTCTCCTGCGTGAGGG 4911 TG      GGAA __   II
                        ACAACTGAG  CTGC GAGGG
                        ||||||||| |||| |||||
                        TGTTGACTC  GACG CTCCC
                          __      AGAG  CA  TI
GAM320 IL1RAP       CACAGCAGATGC--CACTGCA     4899       T TG AA  GG
                        CACAGCAGAT C  C TGCA
                        |||||||||| | | ||||
                        GTGTCGTCTA G  G ACGT
                          C GT __  II
GAM320 LIG1         CACAGCAGATTTGCTAAAAGCA    4892       C  AAT___ GGCI
                        CACAGCAGATT TGC   GCA
                        |||||||||| |||    |||
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                        GTGTCGTCTAA ACG    CGT
                        _   ATTTTT  IIIC
GAM320 LNK              CACAGCAGA-CCTGCCATG     4897      T   A  CAG
                        CACAGCAGAT CTGC ATG
                        IIIIIIIIII IIII III
                        GTGTCGTCTG GACG TAC
                        _   G  III
GAM320 LPIN2           ACAACTGAGGATGCTGCAGGAGG  4876 TGAC      AA  __   I
                        AACTGAGGG CTGC GAGGG
                        IIIIIIIII IIII IIIII
                        TTGACTCCT GACG CTCCT
                        ____        AC   TC   G
GAM320 MAPT           CAATTAACCGAACTGCGAGG    4888 TGACAACTGAGG
                        GAACTGCGAGG
                        IIIIIIIIIII
                        CTTGACGCTCC
                        AATTGG_____
GAM320 MMP16          ACAGCAGATACTG---TGCA     4880 CA      T  CAA   G
                        CAGCAGAT CTG  TGCA
                        IIIIIIII III  IIII
                        GTCGTCTA GAC  ACGT
                        __      T  ___  A
GAM320 NCAM2          CAGAGCAGGTTTCTGCAATG     4893 C   A_      CAGG
                        CA AGCAG TTCTGCAATG
                        II IIIII IIIIIIIIII
                        GT TCGTC AAGACGTTAC
                        C    CA      IIIC
GAM320 NEDD4L         CACGACA-ATTCTGCAATGGAG    4901  A  A      C GC
                        CAC GCAG TTCTGCAATG AG
                        III IIII IIIIIIIIII II
                        GTG TGTT AAGACGTTAC TC
                        C    _        C II
GAM320 OGDH           ACAGCAGATAATGGACACTGCAG  4878 CA      TCT__ A   CI
                        CAGCAGAT   GCA TGCAGG
                        IIIIIIII   III IIIIII
                        GTCGTCTA   TGT ACGTCT
                        __      TTACC  G   II
GAM320 PAG            CATAGCTCACTCTGCAATGTCAG   4898 CAC  AG      _  GCI
                        AGC ATTCTGCAATG CAG
                        III IIIIIIIIIIII III
                        TCG TGAGACGTTAC GTC
                        GTA  AG      A  III
GAM320 PEA15          ACAACTGAGTGGAA----GAGGG   4875 TGAC     _   CTGC
                        AACTGAG GGAA   GAGG
                        IIIIIII IIII   IIII
                        TTGACTC CCTT   CTCC
                        ____        A   ____
GAM320 PKIA           AGCAGGTTCCTGCAATGCAG     4883 CACAGCAGA        G
                        TTCTGCAATGCAG
                        IIIIIIIIIIII
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                              AGGACGTTACGTC
                    TCCA_____          G
GAM320 PPARG        AGCAGAATGCAGAAATGCAGGC   4882 CACA_    TTCTGC
                       GCAGA     AATGCAGGC
                       |||||     |||||||||
                       CGTCT     TTACGTCCG
                    TCTTA     _____
GAM320 PPP1R2       CACAGCAGAGACTCGC-AGGCAG   4894       TT GCAA
                       CACAGCAGA CT  TGCAGGC
                       ||||||||| ||  |||||||
                       GTGTCGTCT GA  GCGTCCG
                          CT ____
GAM320 PRKY         CACAGCAGATTTGAGCAATGC   4891        CT_    AGGC
                       CACAGCAGATT GCAATGC
                       ||||||||||| |||||||
                       GTGTCGTCTAA CGTTACG
                          ACT   IIIC
GAM320 PTPRF         CACACCATA--CTGCAATGCTGG   4902   G GATT     A C
                       CACA CA  CTGCAATGC GG
                       |||| ||  ||||||||| ||
                       GTGT GT  GACGTTACG CC
                         G AT__       A I
GAM320 RHO          AGCAGATTCTCCAGAATGGAG   4884 CACAGC   G __   C C
                          AGATTCT CA ATG AGG
                          ||||||| || ||| |||
                          TCTAAGA GT  TAC TCT
                       _____       G CT C  T
GAM320 SF3B2        TGACAAGTCCTTGGGAACTGCG   4916    __ GA      AGGG
                       TGACAA CT GGGAACTGCG
                       |||||| || ||||||||||
                       ACTGTT GG CCCTTGACGC
                          CA AA      IIIG
GAM320 SLC4A10       CACA-CAGATTCTGCATTG     4896   G       ATGCAG
                       CACA CAGATTCTGCA
                       |||| |||||||||||
                       GTGT GTCTAAGACGT
                          _       AACIII
GAM320 SWAP70        AGGACATTCTGCAAAAGTGCAGG   4885 CACAGCAG       ___   CI
                          ATTCTGCAA TGCAGG
                          ||||||||| ||||||
                          TAAGACGTT ACGTCC
                       TG_____       TTC   TG
GAM320 TAF1C         TGAGAACTGAGGGACCTGCCTGAGG 4917  C      A  __  GII
                       TGA AACTGAGGGA CTGC GAGG
                       ||| ||||||||||| |||| ||||
                       ACT TTGACTCCCT GACG CTCC
                          C     G  GA  III
GAM320 TCF2         CACAGCAGAGGCATTCT--AATCCAGGC4889         ____    CA G   II
                       CACAGCAGA  TTCTG AT CAGGC
                       |||||||||  ||||| || |||||
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                    GTGTCGTCT    AAGAT  TA GTCCG
                       CCGT    __  G    II
GAM320  TGM4          CAGATTCTCTCCTGCAATGCCAGG  4905 CACAGCAGA        _  CI
                     TTCTGCAATGC AGG
                     IIIIIIIIIII III
                     AGGACGTTACG TCC
                    AGAG_____        G   CT
GAM320  TSTA3        CAGAGCGGAT---GGAATGCAGGC  4904  C  A TTC  C
                    CA AGC GA  TG AATGCAGGC
                    II III II  II IIIIIIIII
                    GT TCG CT  AC TTACGTCCG
                     C  C ___  C
GAM320  WBP2         TGCCAGACTGAGGGAGCTG    4915 TGA _      A  CGAGG
                     CA ACTGAGGGA CTG
                     II IIIIIIIII III
                     GT TGACTCCCT GAC
                    ACG  C     C  IIIGG
GAM321  GABRA2        GCAGCCAAGAGAGCGTGGAGCG  4920 AGGC      AA  _
                     AGCCAAGAGG GTGG GCGG
                     IIIIIIIIII IIII IIII
                     TCGGTTCTCT CACC CGCT
                     ____        CG   T
GAM321  GABRA2        GCAGCCAAGAGAGCGTGGAGCG  4920 C       AA  _ I
                     AGCCAAGAGG GTGG GC
                     IIIIIIIIII IIII II
                     TCGGTTCTCT CACC CG
                     _       CG   T  I
GAM321  TCEA1        GCTGGCAAGGGGAAGTGGGCG    4921 A   GCCA  A
                     GGCA  AG GGAAGTGGGCGG
                     IIII  II IIIIIIIIIIII
                     CCGT  TC CCTTCACCCGCT
                    A ____   C
GAM321  TCEA1        GCTGGCAAGGGGAAGTGGGCG    4921 CAGC   A       I
                     CAAG GGAAGTGGGC
                     IIII IIIIIIIIII
                     GTTC CCTTCACCCG
                    GACC  C      I
GAM321  TSN          GGCGGCCAAG--GAAGTGGACG   4922 _ A  AG       I
                     GC GCCA AGGAAGTGGGC
                     II IIII IIIIIIIIIII
                     CG CGGT TCCTTCACCTG
                     C C  __      I
GAM321  TSN          GGCGGCCAAG--GAAGTGGACG   4922 AG A  AG
                     GC GCCA AGGAAGTGGGCG
                     II IIII IIIIIIIIIII
                     CG CGGT TCCTTCACCTGC
                     __  C  __
GAM322  ALDH1A3      TAAAAATAACAAGGCTGTGT     4938         CTCT   GG
                     TAAAAATAACAA  TTGTG
                     IIIIIIIIIII   IIIII
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                        ATTTTTATTGTT   GACAC
                             CC__    AI
GAM322 AXUD1        TAAAAATAAAGCCTCTTTATTGG  4940      CAA      _ GCI
                        TAAAAATAA  CTCTTTGT GG
                        |||||||||  ||||||||| ||
                        ATTTTTATT  GAGAAATA CC
                            TCG      A III
GAM322 AXUD1        TAAAAATAAAGCCTCTTTATTGG  4940      CAA      GGI
                          AAAAATAA  CTCTTTGT
                          |||||||| |||||||||
                          TTTTTATT  GAGAAATA
                            TCG      ACI
GAM322 CDKN1B         TAAAAATAAC-ACTTTCCTGTGG   4937       AC_  T  GC
                        TAAAAATAACA  TCTT GTGG
                        ||||||||||| |||| ||||
                        ATTTTTATTGT  AGGA CACC
                             GAA   _  II
GAM322 CDKN1B         TAAAAATAAC-ACTTTCCTGTGG   4937       AC_  T  I
                         AAAAATAACA  TCTT GTG
                         ||||||||| |||| |||
                         TTTTTATTGT  AGGA CAC
                             GAA   _  I
GAM322 CHN2        AAAATAACAACATTCTCGTGGG   4927 A       TC_      I
                        AATAACAAC  TTTGTGG
                        |||||||| |||||||
                        TTATTGTTG  GAGCACC
                         _       TAA      I
GAM322 CHN2        AAAATAACAACATTCTCGTGGG   4927 TAAA      TC_      C
                        AATAACAAC  TTTGTGGG
                        ||||||||| |||||||||
                        TTATTGTTG  GAGCACCC
                         ____        TAA      A
GAM322 GABRE          AAAGAGCAGC-CTTTGTGGG     4930 AATAACAAC       I
                            TCTTTGTGG
                            |||||||||
                            GGAAACACC
                        TTTCTCGTC      I
GAM322 GABRE          AAAGAGCAGC-CTTTGTGGG     4930 TAAAAATAACAAC
                            TCTTTGTGGG
                            ||||||||||
                            GGAAACACCC
                        CTCGTC_____
GAM322 GPC4        TAACACAAACAACCTCTTTGTGGG  4936 AA__     AA       I
                          AAATAAC  CTCTTTGTGG
                          ||||||| ||||||||||
                          TTTGTTG  GAGAAACACC
                        TGTG      __          I
GAM322 GPC4        TAACACAAACAACCTCTTTGTGGG  4936 TAA___     AA       CI
                          AAATAAC  CTCTTTGTGGG
                          ||||||| |||||||||||
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                        TTTGTTG  GAGAAACACCC
                        ATTGTG      __         ||
GAM322  HGF             AAAATAACATTTAATTTGTGG   4928 TAAA     ACTC_     GC
                        AATAACA   TTTGTGG
                        |||||||   |||||||
                        TTATTGT   AAACACC
                            ____      AAATT    AA
GAM322  HIP2            TAAAAATAACAGATGTTGGTG   4939         ACTCTT  G C
                        TAAAAATAACA    TGT GG
                        |||||||||||    ||| ||
                        ATTTTTATTGT    ACA CC
                            CT____   A A
GAM322  MEN1            TAAAAATAACAGTACACCTTGT   4934        __ T    GGGC
                        TAAAAATAACA AC CTTTGT
                        ||||||||||| || ||||||
                        ATTTTTATTGT TG GGAACA
                            CA  T    |||C
GAM322  MGAT4A            TAACAATATGTACAACTCTTATGT  4933 TAAAAATA      TI
                        ACAACTCTT
                        |||||||||
                        TGTTGAGAA
                        ATACA___       TA
GAM322  MGAT4A            TAACAATATGTACAACTCTTATGT  4933 TAAAAATA___     T GGCI
                        ACAACTCTT GTG
                        ||||||||| |||
                        TGTTGAGAA TAC
                        ATTGTTATACA      _  AIII
GAM322  MTRR            TAAAAATAA-ATCCCTCTGTAGGC   4941         CAA       I
                        TAAAAATAA  CTCTTTGTGGGC
                        |||||||||  |||||||||||||
                        ATTTTTATT  GGGAGACATCCG
                            TA_        I
GAM322  MTRR            TAAAAATAA-ATCCCTCTGTAGGC   4941 _       CAA       I
                        AAAAATAA  CTCTTTGTGGG
                        ||||||||  |||||||||||
                        TTTTTATT  GGGAGACATCC
                        A    TA_        I
GAM322  OPTN           AAAAGCACAACTCTTGGAGG      4929 AAAATA       TGTI
                        ACAACTCTT
                        |||||||||
                        TGTTGAGAA
                        TTCG__       CCTC
GAM322  OPTN           AAAAGCACAACTCTTGGAGG      4929 TAAAAATA      T TG
                        ACAACTCTT G GG
                        ||||||||| | ||
                        TGTTGAGAA C CC
                        TTCG____      _CT
GAM322  PCDHB9          AAAAATAGTACCTTCTTTGTGG   4925 TA    __ AAC      GC
                        AAAATA AC  TCTTTGTGG
                        |||||| || |||||||||
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                              TTTTAT TG  AGAAACACC
                         __     CA  GA_        AI
GAM322  TJP1          TAAAAATGTAACAACTCTGTG    4932   __       TT  GGC
                         TAAAAA TAACAACTCT GTG
                         |||||| |||||||||| |||
                         ATTTTT ATTGTTGAGA CAC
                           AC          __  III
GAM322  TJP1          TAAAAATGTAACAACTCTGTG    4932   __       TTIII
                         TAAAAA TAACAACTCT
                         |||||| ||||||||||
                         ATTTTT ATTGTTGAGA
                          AC          CACII
GAM322  TWIST          TAAAAATAAAAACATTCTTCGT   4935     C  __    GGGC
                         TAAAAATAA AAC  TCTTTGT
                         ||||||||| ||| |||||||
                         ATTTTTATT TTG AGAAGCA
                          T  TA     IIIC
GAM322  VBP1          TAAAAAGCTCACAACTCTTT     4931   TA___      GTGGGC
                         TAAAAA   ACAACTCTTT
                         ||||||   ||||||||||
                         ATTTTT   TGTTGAGAAA
                          TCGAG       IIICGG
GAM322  VBP1          TAAAAAGCTCACAACTCTTT     4931   TA___      III
                         TAAAAA   ACAACTCTT
                         ||||||   |||||||||
                         ATTTTT   TGTTGAGAA
                          TCGAG       AII
GAM322  XRCC5          AAAATAACAATGACTCTTT      4926      ___    III
                         AAAATAACA  ACTCTT
                         ||||||||| ||||||
                         TTTTATTGT  TGAGAA
                           TAC    AII
GAM322  XRCC5          AAAATAACAATGACTCTTT      4926 TAAA    ___    GGG
                         AATAACA  ACTCTTTGT
                         ||||||| |||||||||
                         TTATTGT  TGAGAAATA
                          ____        TAC     III
GAM323  BCL11B          TGTGTTCCACG-AGACCTT     4956 AATGA    A  A  G
                           GTTCCACGA GA CTT
                           ||||||||| || |||
                           CAAGGTGCT CT GAA
                           A____       _  G  G
GAM323  DDX3           GAGATCTCGCGA-GAACTTGC    4951 AATGAG  CA  A
                             TTC CGA GAACTTGC
                             ||| ||| ||||||||
                             GAG GCT CTTGAACG
                           TA____   C_  _
GAM323  DHCR24          AATGAGTTCTAAACGGGGAACT   4944      C__ AA  TGCC
                           AATGAGTTC ACG GAACT
                           ||||||||| ||| |||||
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                          TTACTCAAG  TGC CTTGA
                             ATT  CC    IIIC
GAM323 FACL6        TTACACTGAGAAGAACTTTCC     4957 AATGAGTTCCAC       G
                             GAAGAACTT CC
                             |||||||||| ||
                             CTTCTTGAA GG
                          ACT_____        A
GAM323 FMR2         AATGAGTTCCCCAATAGGAAC     4946      A A__  TTGCC
                             AATGAGTTCC CGA  GAAC
                             ||||||||| |||  ||||
                             TTACTCAAGG GTT  CTTG
                              G  ATC   IIICC
GAM323 IL13RA1      AATGAGTTCCCCTACAAATAA     4945       ___   GAACTTGCC
                             AATGAGTTCC  ACGAA
                             |||||||||  |||||
                             TTACTCAAGG  TGTTT
                              GGA   ATTIIICCG
GAM323 MAPRE1        GAGGTCCAGAAAGAACTTGC     4952 AATGAGT   C
                             TCCA GAAGAACTTGC
                             |||| |||||||||||
                             AGGT TTTCTTGAACG
                          C_____    C
GAM323 PMM2         AGTTTCACGAAGAACGTGC     4949 AATGAGTTC       T
                             CACGAAGAAC TGC
                             |||||||||| |||
                             GTGCTTCTTG ACG
                          A_____         C
GAM323 RAD52        GACTCCCACGTAGAACTTGCC     4953 AATGAG    A
                             TTCCACG AGAACTTGCC
                             ||||||| ||||||||||
                             AGGGTGC TCTTGAACGG
                          _____         A
GAM323 RBM3         TGAGCCCTCCCACGAAGAGCTTTCC 4954 AATGAG        A G II
                             TTCCACGAAGA CTT CC
                             ||||||||||| ||| ||
                             AGGGTGCTTCT GAA GG
                          TCGGG_         C A AA
GAM323 STARD4        AATGGGT---ATGAAGAACTT     4948   A TCCAC       G
                             AATG GT   GAAGAACTT
                             |||| ||    |||||||||
                             TTAC CA    CTTCTTGAA
                              C TA___        I
GAM323 TEM6         AATGAGTT-CAAAAAGCACGTTTGC 4947       CAC  A __  CI
                             AATGAGTTC  GAAG AC  TTGC
                             ||||||||| |||| || ||||
                             TTACTCAAG  TTTC TG  AACG
                              TT_  G  CA  II
GAM323 TRIP12      ATAATTTAAAC-AAGAACTTGC     4950 AATGAGTTCCACG       C
                             AAGAACTTGC
                             ||||||||||
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                        TTCTTGAACG
                    ATTAAATTTG___          A
GAM323  XT3         TGAGTTCCATGAGCAAAAACT    4955 AATG    C ___       TGCC
                    AGTTCCA GA  AGAACT
                    |||||||| ||  ||||||
                    TCAAGGT CT  TTTTGA
                    ____      A  CGT       TAII
GAM324  ABCA1           TGAGAATACACAGGAACAAAA   4968       CTGAAAC  CCGT
                    TGAGAATAC      CAAA
                    |||||||||      ||||
                    ACTCTTATG      GTTT
                      TGTCCTT   TIII
GAM324  CACNA1C         AATACAAGAAAACCAAACC      4960 TGAGAATACCT        G
                    GAAACCAAACC
                    |||||||||||
                    TTTTGGTTTGG
                    GTTC_____          G
GAM324  CNTN3           AGCATACC--AAACCAAAC     4964 TGAGA    TG      C
                    ATACC AAACCAAAC
                    ||||| |||||||||
                    TATGG TTTGGTTTG
                    G____   __        T
GAM324  DDX6           GAGACTTCAACCTGAAACCAAA   4967 TG  AT___        CCGT
                    AGA    ACCTGAAACCAAA
                    |||    |||||||||||||
                    TCT    TGGACTTTGGTTT
                    __  GAAGT          TIII
GAM324  HTN3        TGAGAATACACGAGTCCAAAGCG   4969      C AA   C TI
                    TGAGAATAC TGA  CCAAA CG
                    ||||||||| |||  ||||| ||
                    ACTCTTATG GCT  GGTTT GC
                      T CA   C II
GAM324  PDGFRA          GAAAACCTGTCAAAACCAAAC   4966 TGAGAAT   ___       CGT
                    ACCTG AAACCAAAC
                    ||||| |||||||||
                    TGGAC TTTGGTTTG
                    T_____  AGT       AAA
GAM324  PRDM1       AATCCCTGAAACCTCACAGT    4962 TGAGAATA     AA  C
                    CCTGAAACC AC G
                    ||||||||| || |
                    GGACTTTGG TG C
                    _____      AG  T
GAM324  RAB11A          AGACATAC-TGAAACCAAA    4963 TGAGA   C       CC
                    ATAC TGAAACCAAA
                    |||| ||||||||||
                    TATG ACTTTGGTTT
                    TG___  _       CT
GAM324  STCH        AATACCTGACATCAACACGGT    4961 TGAGAATA   AAC  AC T
                    CCTGA  CAA  CG
                    |||||  |||  ||
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                              GGACT  GTT GC
                   _____      GTA  GT C
GAM324 STIM1       AGAA-ACAAGAAACCAAACC   4965 TGAGAAT CT       G
                         AC GAAACCAAACC
                         || |||||||||||
                         TG CTTTGGTTTGG
                   TT_____ TT        A
GAM325 COL4A6      AAACTAAACACTGCTTCTAGAT   4973 TAAAAGTAAAA     CCTG
                            CTTCTAGAT
                            |||||||||
                            GAAGATCTA
                   TGATTTGTGAC       TTII
GAM325 F8          AAAAGTAAAATTTCT-GAT    4972       C  AGAI
                         AAAAGTAAAA TTCT
                         |||||||||| ||||
                         TTTTCATTTT AAGA
                            A   CTAI
GAM325 F8          AAAAGTAAAATTTCT-GAT    4972 TA     C  A CC
                         AAAGTAAAA TTCT GAT
                         ||||||||| |||| |||
                         TTTCATTTT AAGA CTA
                      __       A  _  AI
GAM326 HAO2         GTGGTGGTATTAGAAATGTG    4976   C_      TG CCI
                         GTGG GTATTAGAA GTG
                         |||| ||||||||| |||
                         CACC CATAATCTT CAC
                           AC      TA III
GAM326 TTC3        GTGGGGAAGGAGAATGGTG    4978  CGTATT     CC
                         GTGG  AGAATGGTG
                         ||||  |||||||||
                         CACC  TCTTACCAC
                         CCTTCC        II
GAM326 USP14       GTGGC-TAC-AGAATGGTG    4977   GTAT      C
                         GTGGC  TAGAATGGTG
                         |||||  ||||||||||
                         CACCG  GTCTTACCAC
                         AT__       I
GAM327 ADRA1A       TCACCAGTCACCATGGAGAGAA   4985 TCACCC      AI
                          CACCATGGAGA
                          |||||||||||
                          GTGGTACCTCT
                   GTCA__        CT
GAM327 ADRA1A       TCACCAGTCACCATGGAGAGAA   4985 TGTC C__      AAAGA
                         ACC  CACCATGGAGA
                         |||  |||||||||||
                         TGG  GTGGTACCTCT
                      ____    TCA      CTTAC
GAM327 CHD4        CCCCAAAAAGGAGAAAAGA    4982   CCAT     II
                         CCCCA  GGAGAAAAG
                         |||||  |||||||||
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                         GGGGT    CCTCTTTTC
                          TTTT        TI
GAM327  FTH1            GTCACCCCACGGCTATGGGGAAA  4983 TCA      C___   A    I
                          CCCCAC    ATGG GAA
                          ||||||    |||| |||
                          GGGGTG    TACC CTT
                             ___    CCGA  C   I
GAM327  FTH1            GTCACCCCACGGCTATGGGGAAA  4983 TG       C___   A  AGAI
                          TCACCCCAC    ATGG GAAA
                          |||||||||    |||| ||||
                          AGTGGGGTG    TACC CTTT
                              __       CCGA  C  AIII
GAM327  MGAT5             TCACTCCCACCATGAGGCAAA   4984 C  _        AGAAAI
                           AC CCCACCATGG
                           || |||||||||||
                           TG GGGTGGTACT
                            _  A        CCGTTI
GAM327  MGAT5             TCACTCCCACCATGAGGCAAA   4984 TGTC _       AGAAAAGA
                           AC CCCACCATGG
                           || |||||||||||
                           TG GGGTGGTACT
                             ____  A       CCGTTTTA
GAM327  MUC4             ACCCCACCAGGAAAGAAAA      4981       T    AAII
                          ACCCCACCA GGAGA
                          ||||||||| |||||
                          TGGGGTGGT CCTTT
                              _    CTTT
GAM327  MUC4             ACCCCACCAGGAAAGAAAA      4981 TGTCACCC    T    AAAG
                           CACCA GGAGA
                           ||||| |||||
                           GTGGT CCTTT
                           _____  _    CTTT
GAM327  SEPN1           TGTCTACCCGCCACCATGGAGCCAAG 4986   _  ___      AA  AII
                          TGTC ACCC  CACCATGGAG  AAG
                          |||| ||||  |||||||||| |||
                          ACAG TGGG  GTGGTACCTC TTC
                             A    CG       GG  III
GAM327  SEPN1           TGTCTACCCGCCACCATGGAGCCAAG 4986 TCA _       AAI
                           CC CCACCATGGAG
                           || ||||||||||
                           GG GGTGGTACCTC
                             G__ C       GGT
GAM328  ATP2A3          TGCAGA--CAGCGCGGCGGCCGC   4998   AAAC             G
                           TGCA   CAGCGTGGCGGCCGC
                           ||||   ||||||||||||||
                           ACGT   GTCGCGCCGCCGGCG
                             CT__            I
GAM328  CHRNA7            TGCAAAACCAACTGTCTCGG     4995        _ GG  CCGC
                           TGCAAAACCAGC GT CGG
                           |||||||||||| || |||
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                          ACGTTTTGGTTG CA  GCC
                            A  GA   IIIG
GAM328 CUGBP1           GCAAAACCAATTTGGCAGC     4992 TG      CG      CGC
                          CAAAACCAG TGGCGGC
                          |||||||| |||||||
                          GTTTTGGTT ACCGTCG
                                  AA      TII
GAM328 FLNB         GCAAAACCA---TGACTGCCG    4993 TG      GCG   G
                          CAAAACCA  TGGC GCCG
                          |||||||| |||| ||||
                          GTTTTGGT  ACTG CGGC
                          __      ___     A
GAM328 GRLF1          GCAAAACCAAGGCGGTGGAGGC    4991 TG       C   C CC
                          CAAAACCAG GTGG GG  GCG
                          ||||||||| |||| ||  |||
                          GTTTTGGTT CGCC CC  CGT
                          __          C   A TC
GAM328 HNF3A        TGCGAAGCGA-CG-GGCGGCCGCG    5000    AAAACCA  T
                          TGC     GCG GGCGGCCGCG
                          |||     ||| ||||||||||
                          ACG     TGC CCGCCGGCGC
                          CTTCGC_  _
GAM328 JUND         TGCAA---CA-CGGGGCGGCCGCG    4999     AACCA  T
                          TGCAA    GCG GGCGGCCGC
                          |||||    ||| |||||||||
                          ACGTT    TGC CCGCCGGCG
                            G____    C
GAM328 MECP2         TGCAAAACCTGGGT-GCTGCC     4997        AGCG  CG  C
                          TGCAAAACC  TGG GC GC
                          |||||||||  ||| || ||
                          ACGTTTTGG  ACC CG CG
                            ____   CA  A
GAM328 PACE        CAAAACCAGCCGGGCTGGCCACG    4989 TGCA     GT  _    I
                          AAACCAGC GGC GGCCGCG
                          |||||||| ||| |||||||
                          TTTGGTCG CCG CCGGTGC
                          ____      GC  A   T
GAM328 PDGFB         TGAAAAATGGGCGCTGGCGGCCG    4996 TGCAAAACCA _      CGI
                          GCG TGGCGGCCG
                          ||| |||||||||
                          CGC ACCGCCGGC
                          ACTTTTTACC G      III
GAM328 SCA1        TGCACAGAAACCAGCGTGG     4994   ___      CGGCCGC
                          TGCA AAACCAGCGTGG
                          |||| |||||||||||
                          ACGT TTTGGTCGCACC
                            GTC        IIIGCGC
GAM328 TNFRSF6B       GCAGAAACCAGCGTGCGCG    4990 TGCA       _  CCGC
                          AAACCAGCGTG GCGG
                          ||||||||||| ||||
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                          TTTGGTCGCAC CGCT
                          GTC_        G  IIIG
GAM329  DBP           CCTGCAAATCTAGGAGCACGGAT  5003 C     GA   GA_  I
                          TGCAAAT AGGAG  GGA
                          IIIIIII IIIII  III
                          ACGTTTA TCCTC  CCT
                          _       GA   GTG  I
GAM329  DBP           CCTGCAAATCTAGGAGCACGGAT  5003 GTCC    GA   GA_  I
                          TGCAAAT AGGAG  GGAT
                          IIIIIII IIIII  IIII
                          ACGTTTA TCCTC  CCTA
                          ____        GA   GTG  A
GAM329  NPDC1         TGCCAAGGAGGAGGAGGAGGA    5004   AAAT A      III
                          TGC   GA GGAGGAGG
                          III   II IIIIIIIII
                          ACG   CT CCTCCTCC
                           GTTC _       TCC
GAM329  SLC2A2        TGCAT-TGCAGGAGGAGGA     5005   AA A      I
                          TGCA TG AGGAGGAGG
                          IIII II IIIIIIIII
                          ACGT AC TCCTCCTCC
                           A_  G      T
GAM329  SLC2A2        TGCAT-TGCAGGAGGAGGA     5005 GTCCTGCAAA A
                             TG AGGAGGAGG
                             II IIIIIIIII
                             AC TCCTCCTCC
                          A_____ G
GAM330  ABCC1         GGTGGCGCGGGCGGCGGCGGGCA  5031 TGGGC        A_  I
                          GGCGCGGGCGGCG GGGCA
                          IIIIIIIIIIIII IIIII
                          CCGCGCCCGCCGC CCCGT
                          A____        CG   G
GAM330  ABCC1         GGCGCGGGCGGCGGCGGGCA     5019 T     _   G A GC
                          GGGCGGCG CGGGCG CG GG
                          IIIIIIII IIIIII II II
                          CCCGCCGC GCCCGT GC CC
                          _     C   G _ II
GAM330  ABCC1         GGCGGCGGGCACCGGGCGGCG    5021 TG    _ _      A GCA
                          GGCGG CGC GGGCGGCG GG
                          IIIII III IIIIIIIII II
                          CCGCC GTG CCCGCCGC CC
                          G_   C  G      _ III
GAM330  ADAM12        CGGGCCCGGCGGCGAGCGC      5012 TGGGCGGCGCG      G
                          GGCGGCGAG GC
                          IIIIIIIII II
                          CCGCCGCTC CG
                          GGG_____      G
GAM330  ARHC          GGCGGCGTGGGC---GAGGGCA   5045 TGGG   C  GGC
                          CGGCG GGGC  GAGGGC
                          IIIII IIII  IIIIII
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                               GCCGC CCCG   CTCCCG
                               ____       A    ___
GAM330 ARHC          GGGCGGCGCCGAGGCGGCGTTGGGCA 5050 TG       __       A_    II
                               GGCGGCGC GGGCGGCG GGGCA
                               |||||||| ||||||||| |||||
                               CCGCCGCG TCCGCCGC CCCGT
                                     __       GC    AA    CI
GAM330 ARHC          TGGAGCGGCGGCGGGCGGCG    5070  _   _      AGGGC
                               TGG GCGGCG CGGGCGGCG
                               ||| |||||| |||||||||
                               ACC CGCCGC GCCCGCCGC
                                      T    C       IIIAC
GAM330 BACE          GGCGGCGCGGGCAGGGGCAAGGGC  5026 TGGG       ___       AI
                               CGGCGCGGGC  GGCGAGGGC
                               ||||||||||  |||||||||
                               GCCGCGCCCG  CCGTTCCCG
                               ____         TCC      AG
GAM330 BACE          GCGGGCGGCGGCGCGGGCA     5013 TGGG        CGA
                               CGGCGCGGGCGG  GGGC
                               ||||||||||||  ||||
                               GCCGCGCCCGTC  CCCG

                               ____         ___
GAM330 BACH2       TGGGCAGGCG-GGGTGGCGAGGGC 5073  _   C    C      AI
                               TGGGC GGCG GGG GGCGAGGGC
                               ||||| |||| ||| |||||||||
                               ACCCG CCGC CCC CCGCTCCCG
                                     T   _  A      II
GAM330 BCL11A       GCGGGGCGGGCGGCGGCGGC    5017 T    C    G    AG
                               GGGCGG GCGG CGGCG  GGC
                               |||||| |||| ||||| |||
                               CCCGCC CGCC GCCGC  CCG
                                    _     _    _     CG
GAM330 BMP1        GGCGGGGCGG-CGGCGAGGG      5039 TG  C    GCG        C
                               GG GGC  GGCGGCGAGGG
                               || |||  ||||||||||
                               CC CCG  CCGCCGCTCCC
                                  G_   _   ___         T
GAM330 BTEB1       CGACGCGGGTGGCGAGGGC      5011 TGGGCGGC    C
                               GCGGG GGCGAGGGC
                               ||||| |||||||||
                               CGCCC CCGCTCCCG
                               _____      A
GAM330 CAPN7       GGCGGCCCGGCGGCGGCGAGG     5024 TGGG   G  __        A
                               CGGC CGG  GCGGCGAGGGC
                               |||| |||  |||||||||||
                               GCCG GCC  CGCCGCTCCTG
                               ____     G  GC       I
GAM330 CD81        GGCGGCGCGGGCGGCGGGCGGC    5032 TGGG      GA   A
                               CGGCGCGGGCGGC GGGC
                               ||||||||||||| ||||
```

```
                          GCCGCGCCCGCCG  CCCG
                          ____         __   C
GAM330  CDK2AP1           GGCGGCGGCGGCGGCGAGG      5035 TG    GCG      GC
                          GGCGGC  GGCGGCGAGG
                          ||||||  ||||||||||
                          CCGCCG  CCGCCGCTCC
                          G_    ___        GG
GAM330  CREBBP            GGGCGGC-CGGGCCGGCGAGGGC   5058 TG   G    _     A
                          GGCGGC CGGGC GGCGAGGGC
                          |||||| ||||| |||||||||
                          CCGCCG GCCCG CCGCTCCCG
                          __    _    G    G
GAM330  CSNK2A2           GGGCGGCGCGGGGCGCAGAGGG    5053 TG      CG _  CA
                          GGCGGCGCGGG GC GAGGG
                          ||||||||||| || |||||
                          CCGCCGCGCCC CG CTCCC
                          __        CG  T   AI
GAM330  DLK1              GGGGGCGCGGGCGCGCAGCGAGGG  5027 T _  C  G     CAI
                          GG GCGG GCG GCGGCGAGGG
                          || |||| ||| ||||||||||
                          CC CGCC CGC CGTCGCTCCC
                          C  G  _  G      CTI
GAM330  DUSP7             TGGGGAGCGCGGGCGGCCCGGG    5077   C      GA  CA
                          TGGG GGCGCGGGCGGC GGG
                          |||| ||||||||||| |||
                          ACCC TCGCGCCCGCCG CCC
                          C       GG  II
GAM330  DVL3              GGCGGCGC--GCGGCGCGG       5034 TG  G   _   GAGGG
                          GGCG CGCGG GCGGC
                          |||| ||||| |||||
                          CCGC GCGCC CGCCG
                          G_  _   G   GIIIA
GAM330  FASN              GGCGGTGCGGGCGGCGGAGAGC    5030 TGGG  C       _   A
                          CGG GCGGGCGGCG AGGGC
                          ||| |||||||||| |||||
                          GCC CGCCGCCGC TCTCG
                          ____   A      C   C
GAM330  FKBP1A            GGGCGGCGCGACGGGCGGCGTGG   5049 TG       ___     A  CAI
                          GGCGGCGC  GGGCGGCG GGG
                          ||||||||  |||||||| |||
                          CCGCCGCG  CCCGCCGC CCT
                          __        CTG    A  III
GAM330  FOXG1B            GGGGGGCGGCGGGCGGC-AGCGGC  5051 T  C  _    G  _  AI
                          GGG GGCG CGGGCGGC AG GGC
                          ||| |||| |||||||| || |||
                          CCC CCGC GCCCGCCG TC CCG
                          _  _   C   _ G  CI
GAM330  FOXG1B            GGCGGCGCGGG-AGCG-GGACA    5042 TGGG     C  A
                          CGGCGCGGG GGCG GGGC
                          ||||||||| |||| ||||
```

```
                            GCCGCGCCC TCGC CCTG
                            ___        _  _
GAM330  FOXG1B        GGCG-CGCGGGCGGCGCGG    5033 TGGGCG         AG
                          GCGCGGGCGGCG GG
                          IIIIIIIIIII II
                          CGCGCCCGCCGC CC
                      G_____          G_
GAM330  G6PD         GGGCGGGGCGGG--GCGAGGGCA  5069 TG    C    CG
                          GGCGG GCGGG  GCGAGGGCA
                          IIIII IIIII  IIIIIIIII
                          CCGCC CGCCC  CGCTCCCGT
                         __    C    __
GAM330  GAD2         GCGGGGCCGAGCGGCGAGGGC    5014 TGGGC  G            A
                          GGC CGGGCGGCGAGGGC
                          III IIIIIIIIIIIIII
                          CCG GCTCGCCGCTCCCG
                      C____ _          C
GAM330  GATA2         GGCCGGCGCGGGCGGCTCAGGG  5060 TG G        G_  CA
                          G CGGCGCGGGCGGC AGGG
                          I IIIIIIIIIIIII IIII
                          C GCCGCGCCCGCCG TCCC
                         __G       AG   AI
GAM330  GPC1         GGCGGCGCGGGGCGCGCGGG     5037 TGGG      _ _  A  C
                          CGGCGCGGG CG GCG GGG
                          IIIIIIIII II III III
                          GCCGCGCCC GC CGC CCC
                         ____        C G _  A
GAM330  GRB14        TGGGGCGCGCGGGCGGCGAGG    5076 T_  G         GCA
                          GGGCG CGCGGGCGGCGAGG
                          IIIII IIIIIIIIIIIII
                          CCCGC GCGCCGCCGCTCC
                         AC   _        III
GAM330  GTF2IRD1     GGACGGCG-GCGCGGCGAGGGC   5065 TG_     GGGC      A
                          GGCGGCGC  GGCGAGGGC
                          IIIIIIII  IIIIIIIII
                          CCGCCGCG  CCGCTCCCG
                         CTG   ____     C
GAM330  GTF2IRD1     GGGCGGCGCGG--GGAGAGG     5061 TG      C C
                          GGCGGCGCGGG GG GAGGG
                          IIIIIIIIIII II IIIII
                          CCGCCGCGCCC CT CTCCT
                         __       _  _
GAM330  GTF2IRD1     CGGCGCGGGCTGCGGCGGAGGGC  5009 TGG  C GG   _   AI
                          GCGG GC GCGGCG AGGGC
                          IIII II IIIIII IIIII
                          CGCC CG CGCCGC TCCCG
                         ___   _ A_   C  CC
GAM330  HDAC4        TGGGAGGCTGTTCGGGCGGCGGCGGC 5074  C G___     AG AII
                          TGGG GGC  CGGGCGGCG GGC
                          IIII III  IIIIIIIII III
```

```
                         ACCC CCG   GCCCGCCGC CCG
                         T   ACAA         CG   III
GAM330 HDAC4             GGGCTCGGGCTCGGGCGGCGA    5047 TG ___  G      GGGCA
                            GGC  GGC CGGGCGGCGA
                            III  III IIIIIIIIII
                            CCG  CCG GCCCGCCGCT
                            __ AGC  A        GIIIA
GAM330 HDAC4             GGCGGCGCGGGCGGGTGCGCGGGC 5028 TGGG      ___  A  AI
                            CGGCGCGGGCG  GCG GGGC
                            IIIIIIIIIII  III IIII
                            GCCGCGCCCGC  CGC CCCG
                            ____          CCA G  AG
GAM330 HDAC5             GGCTTCGCGGGCGGCGGCGGCA   5046 TGGGCGG      AG
                            CGCGGGCGGCG  GGCA
                            IIIIIIIIIII  IIII
                            GCGCCCGCCGC  CCGT
                         GAA____          CG
GAM330 HSF4             TGCGCAGGCGCGGGCAGTGCGCGC  5072 G _      __ AGG AI
                            TG GC GGCGCGGGCG GCG  GC
                            II II IIIIIIIIII III  II
                            AC CG CCGCGCCCGT CGC  CG
                             G  T        CA G__ II
GAM330 IGFBP4           GGCGGCGGGGGGCGGCGAGGG    5025 TG   CGC     _ A
                            GGCGG  GGGCGGCGAGGG C
                            IIIII  IIIIIIIIIII I
                            CCGCC  CCCGCCGCTCCC G
                         G_  C__        C I
GAM330 JAG2             GGCGGCGCGGGCGGGGTCGAGCGCA 5029 TGGG       ___   G  II
                            CGGCGCGGGCGG  CGAG GCA
                            IIIIIIIIIII   IIII III
                            GCCGCGCCCGCC  GCTC CGT
                            ____          CCA  G CG
GAM330 JAG2             TGGGCG--GCGGGCGTGCAGGGC   5075     GC  _ A  A
                            TGGGCGGC GGGCG GCG GGGC
                            IIIIIIII IIIII III IIII
                            ACCCGCCG CCCGC CGT CCCG
                             __  A  C  I
GAM330 LBX1             TGGGCAGGGCGCGGGCCGGCGCGGG 5071    __    _ A CAII
                            TGGGC GGCGCGGGC GGCG GGG
                            IIIII IIIIIIIII IIII III
                            ACCCG CCGCGCCCG CCGC CCC
                             TC      G  G  IIIA
GAM330 LBX1             GGACGGCGCGGGCCAGGC-AGCGGC 5057 TG       __  G _ AI
                            GGCGGCGCGGGC GGC AG GGC
                            IIIIIIIIIII  III II III
                            CTGCCGCGCCCG CCG TC CCG
                             __          GT _ G CI
GAM330 MADH3           GGGCGT-GCGGGCGGCGAGG       5062 TG  GC         C
                            GGCG GCGGGCGGCGAGGG
                            IIII IIIIIIIIIIIII
```

```
                        CCGC  CGCCCGCCGCTCCT
                         __     A_           I
GAM330 MAF        GGGCGTCTGTCCGGGCGGCGCGGGC 5048 TG   GCG___      A  AII
                        GGCG     CGGGCGGCG GGGC
                        ||||     ||||||||| ||||
                        CCGC     GCCCGCCGC CCCG
                         __    AGACAG      G  GII
GAM330 MAF        GGGCGGCGCGGGCCTTGGCACGGG 5056 TG       ___    A  CAI
                        GGCGGCGCGGGC  GGCG GGG
                        ||||||||||||  |||| |||
                        CCGCCGCGCCCG  CCGT CCC
                         __         GAA  G  CII
GAM330 MAFF       GGGCGGCGCAGGGGGCCGAGG    5052 TG      C  GA  A
                        GGCGGCGCGGG GGC  GGGC
                        ||||||||||| ||| ||||
                        CCGCCGCGTCC CCG  TCCG
                         __         C  GC  I
GAM330 MAP4K2     GGGCGGCGCGGGGCGGGGCGGGC  5054 TG      _  CGA  AI
                        GGCGGCGCGGG CGG  GGGC
                        ||||||||||| ||| ||||
                        CCGCCGCGCCC GCC  CCCG
                         __         C  CCG  CI
GAM330 MAP4K2     CGGCGCGGGGCGGCGCGGG      5008 T__      _  CGAGGGC
                         GGGCGGCGCGGG CGG
                         |||||||||||| |||
                         CCCGCCGCGCCC GCC
                   CGC         C  IIIACGG
GAM330 MET        GGGCGCCGCGGGCGGCGAGGGC   5066 TG  G         A
                        GGCG CGCGGGCGGCGAGGGC
                        |||| ||||||||||||||||
                        CCGC GCGCCCGCCGCTCCCG
                         __   G             I
GAM330 MSI1       GGGAGCCGCGGGCGGCGCGGGCA  5068 T  GG       A   I
                        GGGC CGCGGGCGGCG GGGCA
                        |||| ||||||||||| |||||
                        CTCG GCGCCCGCCGC CCCGT
                   C    __        G  C
GAM330 MSI1       GGGCGGCGCGGGCAGCGGAGCGGC 5059 TG         _ _  AI
                        GGCGGCGCGGGCGGCG AG GGC
                        |||||||||||||||| || |||
                        CCGCCGCGCCCGTCGC TC CCG
                         __          C  G  CI
GAM330 NFATC2     GCGGGGCCGGGGGCGAGGGC     5016 TGGGC  G  C
                          GGC CGGG GGCGAGGGC
                          ||| |||| |||||||||
                          CCG GCCC CCGCTCCCG
                   C____  _  _
GAM330 PABPC4     CGG-GCGGGCGGCGAAGGGCA    5010 T    C_     AGGGC
                          GGGCGGCG GGGCGGCG
                          |||||||| ||||||||
```

```
                    CCCGCCGC  CCCGTCGT
                    G       TT     GIIIA
GAM330  PABPC4          GGTGGCACCGGCGCGGCGAGG      5022 TGGGC   _ _         A
                          GGCGC GG GCGGCGAGGGC
                          |||||| || |||||||||||
                          CCGTG CC CGCCGCTCCTG
                    A____      G G         I
GAM330  PDXK           GGCGGCGCGGGGCCGAGGCGGGGGCA 5023 TGGG      _ ___   A   II
                          CGGCGCGGG C  GGCG GGGCA
                          |||||||||| |  |||| |||||
                          GCCGCGCCC G  CCGC CCCGT
                    ____        C GCT   C  GC
GAM330  PK428          GGCGGCGCGGGCGGCTGGCA      5044 TGGG           GAG
                          CGGCGCGGGCGGC  GGCA
                          ||||||||||||| ||||
                          GCCGCGCCCGCCG  CCGT
                    ____             AGA
GAM330  PK428        GGCGGGCTGCGGGCGGCACTGGCA   5020 T  GGC       AG  I
                          GGGC  GCGGGCGGCG GGCA
                          |||| |||||||||| ||||
                          CCCG  CGCCGCCGT CCGT
                    G   A__         GA  G
GAM330  PLCD1         GGGCGGCGC-GGCGG-GAGGG      5064 TG      G  C  C
                          GGCGGCGCGG CGG GAGGG
                          |||||||||| ||| |||||
                          CCGCCGCGCC GCC CTCCC
                    __        _ _     C
GAM330  SCN8A          GGCAGCGGCGGCGGCGAGGG      5036 TG    GCG       C
                          GGCGGC  GGCGGCGAGGG
                          ||||||  |||||||||||
                          TCGCCG  CCGCCGCTCCC
                    G_     ___        T
GAM330  SLBP         GGCGGCGCGGGCAGAGAGCGCA     5043 TGGG       C  G
                          CGGCGCGGGCGG GAG GCA
                          ||||||||||| ||| |||
                          GCCGCGCCCGTC CTC CGT
                    ____         T  G
GAM330  SLC6A8         GGCGCGGGCCGGCCGGGGGC      5018 T G  G  C  GA  C
                          GG CGGC CGGG GGC  GGG
                          || |||| |||| ||| |||
                          CC GCCG GCCC CCG  CCC
                    C G    _  _  G_  C
GAM330  SLC6A8         GCGGCTCGGGCGGCGGCGGC      5015 ___       GCG   GAGG
                          TGGGCGGC  GGCGGC  GC
                          ||||||||  ||||||  ||
                          GCCCGCCG  CCGCCG  CG
                    CGA       ___     A___
GAM330  SRM          GGGCGG-GCGGGCGGCGCGGG      5063 TG    C       A C
                          GGCGG GCGGGCGGCG GGG
                          ||||| |||||||||| |||
```

```
                         CCGCC CGCCCGCCGC CCC
                         __    _         G  C
GAM330 SRM               GGGCGGCGCGG--GGCGCGGGC  5067 TG      CG  A
                         GGCGGCGCGGG GCG GGGC
                         |||||||||| ||| ||||
                         CCGCCGCGCCC CGC CCCG
                         __        __  G
GAM330 TFAP4             GGCGGCGGCGGCGGCGAGGG    5038 TG   GCG       C
                         GGCGGC GGCGGCGAGGG
                         |||||| |||||||||||
                         CCGCCG CCGCCGCTCCC
                         G_    ___        C
GAM330 TFDP1             GGGCGGCGCGGAGAGGCGCGGGC  5055 TG      _C  A  AI
                         GGCGGCGCGG G GGCG GGGC
                         |||||||||| | |||| ||||
                         CCGCCGCGCC C CCGC CCCG
                         __         T T  G  AI
GAM330 THBS1             GGTGGCGAGGGCGGCGAGGGC    5041 TGGGC  C        A
                         GGCG GGGCGGCGAGGGC
                         |||| |||||||||||||
                         CCGC CCCGCCGCTCCCG
                         A____     T        A
GAM330 ZNF219            GGCGGAGCGGGCGGCGGCGGC    5040 TGGG  C      AG  A
                         CGG GCGGGCGGCG GGC
                         ||| |||||||||| |||
                         GCC CGCCCGCCGC CCG
                         ____    T    CG  C
GAM331 ADRA2A            GGCCGCA-GGGAGGCCGGGCCCG  5092 TG    T  C_      C
                         GCCGTG GGGA CCGGGCCCG
                         |||||| |||| |||||||||
                         CGGCGT CCCT GGCCCGGGC
                         __    _   CC      T
GAM331 AIM1              TGGCCGTGTGCG--CTGCGCCC   5101        GGACCCGG  G
                         TGGCCGTGTG      GCCC
                         ||||||||||      ||||
                         ACCGGCACAC      CGGG
                           GCGACG__    I
GAM331 AIRE              TGGGCGCG-GGGACCCGGG      5099  C  T      CCC
                         TGG CGTG GGGACCCGGG
                         ||| |||| ||||||||||
                         ACC GCGC CCCTGGGCCC
                               C  _      |||
GAM331 ALPL              GGGCTTGTGGGTGCCCGGGCCC   5091 T  CG   A_      GC
                         GGC TGTGGG CCCGGGCCC
                         ||| ||||||  |||||||||
                         CCG ACACCC GGGCCCGGG
                          _  A_   AC      AI
GAM331 ARSB              GCCGCCTCCGACCCGGGCCC     5084 TG GTGTGG       G
                         GCC    GACCCGGGCCC
                         |||    |||||||||||
```

```
                          CGG     CTGGGCCCGGG
                        G_  AGG___          G
GAM331  BCAT1           TGGCCGTGT-GGA-CCGGGTCTGC  5103          AC    CCC
                        TGGCCGTGTGGG CCGGG  GC
                        |||||||||| ||||| ||
                        ACCGGCACACCT GGCCC  CG
                                __    AGA
GAM331  CELSR1          GCCGTGTGGCAACCGTGCCC     5085 TGGC    _  CGG   G
                          CGTGTGG GACC  GCCC
                          ||||||| |||| ||||
                          GCACACC TTGG  CGGG
                          ____    G  CA_  G
GAM331  CHRNA4          GGCCGCTTCGGCCGCCGGGCCCG  5093 TG    GTG  AC_      CI
                          GCCGT  GG  CCGGGCCCG
                          |||||  ||  |||||||||
                          CGGCG  CC  GGCCCGGGC
                          __    AAG  GGC       CI
GAM331  CLTB           GCCGCG-GGGAGCCGGGCCCG     5086 TGGC   T   C
                          CGTG GGGA CCGGGCCCG
                          |||| |||| |||||||||
                          GCGC CCCT GGCCCGGGC
                          ____   _   C
GAM331  DIA1           TGGCCGTGT--GACCGGTGCCCG   5102         GAC   _   C
                          TGGCCGTGTGG  CCGG GCCCG
                          ||||||||||  |||| |||||
                          ACCGGCACACT  GGCC CGGGC
                          ___    A   I
GAM331  DXYS155E        TGTGGGACCTCCGGGACCG      5104 TG  GTG    C  CCCG
                          GCC  TGGGACC GGG
                          |||  ||||||| |||
                          TGG  GCCCTGG CCC
                          __  AG_   _  ACAC
GAM331  FGFR1           GCCCTGCGGAGGCCCCGGGCCCGC 5082 TGG _  TG  A        I
                          CC GTG  GG CCCGGGCCCGC
                          || ||| || |||||||||||
                          GG CGC  CC GGGCCCGGGCG
                          ___  A  CT  G         C
GAM331  FHIT           TGGCCGCCTGAGGGACCCGGG     5097     G __       CCCGC
                          TGGCCGT T GGGACCCGGG
                          ||||||| | |||||||||||
                          ACCGGCG A CCCTGGGCCC
                          G CT         IIICG
GAM331  GNA11          GGCCGAGCGGGGACCCGGCGGCTCGC 5090 TG  T   _   __ C II
                          GCCG GTGGG ACCCGG  GC CGC
                          |||| ||||| |||||| || |||
                          CGGC CGCCC TGGGCC  CG GCG
                          __   T   C   GC  A  GI
GAM331  HPN            GGCCAGGGTGGGACCCTGG        5087 TG   T_     _  CCCG
                          GCCG GTGGGACCC GGG
                          |||| ||||||||| |||
```

```
                              CGGT  CACCCTGGG CCC
                              __    CC       A  IIIC
GAM331  IRS2              GGTCCTGTGGGACCCCGCC      5094 TGG  G      GG  CG
                              CC TGTGGGACCC  GCC
                              || |||||||||| |||
                              GG ACACCCTGGG  CGG
                              CA_  _         GG  TI
GAM331  IRS2              GGCCGCGCGG--CCCGGGCCCG   5096 TG      GA
                              GCCGTGTGG CCCGGGCCCG
                              ||||||||| ||||||||||
                              CGGCGCGCC GGGCCCGGGC

                              __        __
GAM331  MSF              CCG-GCGGGGCCCGGGCCC      5080 TGGCCGT   A
                              GTGGG CCCGGGCCC
                              ||||| |||||||||
                              CGCCC GGGCCCGGG
                              _____      C
GAM331  NEK4            GGCTGTTGAGGCAGCCGGGCCCG   5088 TG  C  GT  AC_      CI
                              GC GT GGG  CCGGGCCCG
                              || || ||| ||||||||||
                              CG CA TCC  GGCCCGGGC
                              __  A  AC  GTC      CI
GAM331  NFRKB           GGCCGTGACGGCGGCTCCGGGCCCG 5089 TG      _ __AC      CII
                              GCCGTG TGG G CCGGGCCCG
                              |||||| ||| | ||||||||||
                              CGGCAC GCC C GGCCCGGGC
                              __    T  GC GA      CII
GAM331  PAFAH1B1          TGGC-GCGCTGGG-CCCGGGCCCG 5098  _ G  A      C
                              TGGC CGT TGGG CCCGGGCCCG
                              |||| ||| |||| |||||||||||
                              ACCG GCG ACCC GGGCCCGGGC
                              C  _  _      I
GAM331  SLC25A13          TGGC-GTTTGGGACCCGGGC     5100  C G      CCG
                              TGGC GT TGGGACCCGGGC
                              |||| || |||||||||||
                              ACCG CA ACCCTGGGCCCG
                              _  A      III
GAM331  SMURF1           GCCGTGTGGCACACACCTGGC    5083 TGGC   G ___ G  CCGC
                              CGTGTGG AC  CC GGC
                              ||||||| ||  || |||
                              GCACACC TG  GG CCG
                              ____      G  TGT A  ACII
GAM331  TBX1             GGCAGGGTGG---CCGGGCCCG   5095 TG CGT   GAC
                              GC GTGG  CCGGGCCCG
                              || |||| |||||||||
                              CG CACC  GGCCCGGGC
                              __ TCC  ___
GAM331  ZNF9            CCGCGTCGGAGC-GGGCCCGC     5081 TGGCCGT G  CC
                              GT GGA CGGGCCCG
                              || ||| |||||||
```

```
                        CA CCT  GCCCGGGC
                      G_____  G  C_
GAM332  AKAP2         GGCAGAGCTGTGCGCACGGC    5117         C  G  I
                      GCGGAGCTGTGC CA GG
                      ||||||||||| || ||
                      CGTCTCGACACG GT CC
                              C  G  I
GAM332  AKAP2         GGCAGAGCTGTGCGCACGGC    5117 TG       C  G  TG
                        GCGGAGCTGTGC CA GGC
                        |||||||||| || |||
                        CGTCTCGACACG GT CCG
                        __       C  G  CI
GAM332  FRAT2         CGGAGCTGTGC---GGGCT      5107         CCA
                      CGGAGCTGTGC  GGGC
                      ||||||||||  ||||
                      GCCTCGACACG  CCCG

                       ___
GAM332  FRAT2         CGGAGCTGTGC---GGGCT      5107 TGGCGG      CCA
                        AGCTGTGC  GGGC
                        ||||||||  ||||
                        TCGACACG  CCCG

                      _____   ___
GAM332  GGT2          TGGAAGAGGCGAGCCCAGGGCAGC  5122   C  C T     T I
                      TGG GGAG TG GCCCAGGGC GC
                      ||| |||| || |||||||| ||
                      ACC TCTC GC CGGGTCCCG CG
                       T  C T     T I
GAM332  GGT2          TGGAAGAGGCGAGCCCAGGGCAGC  5122   C  C T     TGI
                      GG GGAG TG GCCCAGGGC
                      || |||| || ||||||||||
                      CC TCTC GC CGGGTCCCG
                       T  C T     TCI
GAM332  LOXL1         GGCAGGGGCGGTGCCCAGGGCTGC  5114 GC A  T         I
                        GG GC GTGCCCAGGGCTG
                        || || |||||||||||||
                        CC CG CACGGGTCCCGAC
                      GT C  C         I
GAM332  LOXL1         GGCAGGGGCGGTGCCCAGGGCTGC  5114 TG  A_ T         I
                        GCGG  GC GTGCCCAGGGCTGC
                        |||| || |||||||||||||
                        CGTC CG CACGGGTCCCGACG
                        __   CC C        T
GAM332  MARK3         TGGCGGAGCCGAGCCTGCGGGCGGC 5121        T  CA_  T II
                      TGGCGGAGCTG GCC  GGGC GC
                      |||||||||| |||  |||| ||
                      ACCGCCTCGGC CGG  CCCG CG
                       T  ACG   C II
GAM332  MARK3         TGGCGGAGCCGAGCCTGCGGGCGGC 5121        T  CA_  TGI
                        GCGGAGCTG GCC  GGGC
                        |||||||| |||  ||||
```

```
                    CGCCTCGGC CGG   CCCG
                       T  ACG   CII
GAM332 OXTR             GCGGAGCTGGTTCGCCCAGCGTTG 5109 GG    ___      GGCTI
                         AGCTG  TGCCCAG
                         ||||| |||||||
                         TCGAC  GCGGGTC
                          __   CAA    GCAII
GAM332 OXTR             GCGGAGCTGGTTCGCCCAGCGTTG 5109 TGGC    ___       GGCTGCI
                         GGAGCTG  TGCCCAG
                         ||||||| |||||||
                         CCTCGAC  GCGGGTC
                          ____     CAA      GCAACCA
GAM332 P2RX7           GCGGAGCTG-GACCAGAGCT    5112 _      TG  C    I
                        CGGAGCTG CC AGGGC
                        |||||||| || |||||
                        GCCTCGAC GG TCTCG
                        C    CT _   I
GAM332 P2RX7           GCGGAGCTG-GACCAGAGCT    5112 TGGC    TG  C    G
                         GGAGCTG CC AGGGCT
                         ||||||| || ||||||
                         CCTCGAC GG TCTCGA
                          ____     CT _  G
GAM332 PIM2           GCGCAGCTGGGGAGCCAGGGCTG  5111 CGG   TGC__    I
                         AGCTG   CCAGGGCT
                         |||||   ||||||||
                         TCGAC   GGTCCCGA
                         G__   CCCTC     I
GAM332 RBBP9          GCGGAGCTGAGCCCA-GCCTGC   5113 _    T  G G I
                        CGGAGCTG GCCCA G CTG
                        |||||||| ||||| | |||
                        GCCTCGAC CGGGT C GAC
                        C    T   _G I
GAM332 RBBP9          GCGGAGCTGAGCCCA-GCCTGC   5113 TGGC    T   G G
                         GGAGCTG GCCCA G CTGC
                         ||||||| ||||| | ||||
                         CCTCGAC CGGGT C GACG
                          ____     T  _G
GAM332 SLC1A2         GAGCGATGCGCCCAGGGCTGC    5108   __           III
                        GAGC TGTGCCCAGGGCTG
                        |||| ||||||||||||||
                        CTCG ACGCGGGTCCCGAC
                          CT       GII
GAM332 SLC1A2         GAGCGATGCGCCCAGGGCTGC    5108 TGGCGGAGC
                          TGTGCCCAGGGCTGC
                          |||||||||||||||
                          ACGCGGGTCCCGACG
                        T_____
GAM332 SLC22A12       TGGCGG--CTGTGGGATGCCAGGGCTGC5120   GA   C____       II
                         TGGCG GCTGTG   CCAGGGCTGC
                         ||||| ||||||   |||||||||
```

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                          ACCGC CGACAC    GGTCCCGACG
                           __      CCTAC       II
GAM332 SLC22A12      TGGCGG--CTGTGGGATGCCAGGGCTGC5120 _ GGAGCT   C    I
                          GGC    GTGCC AGGGCTG
                          III    IIIII IIIIIII
                          CCG    TACGG TCCCGAC
                          G  ACACCC   _      I
GAM332 SYN1         GGCGGACTGCGCGGTGCCCAGG    5115     ____ T    IIIC
                          GGCGGA   GC GTGCCCAG
                          IIIIII   II IIIIIIII
                          CCGCCT   CG CACGGGTC
                           GACG  C      CIII
GAM332 SYN1         GGCGGACTGCGCGGTGCCCAGG    5115 TG   ____ T       CTGC
                          GCGGA   GC GTGCCCAGGG
                          IIIII   II IIIIIIIIII
                          CGCCT   CG CACGGGTCCT
                           __   GACG  C       IIIC
GAM332 TADA2L       TGGTAGAGCTACGCGCTCCAGGGCTG 5119  CG   __ _      CII
                          TGG GAGCT GTGC CCAGGGCTG
                          III IIIII IIII IIIIIIIII
                          ACC CTCGA CGCG GGTCCCGAC
                          AT   TG   A       III
GAM332 TADA2L       TGGTAGAGCTACGCGCTCCAGGGCTG 5119 GGC   __ _       I
                          GGAGCT GTGC CCAGGGCT
                          IIIIII IIII IIIIIIIII
                          TCTCGA CGCG GGTCCCGA
                          ___     TG   A     I
GAM332 TIRAP       TGGCAGAGCAACTG-GCACAGGGCTGC5118        ___ T C      II
                          TGGCGGAGC TG GC CAGGGCTGC
                          IIIIIIIII II II IIIIIIIII
                          ACCGTCTCG  AC CG GTCCCGACG
                          TTG _ T        II
GAM332 TIRAP       TGGCAGAGCAACTG-GCACAGGGCTGC5118 GG   ___ T C      I
                          CGGAGC TG GC CAGGGCTG
                          IIIIII II II IIIIIIIII
                          GTCTCG  AC CG GTCCCGAC
                          __      TTG _ T      I
GAM332 TRPC6         GGCAGACCGGTGCCCAGGG      5116     G _      II
                          GGCGGA CTG TGCCCAGG
                          IIIIII III IIIIIIIII
                          CCGTCT GGC ACGGGTCC
                          _   C      CI
GAM332 TRPC6         GGCAGACCGGTGCCCAGGG      5116 TG   G _       CTG
                          GCGGA CTG TGCCCAGGG
                          IIIII III IIIIIIIIII
                          CGTCT GGC ACGGGTCCC
                          __   _ C      CII
GAM332 UNG         GCGGA-CAGTAAGAGCCCAGGGCTG 5110 _ AGCTGT      I
                          CGG    GCCCAGGGCT
                          III    IIIIIIIIII
```

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                              GTC    CGGGTCCCGA
                          T  ATTCT_         I
GAM332 UNG            GCGGA-CAGTAAGAGCCCAGGGCTG 5110 T   AGCTGT      CI
                         GGCGG    GCCCAGGGCTG
                         |||||    |||||||||||
                         CTGTC    CGGGTCCCGAC
                         C  ATTCT_         CC
GAM333 CASP8         CCAGCTA---AAAACATTCTCA  5127 GCCT   TGA
                        GCTA  AAAACATTCTCA
                        ||||  |||||||||||
                        CGAT  TTTTGTAAGAGT
                        GT__    ___
GAM333 DCK          CCTGCTATGAGAAATAATGTC    5126 GC      AAAACATTCTCAC
                        CTGCTATGA
                        |||||||||
                        GACGATACT
                        __        CTTTATTACAGAI
GAM333 EYA1         GCTGTGCTAAAACATTCTCA     5132 GCC   TGAA
                        TGCTA  AAACATTCTCA
                        |||||  |||||||||||
                        ACGAT  TTTGTAAGAGT
                        ___    ____
GAM333 F11          TGTTATGTAA--CATTCTC     5133 GCCTGC  AAA
                           TATG  AACATTCTC
                           ||||  |||||||||
                           ATAC  TTGTAAGAG
                        _____     A__
GAM333 MAP3K9       GCCT-CT-TGGCGAACATTCTC   5131   G A AAA      A
                        GCCT CT TG  AACATTCTC
                        |||| || ||  |||||||||
                        CGGA GA AC  TTGTAAGAG
                        _ _ CGC     I
GAM333 PSMB2        CCTGTCTCTATGAAAAACA      5125 GC__ G         TCTCA
                        CT CTATGAAAAACAT
                        || |||||||||||||
                        GA GATACTTTTGTG
                        GACA _       IIICA
GAM333 SYT4         TGATATCAAACACATTCTCA     5134 GCCTGC  G  A
                        TAT AAA ACATTCTCA
                        ||| ||| |||||||||
                        ATA TTT TGTAAGAGT
                        _____  G  G
GAM333 TEM5         CTGCTA-GAAA-ACATTCT      5128 GCCT   T  A    C
                        GCTA GAAAA CATTCT
                        |||| ||||| ||||||
                        CGAT CTTTT GTAAGA
                        ____  _  _    T
GAM333 ZNF132       CTTCTAC-AGAAACATTCT      5129 GC   TATGAA      C
                        CTGC    AAACATTCT
                        ||||    |||||||||
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                             GATG      TTTGTAAGA
                        A_    TC____          C
GAM333   ZNF133         GCCTG-TAACACAAAACATTC    5130    CT  A      TCA
                        GCCTG ATG AAAACATTC
                        ||||| ||| |||||||||
                        CGGAC TGT TTTTGTAAG
                          AT  G      |||
GAM334   B3GALT2        ATTGTCTCTTGTAGTCA    5137 TA      CTTTCGCCACCT
                        TTGTCTCTC
                        |||||||||
                        AACAGAGAG
                        __        AACATCAGTAII
GAM334   CEP1           GTCTCCTTCCTCTGGCCAC    5139 TATTG TC    C   CTC
                        TC TCCTTT GCCAC
                        || |||||| |||||
                        AG AGGAGA CGGTG
                        G____ GA   C   TAC
GAM334   FKRP           TTGTCTCTCCAGTCCCAC      5143 TATT    TT G  CT
                        GTCTCTCC TC CCAC
                        |||||||| || ||||
                        CAGAGAGG AG GGTG
                        ____      TC  G   TT
GAM334   GAB2           TTGTCTCT-CTATTGCTAGCCTC  5142 TATT    CT C CA_
                        GTCTCTC TT GC  CCTC
                        ||||||| || || ||||
                        CAGAGAG AA CG  GGAG
                        ____          AT _ ATC
GAM334   HYAL3          TCTCACTCAGTCGCCACCTC    5140 TATTGTCT  CTT
                        CTC  TCGCCACCT
                        |||  |||||||||
                        GAG  AGCGGTGGA
                        _____   TC_
GAM334   IHPK3          TTGTCTCTCAGTGC-CCACC    5144 TATT    CTTTCG   T
                        GTCTCTC    CCACC
                        |||||||    |||||
                        CAGAGAG    GGTGG
                        ____      TCACG_   T
GAM334   MECP2          GTCTCTCCTCCTCGCCTCCTC   5138 TATTGTCT   _   A
                        CTCCTT TCGCC CCTC
                        |||||| ||||| ||||
                        GAGGAG AGCGG GGAG
                        _____      G   A
GAM334   ZIC1           TCTCTCCTTTCTCTCACGCTC   5141 TATTG   CT_   ACCTC
                        TCTCTC TTCGCC
                        |||||| ||||||
                        AGAGAG GAGCGG
                        GGAA_     TGC   AGIII
GAM335   ACHE           GGGAGGGGAGGACGGCACGA     5156         CA  I
                        GGAGGGGAGGGC CACG
                        |||||||||||| ||||
```

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                              CCTCCCCTCCTG GTGC
                                   CC     I
GAM335 ACHE          GGGAGGGGAGGACGGCACGA     5156 TG         CA    TG
                          GGAGGGGAGGGC CACGA
                          IIIIIIIIIII IIIII
                          CCTCCCCTCCTG GTGCT
                              __         CC    CI
GAM335 BCL7A         GGAGGGGAGAG-CACAGCGAGTGC  5151        C _  TGI
                         AGGGGAGGGC ACA CGA
                         IIIIIIIIII III III
                         TCCCCTCTCG TGT GCT
                             _   C  CAI
GAM335 BCL7A         GGAGGGGAGAG-CACAGCGAGTGC  5151 TGGG        C _  _  I
                          AGGGGAGGGC ACA CGA TGC
                          IIIIIIIIII III III III
                          TCCCCTCTCG TGT GCT ACG
                            ____        _  C  C  G
GAM335 CELSR1         GGCGGGGAGGGCCCACACCAT     5150 GA      _   GAI
                          GGGGAGGGCC ACAC
                          IIIIIIIIII IIII
                          CCCCTCCCGG TGTG
                          G_       G  GTI
GAM335 CELSR1         GGCGGGGAGGGCCCACACCAT     5150 TGGGA      _  G GC
                            GGGGAGGGCC ACAC AT
                            IIIIIIIIII IIII II
                            CCCCTCCCGG TGTG TA
                          G____        G  G GG
GAM335 CNTN2         TGGGAGCAGGCAGGGCCACA     5158    _  _      CGATG
                          TGGGAG GGG AGGGCCACA
                          IIIIII III IIIIIIIII
                          ACCCTC TCC TCCCGGTGT
                            G  G      IIICG
GAM335 CNTN2         TGGGAGCAGGCAGGGCCACA     5158    _  _      III
                          TGGGAG GGG AGGGCCAC
                          IIIIII III IIIIIIII
                          ACCCTC TCC TCCCGGTG
                            G  G     TII
GAM335 CRHR2           GGGAGGGGA----CACAGGA    5154      GGGC  C
                          GGGAGGGGA  CACA
                          IIIIIIIII  IIII
                          CCCTCCCCT  GTGT
                             ____   C
GAM335 CRHR2           GGGAGGGGA----CACAGGA    5154 TG     GGGC  C
                          GGAGGGGA   CACA GA
                          IIIIIIII   IIII II
                          CCTCCCCT   GTGT CT
                          __      ____   C
GAM335 DRPLA          GGGAGGGGCAGGGGTGGCACACGATGC5153 _  _    AG  C      I
                          GG AGGGG GGC ACACGATG
                          II IIIII III IIIIIIII
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                        CC TCCCC  CCG TGTGCTAC
                         C  G    A_  _     I
GAM335 DRPLA          GGGAGGGGCAGGGGTGGCACACGATGC5153 TG    _  C___        III
                        GGAGGGG AGGG  CACACGATGC
                        |||||| |||| |||||||||||
                        CCTCCCC TCCC  GTGTGCTACG
                          __   G  CACC     AII
GAM335 GFPT2          GGAGGGATGTGGGCCACAC    5148    A__      III
                        GGAGGGG GGGCCACA
                        ||||||| ||||||||
                        CCTCCCT CCCGGTGT
                           ACA      GII
GAM335 GFPT2          GGAGGGATGTGGGCCACAC    5148 T  GGGGA      ATG
                        GGGA   GGGCCACACG
                        ||||   ||||||||||
                        CCCT   CCCGGTGTGT
                         T  ACA__      GII
GAM335 KIAA0857       GGGAGGGGGAAGACAGCAGGA    5155        CA CGI
                        GGAGGGGAGGGC CA
                        |||||||||||| ||
                        CCTCCCCTTCTG GT
                          TC  CCI
GAM335 KIAA0857       GGGAGGGGGAAGACAGCAGGA    5155 TG      CA C TG
                        GGAGGGGAGGGC CA GA
                        |||||||||||| || ||
                        CCTCCCCTTCTG GT CT
                         __      TC C TI
GAM335 KIAA0857       TGGGAGGGGGACGCCACAC    5160      A _    GATG
                        TGGGAGGGG GG GCCACAC
                        ||||||||| || |||||||
                        ACCCTCCCC CT CGGTGTG
                          _ G    IIIC
GAM335 KIAA0857       TGGGAGGGGGACGCCACAC    5160      A _    II
                        TGGGAGGGG GG GCCACA
                        ||||||||| || ||||||
                        ACCCTCCCC CT CGGTGT
                          _ G    GI
GAM335 MEF2D          GGGAGGGGGAGGGCCATTAGATG  5152 GA      CAC  I
                        G GGGGAGGGCCA  GAT
                        | ||||||||||  |||
                        C CCCCTCCCGGT CTA
                         TC      AAT I
GAM335 MEF2D          GGGAGGGGGAGGGCCATTAGATG  5152 T GA      CAC  CI
                        GG GGGGAGGGCCA GATG
                        || |||||||||| ||||
                        CC CCCCTCCCGGT CTAC
                         _ TC      AAT TI
GAM335 MTM1           GGGAGGGGAAGCCAACACCAT    5157      G _ GAI
                        GGAGGGGAGG CCA CAC
                        ||||||||| ||| |||
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                              CCTCCCCTTC GGT GTG
                                 _   T  GTI
GAM335 MTM1              GGGAGGGGAAGCCAACACCAT   5157 TG      G _  G GC
                              GGAGGGGAGG CCA CAC AT
                              ||||||||| ||| ||| ||
                              CCTCCCCTTC GGT GTG TA
                              __      _  T  G  AI
GAM335 SOX13            TGGGAGGGGTGTTGGTCCCACA   5159      A___ G_  IIIT
                              TGGGAGGGG  GG  CCAC
                              |||||||||  ||  ||||
                              ACCCTCCCC  CC  GGTG
                               ACAA  AG   TIII
GAM335 SOX13            TGGGAGGGGTGTTGGTCCCACA   5159      AG__ _ A  ATGC
                              TGGGAGGGG  GG CC CACG
                              |||||||||  || || ||||
                              ACCCTCCCC  CC GG GTGT
                               ACAA  A  _   IIIC
GAM335 STIM1           GGAGGTTTGGGGGCCACACGCTG  5149 GAGG A      AI
                              GG GGGCCACACG
                              || ||||||||||
                              CC CCCGGTGTGC
                              CAAA _      GA
GAM335 STIM1           GGAGGTTTGGGGGCCACACGCTG  5149 T AGG A      AT_ I
                              GGG  GG GGGCCACACG  GC
                              |||  || |||||||||  ||
                              TCC  CC CCCGGTGTGC  CG
                              _  AAA _      GAC I
GAM335 TLR9            AGGGGAGGGTCAGACCAGGC     5147      C C GATGI
                              GGGGAGGG CA AC
                              |||||||| || ||
                              CCCCTCCC GT TG
                               A C GTCCI
GAM335 TLR9            AGGGGAGGGTCAGACCAGGC     5147 TGG   GA   CA ATG
                              GAGGG GGGCCA CG
                              ||||| ||||| ||
                              CTCCC TCTGGT GT
                              ___   AG   CC CCG
GAM336 AMPD1            TAGCACAGT----AGAAAAGA   5174      TGTC C  T
                              TAGCACAGT   AGA AAGA
                              |||||||||   ||| ||||
                              ATCGTGTCA   TCT TTCT
                              ____  T   I
GAM336 AMPD1            TAGCACAGT----AGAAAAGA   5174      TGTC_ CAI
                              TAGCACAGT   AGA
                              |||||||||   |||
                              ATCGTGTCA   TCT
                               TCTTT  III
GAM336 B4GALT5          CACAGCAATCAAAGACAAGATT  5168 AC  T __    I
                              AGT GTCA GACAAGAT
                              ||| |||| ||||||||
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                              TCG TAGT  CTGTTCTA
                              __   T  TT      I
GAM336 B4GALT5        CACAGCAATCAAAGACAAGATT   5168 TAGCAC  T  __       C
                         AGT GTCA  GACAAGATT
                         ||| |||| |||||||||
                         TCG TAGT  CTGTTCTAA
                         _____   T  TT      T
GAM336 EIF4A2         AGCA---TTG--AGACAAGATTC  5167 _  CAG  TC
                         GCA  TTG AGACAAGAT
                         |||  ||| |||||||||
                         CGT  AAC TCTGTTCTA
                           T  ___ __
GAM336 EIF4A2         AGCA---TTG--AGACAAGATTC  5167 TAGCACA   TC
                             GTTG  AGACAAGAT
                             ||||  |||||||||
                             TAAC  TCTGTTCTA
                          CG_____   __
GAM336 EN2           AGCACAGTTGTAAATAGA-AACATTC 5165       C  CA  TTI
                        ACAGTTGT AGA  AGA
                        ||||||||| |||  |||
                        TGTCAACA TTT  TCT
                          _  A_  TTG
GAM336 EN2           AGCACAGTTGTAAATAGA-AACATTC 5165 TA       C___  C G  II
                        GCACAGTTGT   AGA AA ATTC
                        |||||||||    ||| || ||||
                        CGTGTCAACA   TCT TT TAAG
                          __        TTTA _ G  TI
GAM336 HSD17B1       TATCACAGTTGTC---CATGCTTC  5175 AG       AGACAAI
                        CACAGTTGTC
                        ||||||||||
                        GTGTCAACAG
                        A_        GTACGAA
GAM336 HSD17B1       TATCACAGTTGTC---CATGCTTC  5175 TAG        AGACAAGATTC
                        CACAGTTGTC
                        ||||||||||
                        GTGTCAACAG
                        ATA        GTACGAAGIII
GAM336 IFNG          CACAGTTGTCA-ACAATATT     5171 _        A  GATI
                        ACAGTTGTCAG CAA
                        |||||||||| |||
                        TGTCAACAGTT GTT
                        G        _ ATAI
GAM336 IFNG          CACAGTTGTCA-ACAATATT     5171 TAGCAC     A  G
                        AGTTGTCAG CAA ATT
                        ||||||||| ||| |||
                        TCAACAGTT GTT TAA
                        _____       _  A
GAM336 M11S1         CACAGTTGTTTGGCCAGAT      5169        _____  CAAGAII
                        CACAGTTGT  CAGA
                        ||||||||   ||||
```

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                         GTGTCAACA   GTCT
                          AACCG   AIIIAGA
GAM336 MCF2        TAGCACAG-TGGCAG-CAA     5173      T T  A  GAT
                     TAGCACAGT G CAG CAA
                     IIIIIIIII I III III
                     ATCGTGTCA C GTC GTT
                          C _  _   III
GAM336 MCF2        TAGCACAG-TGGCAG-CAA     5173      T T  A  I
                     TAGCACAGT G CAG CA
                     IIIIIIIII I III II
                     ATCGTGTCA C GTC GT
                          C _  _ T
GAM336 MOCS2       AGCACAGTTCT-TCACAAGAATTC 5166      G_ AG    TTI
                     GCACAGTT TC ACAAGA
                     IIIIIIII II IIIIII
                     CGTGTCAA AG TGTTCT
                          GA __    TAA
GAM336 MOCS2       AGCACAGTTCT-TCACAAGAATTC 5166 TA     G_ AG    TTCI
                      GCACAGTT TC ACAAGA
                      IIIIIIII II IIIIII
                      CGTGTCAA AG TGTTCT
                         __    GA __    TAAG
GAM336 PLAC1       AGCACTTATTTGTCAGACA     5164    AG__      III
                       AGCAC  TTGTCAGAC
                       IIIII  IIIIIIIII
                       TCGTG  AACAGTCTG
                        AATA        TII
GAM336 PLAC1       AGCACTTATTTGTCAGACA     5164 TA  AG__       AGATT
                        GCAC  TTGTCAGACA
                        IIII  IIIIIIIIII
                        CGTG  AACAGTCTGT
                         __   AATA      AIIIC
GAM336 RDX         CACATTTGTCAGACGTGAT     5170    G      AAGAII
                       CACA TTGTCAGAC
                       IIII IIIIIIIII
                       GTGT AACAGTCTG
                        A      CACTAI
GAM336 RDX         CACATTTGTCAGACGTGAT     5170 TAGCACAG      AA T
                         TTGTCAGAC GAT
                         IIIIIIIII III
                         AACAGTCTG CTA
                      TA_____      CA  T
GAM336 SLC7A9      AGCAGCAG----CAGACAAGA   5163 GCA   T T
                       CAGT G CAGACAAG
                       IIII I IIIIIIII
                       GTCG C GTCTGTTC
                        TC_  T _
GAM336 SLC7A9      AGCAGCAG----CAGACAAGA   5163 TAGCA  T T
                        CAGT G CAGACAAGAT
                        IIII I IIIIIIIIII
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                            GTCG C GTCTGTTCTG
                            C____     T _
GAM336 STAU          CAGTC-TCAGACAAGTTTC    5172    G       ATTI
                        CAGTT TCAGACAAG
                        ||||| |||||||||
                        GTCAG AGTCTGTTC
                                _   AAAG
GAM337 ALCAM          TAACAGCAA--CTCCCAGAACAAA 5196        GT AG
                        TAACAGCAAT TC GGAACAAA
                        |||||||||| || ||||||||
                        ATTGTCGTTG AG TCTTGTTT
                                  __ GG
GAM337 ALCAM          TAACAGCAA--CTCCCAGAACAAA 5196 _       GT AG      I
                         AACAGCAAT TC GGAACAA
                         ||||||||| || |||||||
                         TTGTCGTTG AG TCTTGTT
                         A       __ GG       I
GAM337 ATP1A2        ACAGGAAGGTTCAGGGAAC      5186    C T       II
                        ACAG AA GTTCAGGGAA
                        |||| || |||||||||||
                        TGTC TT CAAGTCCCTT
                           C C       GI
GAM337 ATP1A2        ACAGGAAGGTTCAGGGAAC      5186 TAACAGCAAT        AA
                              GTTCAGGGAAC
                              |||||||||||
                              CAAGTCCCTTG
                        TCCTTC____          AA
GAM337 CDC23         AAAAGCA---TTCAGGGAAGAA  5181 C__   ATG      CI
                          AGCA  TTCAGGGAA
                          ||||  |||||||||
                          TCGT  AAGTCCCTT
                        TTT  ___      CI
GAM337 CDC23         AAAAGCA---TTCAGGGAAGAA  5181 TAAC  ATG      CAA
                          AGCA  TTCAGGGAA
                          ||||  |||||||||
                          TCGT  AAGTCCCTT
                        TT__  ___       CTT
GAM337 CLASP1        TAACAGCAAAGCATCA-GCAACA  5193     T TCA G  AA
                        TAACAGCAA GT  GG AACA
                        ||||||||| ||  || ||||
                        ATTGTCGTT CG  TC TTGT
                          T TAG G  II
GAM337 CLASP1        TAACAGCAAAGCATCA-GCAACA  5193     T _ G ACI
                        AACAGCAA GT TCAG GA
                        |||||||| || |||| ||
                        TTGTCGTT CG AGTC TT
                          T T  G GII
GAM337 FLNB          AACAGCAATATTTTAGGGA     5178          C_ II
                        AACAGCAATGTT AGGG
                        |||||||||| ||||
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                    TTGTCGTTATAA TCCC
                      AA    TI
GAM337 FLNB         AACAGCAATATTTTAGGGA     5178 TA      C_    ACAA
                    ACAGCAATGTT AGGGA
                    IIIIIIIIII IIIII
                    TGTCGTTATAA TCCCT
                      __       AA   AIII
GAM337 GJB3         CAGCGAAAATGTTCAGGGAA    5187 ___          III
                    CAGC AATGTTCAGGGA
                    IIII IIIIIIIIIII
                    GTCG TTACAAGTCCCT
                     CTT        TII
GAM337 GJB3         CAGCGAAAATGTTCAGGGAA    5187 TAACAGC        CAA
                    AATGTTCAGGGAA
                    IIIIIIIIIIII
                    TTACAAGTCCCTT
                  GCTT___        TTA
GAM337 GTF2E2       TAACAG-AAGGTTAACAGGGAACA 5194    C T __      AAI
                   TAACAG AA GTT CAGGGAACA
                   IIIIII II III IIIIIIIII
                   ATTGTC TT CAA GTCCCTTGT
                    _  C  TT     III
GAM337 GTF2E2       TAACAG-AAGGTTAACAGGGAACA 5194 A  C T __     I
                    ACAG AA GTT CAGGGAAC
                    IIII II III IIIIIIII
                    TGTC TT CAA GTCCCTTG
                    _  _ C TT    I
GAM337 HNF3B       AACAGCAATG--GAGGAGAACAA  5180 _      TTC _  I
                   ACAGCAATG AGG GAACA
                   IIIIIIIII III IIIII
                   TGTCGTTAC TCC CTTGT
                   T     C__ T  I
GAM337 HNF3B       AACAGCAATG--GAGGAGAACAA  5180 TA      TTC _   A
                   ACAGCAATG AGG GAACAA
                   IIIIIIIII III IIIIII
                   TGTCGTTAC TCC CTTGTT
                   __      C__ T   G
GAM337 IL12RB2     ACAGCCAT---CAGGGAAC      5185   AATGT
                   ACAGC  TCAGGGAA
                   IIIII  IIIIIIIII
                   TGTCG  AGTCCCTT
                    GT___
GAM337 IL12RB2     ACAGCCAT---CAGGGAAC      5185 TAAC  AATGT
                    AGC   TCAGGGAAC
                    III   IIIIIIIII
                    TCG   AGTCCCTTG
                    ____  GT___
GAM337 MCF2        CAGCAATGTTGGGAGGAAAAAA   5189 A     CA   ACAAI
                    GCAATGTT GGGA
                    IIIIIIII IIII
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                              CGTTACAA  CCCT
                          _      __    CCTTT
GAM337 MCF2        CAGCAATGTTGGGAGGAAAAAA  5189 TAACAG     CA   ACAAA
                          CAATGTT  GGGA
                          |||||||  ||||
                          GTTACAA  CCCT
                       _____     __    CCTTT
GAM337 NLGN3         CAGCAATGT--AGAGAGCA    5190      TC   ACI
                          CAGCAATGT  AGGGA
                          |||||||||  |||||
                          GTCGTTACA  TCTCT
                             __    CGT
GAM337 NLGN3         CAGCAATGT--AGAGAGCA       5190 TAACAG    TC    A
                          CAATGT  AGGGA CA
                          ||||||  ||||| ||
                          GTTACA  TCTCT GT
                       _____    __    C
GAM337 NPTX2        AACAG-AATATTGGTAGGGAACAAA 5179 A  C     C__       I
                          CAG AATGTT  AGGGAACAA
                          ||| ||||||  |||||||||
                          GTC TTATAA  TCCCTTGTT
                          _  _    CCA      I
GAM337 NPTX2        AACAG-AATATTGGTAGGGAACAAA 5179 TA   C    C__       I
                          ACAG AATGTT  AGGGAACAAA
                          |||| ||||||  ||||||||||
                          TGTC TTATAA  TCCCTTGTTT
                          __  _    CCA        G
GAM337 PPP2R4      TAAAAGCAATGGACAGTTCAGGGA 5192  C   _____       ACAAAI
                          TAA AGCAAT    GTTCAGGGA
                          ||| ||||||    |||||||||
                          ATT TCGTTA    CAAGTCCCT
                           T    CCTGT      IIIAAA
GAM337 PPP2R4      TAAAAGCAATGGACAGTTCAGGGA 5192  C   _____       IIIT
                          TAA AGCAAT    GTTCAGGG
                          ||| ||||||    ||||||||
                          ATT TCGTTA    CAAGTCCC
                           T    CCTGT      TIII
GAM337 PPP2R4      AACAGCAATG---AGGGTGCAA   5182        TTC  AAI
                          AACAGCAATG  AGGG
                          ||||||||||  ||||
                          TTGTCGTTAC  TCCC
                              ___  ACG
GAM337 PPP2R4      AACAGCAATG---AGGGTGCAA   5182 TA     TTC   AA
                          ACAGCAATG  AGGG  CAA
                          |||||||||  ||||  |||
                          TGTCGTTAC  TCCC  GTT
                          __     ___   AC
GAM337 PTPRN        ACAG--ATGTTCAGGGAAC     5184  CA       I
                          ACAG ATGTTCAGGGAA
                          |||| |||||||||||||
```

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                              TGTC  TACAAGTCCCTT
                               __         G
GAM337  PTPRN           ACAG--ATGTTCAGGGAAC      5184 TAACAGCA         A
                            ATGTTCAGGGAAC
                            |||||||||||||
                            TACAAGTCCCTTG
                        TC_____          A
GAM337  RNPEP           AACAGGAAT-TT--GGGAACAAA   5183    C  GTTCA      I
                        AACAG AAT   GGGAACA
                        ||||| |||   |||||||
                        TTGTC TTA   CCCTTGT
                          C  AA___      T
GAM337  RNPEP           CAGGAAGTTGATCAGGGAACA     5188 CAGCAA__ T      III
                            TG TCAGGGAAC
                            || |||||||||
                            AC AGTCCCTTG
                        GTCCTTCA  T      TII
GAM337  RNPEP           CAGGAAGTTGATCAGGGAACA     5188 TAACAGCAA  T      AA
                            TG TCAGGGAACA
                            || ||||||||||
                            AC AGTCCCTTGT
                        CTTCA____  T      CC
GAM337  ZFX             TAA-AGCACAGCTCAGGGAACA    5195 AAC   AT        I
                            AGCA  GTTCAGGGAAC
                            ||||  |||||||||||
                            TCGT  CGAGTCCCTTG
                        ATT  GT        I
GAM337  ZFX             TAA-AGCACAGCTCAGGGAACA    5195 TAAC   AT       AA
                            AGCA  GTTCAGGGAACA
                            ||||  ||||||||||||
                            TCGT  CGAGTCCCTTGT
                        ATT_  GT         II
GAM337  ZNF215          GCAATGGT--GGGAACAAA       5191     TTCA       I
                        GCAATG  GGGAACAA
                        ||||||  ||||||||
                        CGTTAC  CCCTTGTT
                          CA__       T
GAM338  APOD            AGTGGGTGCA-GCCTCCCTG      5206 _   _ CAT      I
                          GTGGG GC  GCCTCCCT
                          ||||| ||  |||||||||
                          CACCC CG  CGGAGGGA
                          T   A T__      I
GAM338  APOD            AGTGGGTGCA-GCCTCCCTG      5206 TACAAGT G CAT
                            GG GC  GCCTCCCT
                            || ||  |||||||||
                            CC CG  CGGAGGGA
                        _____ A T__
GAM338  ATP2B2          AGTGGGGCCCATGCTGCTCCCTG   5204 GT  G    __     I
                            GGG CCATGC CTCCCT
                            ||| |||||| ||||||
```

```
                        CCC GGTACG  GAGGGA
                        __   G    AC    I
GAM338 ATP2B2           AGTGGGGCCCATGCTGCTCCCTG  5204 TACAAGT  G     __      I
                        GGG CCATGC  CTCCCTG
                        ||| ||||||  |||||||
                        CCC GGTACG  GAGGGAC
                        _____   G    AC    C
GAM338 ATP2B4           ACCAGTGTCTCC-TGCCTCCCTG  5202 CA_   GGG  A       I
                        AGTG   CC TGCCTCCCT
                        ||||   || |||||||||
                        TCAC   GG ACGGAGGGA
                        TGG   AGA  _      I
GAM338 ATP2B4           ACCAGTGTCTCC-TGCCTCCCTG  5202 TACA   GGG  A       I
                        AGTG   CC TGCCTCCCTG
                        ||||   || ||||||||||
                        TCAC   GG ACGGAGGGAC
                        GG__   AGA  _
GAM338 CALM1            TACCAGTGGGGCCACGTCTC      5211  A        C  CCT
                        TAC AGTGGGGCCATG CTC
                        ||| |||||||||||| |||
                        ATG TCACCCCGGTGC GAG
                         G      A  III
GAM338 CALM1            TACCAGTGGGGCCACGTCTC      5211  A        C  I
                        AC AGTGGGGCCATG CT
                        || |||||||||||| ||
                        TG TCACCCCGGTGC GA
                         G      A  I
GAM338 CD79B            TGGAGGCCAGGGCCTCCCTG      5212  _    T_     III
                        TGG GGCCA GCCTCCCT
                        ||| ||||| |||||||||
                        ACC CCGGT CGGAGGGA
                         T   CC     CII
GAM338 GAB2             ACAAGCTGTCAGCCATGCCT      5199     GG__      III
                        ACAAGT  GGCCATGCC
                        ||||||  |||||||||
                        TGTTCG  TCGGTACGG
                          ACAG      AII
GAM338 GAB2             ACAAGCTGTCAGCCATGCCT      5199 TA  GG__      CCCT
                        CAAGT  GGCCATGCCT
                        |||||  ||||||||||
                        GTTCG  TCGGTACGGA
                          ACAG      CIII
GAM338 KCNQ1            CAGGTGGGGCCACTCTTGGCCTCCC 5207 TACAA      _____    GII
                        GTGGGGCCAT   GCCTCCCT
                        ||||||||||   ||||||||
                        CACCCCGGTG   CGGAGGGG
                          C____       AGAAC    AII
GAM338 NUMA1            ACAGGTGGGGCCA---CTCACTG   5201  A       GC_ CCI
                        ACA GTGGGGCCAT  CT
                        ||| |||||||||| ||
```

```
                         TGT CACCCCGGTG  GA
                          C        AGT  CII
GAM338 NUMA1        ACAGGTGGGGCCA---CTCACTG  5201 TA A      TGC  C
                         CA GTGGGGCCA  CTC CT
                         II IIIIIIIII  III II
                         GT CACCCCGGT  GAG GA
                         __  C        ___  T
GAM338 PTPRO       CATGTGTGGCCATGCCTCC      5208 CAA  G       II
                          GTG GGCCATGCCTC
                          III IIIIIIIIIII
                          CAC CCGGTACGGAG
                          GTA  A      GI
GAM338 PTPRO       CATGTGTGGCCATGCCTCC      5208 TACAA  G      CT
                          GTG GGCCATGCCTCC
                          III IIIIIIIIIIII
                          CAC CCGGTACGGAGG
                         A____  A      AA
GAM338 RNASE1     GTGGAGCTTCCATGCCTCCCTG   5209     ___       III
                         GTGGGGC CATGCCTCCCT
                         IIIIIII IIIIIIIIIII
                         CACCTCG GTACGGAGGGA
                          AAG       CII
GAM338 RNASE1     GTGGAGCTTCCATGCCTCCCTG   5209 TACAAGTGGGG
                             CCATGCCTCCCTG
                             IIIIIIIIIIIII
                             GGTACGGAGGGAC
                         CGAA_____
GAM338 RNMT       GTGGCTCCAGTAAGCCTCCCTG   5210   GG  T___       III
                         GTGG CCA  GCCTCCCT
                         IIII III  IIIIIIII
                         CACC GGT  CGGAGGGA
                          GA  CATT     CII
GAM338 SURF5      AGTGGA---AGGCCTCCCTG     5205 _    CCAT
                          GTGGGG  GCCTCCCT
                          IIIIII  IIIIIIII
                          CACCTT  CGGAGGGA
                          T   C___
GAM338 TM7SF2     AGTGGGGGCCATGGTCTCC      5203    _   C_  III
                          AGTGGGG CCATG CTC
                          IIIIIII IIIII III
                          TCACCCC GGTAC GAG
                           C   CA  GII
GAM338 TM7SF2     AGTGGGGGCCATGGTCTCC      5203 TACAAGT     C_   _
                          GGGGCCATG CTCC CT
                          IIIIIIIII IIII II
                          CCCCGGTAC GAGG GA
                         _____      CA  C
GAM338 TNNC2      ACAAG--GGGCCGCGCCTCCCTG  5200 CAAGT    A      I
                          GGGGCC TGCCTCCCT
                          IIIIII IIIIIIIII
```

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                        CCCCGG GCGGAGGGA
                       TGTT_      C        I
GAM338  TNNC2          ACAAG--GGGCCGCGCCTCCCTG    5200 TACAAGT     A
                       GGGGCC TGCCTCCCTG
                       ||||||  |||||||||||
                       CCCCGG GCGGAGGGAC
                      GTT____       C
GAM339  C4BPB          TCACTCAGAAGCAA-CAGC    5217       TTAA   I
                       TCACTCAGA  AGCAG
                       ||||||||||  |||||
                       AGTGAGTCT  TTGTC
                         TCG_   G
GAM339  ITGA4          TATCAAGAGCCACAGATTAAA    5215    TCA_ _       GCAGC
                       TATCA   CT CAGATTAAA
                       |||||   || |||||||||
                       ATAGT   GG GTCTAATTT
                        TCTC  T       |||CG
GAM339  ITGA4          TATCAAGAGCCACAGATTAAA    5215    TCA_ _      |||
                       TATCA   CT CAGATTAA
                       |||||   || ||||||||
                       ATAGT   GG GTCTAATT
                        TCTC  T      T||
GAM339  KRTHA7         TCCTCAGCTCA--TTAAAGCA    5218 CA A    ___        I
                       TC CTCAG  ATTAAAGC
                       || |||||  |||||||||
                       AG GAGTC  TAATTTCG
                       __ _    GAG      I
GAM339  NOS1           TATCATCACTGAAACGAATTAGCAG 5216 AT    C   T __   I
                       CATCACT AGAT AA  AGCA
                       ||||||| |||| || ||||
                       GTAGTGA TTTG TT  TCGT
                       __    C  C AA  I
GAM339  NOS1           TATCATCACTGAAACGAATTAGCAG 5216        C   T __    C||
                       TATCATCACT AGAT AA  AGCAG
                       |||||||||| |||| || |||||
                       ATAGTAGTGA TTTG TT  TCGTC
                          C  C AA    |||
GAM339  USH3A          TCCTCAC--AGCACTAAAGCAGC    5219 CA_  TC _       I
                       TCAC  AG ATTAAAGCAG
                       ||||  || |||||||||||
                       AGTG  TC TGATTTCGTC
                       AGG  __ G       I
GAM339  USH3A          TCCTCAC--AGCACTAAAGCAGC    5219 TATCA   TC _
                       TCAC  AG ATTAAAGCAGC
                       ||||  || ||||||||||||
                       AGTG  TC TGATTTCGTCG
                       G___  __ G
GAM340  ADAMTS8        ATCGGGTGCAAGGCCGA-CTCGG    5222 TATG       _  G   G
                       GGGTGCAAG TCGA TTCGG
                       ||||||||| |||| |||||
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                          CCCACGTTC GGCT GAGCC
                          AG__       C    _    G
GAM340  ADAMTS8           ATCGGGTGCAAGGCCGA-CTCGG   5222 TG       _   G    I
                          GGGTGCAAG TCGA TTCG
                          |||||||| |||| ||||
                          CCCACGTTC GGCT GAGC
                          AG        C    _    I
GAM340  EPHA1             TGGGGTGCAGAGCAGGGTTC      5227        AGTC   TII
                          TGGGGTGCA   GAGT
                          ||||||||    ||||
                          ACCCCACGT   CTCG
                                ____     TCC
GAM340  EPHA1             TGGGGTGCAGAGCAGGGTTC      5227 TATG    AGTC   TC
                          GGGTGCA   GAGT GG
                          |||||||   |||| ||
                          CCCACGT   CTCG CC
                          ____       ____    T_
GAM340  LARGE             GGTGCCAAGCACAGAGTTCGGG    5224     _   C__      III
                          GGTGC AAGT  GAGTTCGG
                          ||||| ||||  ||||||||
                          CCACG TTCG  CTCAAGCC
                            G    TGT     CII
GAM340  LARGE             GGTGCCAAGCACAGAGTTCGGG    5224 TATG  TG AGTC
                          GGG CA   GAGTTCGGG
                          ||| ||   |||||||||
                          TTC GT   CTCAAGCCC
                          G___    GT ____
GAM340  PDE4D             TATAAGGTGCAAGTAAAATTC     5225        C   GGG
                          TATGGGGTGCAAGT GAGTTC
                          ||||||||||||| ||||||
                          ATATCCACGTTCA TTTAAG
                                T   III
GAM340  PDE4D             TATAAGGTGCAAGTAAAATTC     5225        C   I
                          ATGGGGTGCAAGT GAGTT
                          ||||||||||||| |||||
                          TATTCCACGTTCA TTTAA
                                T    I
GAM340  PPARGC1           ATGGGGTGCA---CGTGTTC      5223        A CGAGTI
                          ATGGGGTGCA GT
                          |||||||||| ||
                          TACCCCACGT CA
                                G CAAGII
GAM340  PPARGC1           ATGGGGTGCA---CGTGTTC      5223 TA    AGT A
                          TGGGGTGCA  CG GTTCG
                          |||||||||  || |||||
                          ACCCCACGT  GC CAAGT
                           __     ___ A
GAM340  SHANK2            TATGGGGTGGAGG--GACTCCGGG  5226        CA TC G
                          TATGGGGTG AG GA TTCGGG
                          ||||||||| || || |||||
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                         ATACCCCAC TC CT AGGCCC
                            C_  C_  G
GAM340  SHANK2       TATGGGGTGGAGG--GACTCCGGG  5226 _      CA TC  G      I
                        ATGGGGTG  AG  GA TTCGG
                        ||||||||  ||  || |||||
                        TACCCCAC  TC  CT AGGCC
                           A    C_  C_  G    I
GAM341  ACK1         GAAAACATGGAACCGCGTGG     5240         _ TCTTGII
                        GAAAACATGGA CC
                        |||||||||| ||
                        CTTTTGTACCT GG
                            T CGCACCI
GAM341  ACK1         GAAAACATGGAACCGCGTGG     5240 TG       _ TCT  AAG
                        AAAACATGGA CC  TGG
                        |||||||||| || |||
                        TTTTGTACCT GG  ACC
                        __       T CGC  CII
GAM341  ADA         TGAGATCATGGTCTTCTTGGAAGG  5247  AAA    ACC       I
                       TGA  CATGG  TCTTGGAAGG
                       |||  |||||  ||||||||||
                       ACT  GTACC  AGAACCTTCC
                       CTA    AGA       I
GAM341  ADA         TGAGATCATGGTCTTCTTGGAAGG  5247 GAAAA    ACC       I
                          CATGG  TCTTGGAAG
                          |||||  |||||||||
                          GTACC  AGAACCTTC
                       CTCTA    AGA       I
GAM341  ADAMTS1       AACTATAGTCCTTCTTGGAAGG    5236 AC  A _       I
                        ATGG CCT CTTGGAAG
                        |||| ||| |||||||||
                        TATC GGA GAACCTTC
                         A_  A  A     I
GAM341  ADAMTS1       AACTATAGTCCTTCTTGGAAGG    5236 TGAAAAC  A _
                        ATGG CCT CTTGGAAGG
                        |||| ||| |||||||||
                        TATC GGA GAACCTTCC
                        _____  A  A
GAM341  COL15A1       GAAAACATGAAGGACATCTT      5239       ___  C  III
                        GAAAACAT GGAC TCT
                        |||||||| |||| |||
                        CTTTTGTA CCTG AGA
                            CTT  T  AII
GAM341  COL15A1       GAAAACATGAAGGACATCTT      5239 TG      ___  C   GAAG
                        AAAACAT GGAC TCTTG
                        ||||||| |||| |||||
                        TTTTGTA CCTG AGAAT
                          __    CTT  T  IIIG
GAM341  ITGB4BP      CATGGAACAACTTGGAAGG        5238    _ CT      II
                        CATGGA C CTTGGAAG
                        |||||| | ||||||||
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                          GTACCT G  GAACCTTC
                            T TT      CI
GAM341 KCNK10            TGATCACATGGACC-CTTG      5244   AA      T   GAA
                          TGA  ACATGGACC CTTG
                          III  IIIIIIIII IIII
                          ACT  TGTACCTGG GAAC
                            AG       _   III
GAM341 KCNK10            TGATCACATGGACC-CTTG      5244   AA        CTTI
                          TGA  ACATGGACCT
                          III  IIIIIIIIII
                          ACT  TGTACCTGGG
                            AG        AACI
GAM341 KCNS2            TGAAACACAAAAGGACCTCTTAAGAAG5242    _  T__      _  GIII
                          TGAAA ACA   GGACCTCTTG GAAG
                          IIIII III   IIIIIIIIII IIII
                          ACTTT TGT   CCTGGAGAAT CTTC
                            G   TTT         T   IIIG
GAM341 KCNS2            TGAAACACAAAAGGACCTCTTAAGAAG5242 GAAA  T__      _  I
                             ACA   GGACCTCTTG GAA
                             III   IIIIIIIIII III
                             TGT   CCTGGAGAAT CTT
                             G___  TTT         T  I
GAM341 LNK             AAAAATTTGACCTCTTGGA        5232 AAAACATG       II
                              GACCTCTTGG
                              IIIIIIIIII
                              CTGGAGAACC
                          TTTTTAAA         TI
GAM341 LNK             AAAAATTTGACCTCTTGGA        5232 TGAAAACATG        AG
                              GACCTCTTGGA
                              IIIIIIIIIII
                              CTGGAGAACCT
                          TTTAAA____         CG
GAM341 MBL2           TGAAAACATTGACTTTTTACAAG    5246      G CTC G  GI
                          TGAAAACAT GAC  TTG AAG
                          IIIIIIIII III  III III
                          ACTTTTGTA CTG  AAT TTC
                            A  AAA  G  II
GAM341 MBL2           TGAAAACATTGACTTTTTACAAG    5246      G  CTCTTGGAAI
                          GAAAACAT GAC
                          IIIIIIII III
                          CTTTTGTA CTG
                            A  AAAAATGTTI
GAM341 MLLT4          GAAAACAT-GACC-CTTGAAA      5241      G T  I
                          GAAAACATG ACC CTTGG
                          IIIIIIIII III IIIII
                          CTTTTGTAC TGG GAACT
                            _  _     T
GAM341 MLLT4          GAAAACAT-GACC-CTTGAAA      5241 TG    G T    G
                          AAAACATG ACC CTTGGAA
                          IIIIIIII III IIIIIII
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                              TTTTGTAC TGG GAACTTT
                              __      _  _     A
GAM341 PSG11        TGAAAACATTATCCTTTTG    5243      GGA  C  GAAG
                       TGAAAACAT  CCT TTG
                       ||||||||| ||| |||
                       ACTTTTGTA  GGA AAC
                        ATA  A  IIIG
GAM341 PSG11        TGAAAACATTATCCTTTTG    5243      GGA  CTTII
                       TGAAAACAT  CCT
                       ||||||||| |||
                       ACTTTTGTA  GGA
                        ATA  AAACI
GAM341 PSG9         TGAAAACATTATCCTTTTG     5243      GGA  C  GAAG
                       TGAAAACAT  CCT TTG
                       ||||||||| ||| |||
                       ACTTTTGTA  GGA AAC
                        ATA  A  IIIG
GAM341 PSG9         TGAAAACATTATCCTTTTG     5243      GGA  CTTII
                       TGAAAACAT  CCT
                       ||||||||| |||
                       ACTTTTGTA  GGA
                        ATA  AAACI
GAM341 RAG1         AAAAAAAGG--CTCTTGGAAG    5233 AAACAT_ AC       I
                         GG  CTCTTGGAA
                         || |||||||||
                         CC  GAGAACCTT
                       TTTTTTT __       I
GAM341 RAG1         AAAAAAAGG--CTCTTGGAAG     5233 TGAAAACAT AC
                         GG  CTCTTGGAAG
                         || |||||||||
                         CC  GAGAACCTTC
                       TTTTT____  __
GAM341 RFC1         AAAACATGGTTGCTCTGGGAA    5230 A      AC_  T  I
                        AACATGG  CTCT GGA
                        ||||||| |||| |||
                        TTGTACC  GAGA CCT
                        _    AAC   C   I
GAM341 RFC1         AAAACATGGTTGCTCTGGGAA    5230 TGAA      AC_   T
                        AACATGG  CTCT GGAAGG
                        ||||||| |||| ||||||
                        TTGTACC  GAGA CCTTTT
                          ____    AAC   C
GAM341 ROBO1        TGAAAACATTAATCACATGGA    5245       GGACCTCT  AGG
                       TGAAAACAT        TGGA
                       |||||||||        ||||
                       ACTTTTGTA        ACCT
                        ATTAGTGT   III
GAM341 SH2D1A       AAAAAAAGG--CTCTTGGAAG    5233 AAACAT_ AC       I
                         GG  CTCTTGGAA
                         || |||||||||
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                           CC  GAGAACCTT
                       TTTTTTT  __         I
GAM341  SH2D1A         AAAAAAAGG--CTCTTGGAAG    5233 TGAAAACAT AC
                           GG  CTCTTGGAAG
                           ||  |||||||||
                           CC  GAGAACCTTC
                       TTTTT____  __
GAM341  SLC13A1        AAAACATGGGCTTCTTGATGAAGG  5231 AA    ACC    __    I
                          ACATGG  TCTTG  GAAG
                          ||||||  ||||| ||||
                          TGTACC  AGAAC  CTTC
                          __    CGA   TA  I
GAM341  SLC13A1        AAAACATGGGCTTCTTGATGAAGG  5231 TGAA    ACC    __    I
                          AACATGG  TCTTG  GAAGG
                          |||||||  ||||| |||||
                          TTGTACC  AGAAC  CTTCC
                          ____      CGA   TA   G
GAM341  TRIM34         AAACATGGATAAATGGGAAGG    5235      CCTCTT   I
                          AACATGGA    GGAAG
                          ||||||||    |||||
                          TTGTACCT    CCTTC
                            ATTTAC    I
GAM341  TRIM34         AAACATGGATAAATGGGAAGG    5235 TGAAAA    CCTCTT
                            CATGGA    GGAAGG
                            ||||||    ||||||
                            GTACCT    CCTTCC
                            _____    ATTTAC
GAM341  TRPM2          AAACATGGAGGCCCTCTTGG    5234       ___      III
                          AAACATGGA  CCTCTTG
                          |||||||||  |||||||
                          TTTGTACCT  GGAGAAC
                            CCG    CII
GAM341  TRPM2          AAACATGGAGGCCCTCTTGG    5234 TGAAAA    ___      AAG
                           CATGGA  CCTCTTGG
                           ||||||  ||||||||
                           GTACCT  GGAGAACC
                           _____    CCG      CCT
GAM341  WISP1          ACA-GTACCTCTTGGCAGG    5237 TGG      AAGI
                          ACA  ACCTCTTGG
                          |||  |||||||||
                          TGT  TGGAGAACC
                          CA_      GTCC
GAM342  ATP5J          AGAAGCCAAACAGGAGGAGGA  5256       __      AGIII
                          AGAAGCCAA  GGGGGGA
                          |||||||||  |||||||
                          TCTTCGGTT  TCCTCCT
                            TG      CCTII
GAM342  ATP5J          AGAAGCCAAACAGGAGGAGGA  5256 TGAG    _____      AGTT
                           AAGCCAA  GGGGGGAAG
                           |||||||   |||||||||
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                              TTCGGTT    TCCTCCTTC
                    ____          TGTCC        IIIT
GAM342 BCL9         AGAAACTGAGGGGGGAA-AGT    5259 _    CA        AGI
                         GAAGC AGGGGGGAAG
                         IIIII IIIIIIIIII
                         CTTTG TCCCCCCTTT
                         T   AC        CII
GAM342 BCL9         AGAAACTGAGGGGGGAA-AGT    5259 TGAG   CA       A
                         AAGC  AGGGGGGA GAGT
                         IIII  IIIIIIII IIII
                         TTTG  TCCCCCCT TTCA
                         ____      AC      _
GAM342 CHRNB4       TGGGAAGCCCTGGG-GGAAGAG    5282  A    AAG       TT
                          TG GAAGCC  GGGGGAAGAG
                          II IIIIII  IIIIIIIIII
                          AC CTTCGG  CCCCCTTCTC
                          C   GA_       II
GAM342 CHRNB4       TGGGAAGCCCTGGG-GGAAGAG    5282 _ A    AAG      I
                           G GAAGCC  GGGGGAAGA
                           I IIIIII  IIIIIIIII
                           C CTTCGG  CCCCCTTCT
                          A C   GA_       I
GAM342 CISH         GAGAAGCCA----GGGCAGAGTT    5267     A  G  AGI
                         GAGAAGCCA GGG GGA
                         IIIIIIIII III III
                         CTCTTCGGT CCC TCT
                          _  G  CAA
GAM342 CISH         GAGAAGCCA----GGGCAGAGTT    5267 TG    A  G  AGAGT
                          AGAAGCCA GGG GGA
                          IIIIIIII III III
                          TCTTCGGT CCC TCT
                          __    _  G  CAACI
GAM342 COL1A1       TGAGAAGCCAGAGGCAGGTGGAGAG    5273      _  G  AA  TTII
                         TGAGAAGCCA AGG GGG  GAG
                         IIIIIIIIII III III  III
                         ACTCTTCGGT TCC TCC  CTC
                          C  G  AC  TCII
GAM342 COL1A1       TGAGAAGCCAGAGGCAGGTGGAGAG    5273 G    _  G  AAGAI
                          AAGCCA AGG GGG
                          IIIIII III III
                          TTCGGT TCC TCC
                          _   C  G  ACCTI
GAM342 CR1          AAACTAAGGGGGGAAAAGT       5251   C       II
                         AAGC AAGGGGGGAAGAG
                         IIII IIIIIIIIIIII
                         TTTG TTCCCCCCTTTTC
                              A        AI
GAM342 CR1          AAACTAAGGGGGGAAAAGT       5251 TGAGAAGCC
                            AAGGGGGGAAGAGT
                            IIIIIIIIIIII
```

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                              TTCCCCCCTTTTCA
                         A_____
GAM342 DBY               AAGC--AGGAGGGGAAGAGTT    5250 _   CA  _         I
                         AGC  AGG GGGGAAGAGT
                         III III IIIIIIIIII
                         TCG  TCC CCCCTTCTCA
                         T  __ T        I
GAM342 DGKB              AAGGAAATTGGGGAAGAGTT      5252 AGCCAAGG          I
                              GGGGAAGAGT
                              IIIIIIIIII
                              CCCCTTCTCA
                         TCCTTTAA           I
GAM342 DGKB              AAGGAAATTGGGGAAGAGTT      5252 TGAGAAGCCAAGG
                              GGGGAAGAGT
                              IIIIIIIIII
                              CCCCTTCTCA
                         TTTAA_____
GAM342 DHCR24            TGAGATCCCAGGGTGGGGAAGAG   5275    AG  A  _       TTI
                         TGAGA  CCA GG GGGGAAGAG
                         IIIII III II IIIIIIIIII
                         ACTCT  GGT CC CCCCTTCTC
                              AG  C  A        III
GAM342 DHCR24            TGAGATCCCAGGGTGGGGAAGAG   5275 G  AG  A  _       I
                         AGA  CCA GG GGGGAAGA
                         III III II IIIIIIIII
                         TCT  GGT CC CCCCTTCT
                         _  AG  C  A      I
GAM342 DSCR5            TGGGGAGCCGCAGTGGGGAAGAG    5274 GAGA  A_ G        I
                         AGCC  AG GGGGAAGA
                         IIII II IIIIIIIII
                         TCGG  TC CCCCTTCT
                         CCC_   CG A       I
GAM342 DSCR5            TGGGGAGCCGCAGTGGGGAAGAG    5274 TGAGA   A_ G      TTI
                         AGCC  AG GGGGAAGAG
                         IIII II IIIIIIIIII
                         TCGG  TC CCCCTTCTC
                         ACCCC   CG A      III
GAM342 EGR3            TGGGGACCCGAGGTGGGGAAGAGTT 5276 GA  AG  A  _        I
                         GA  CC AGG GGGGAAGAGT
                         II  II III IIIIIIIIIII
                         CT  GG TCC CCCCTTCTCA
                         CC G_ C  A        I
GAM342 EGR3            TGGGGACCCGAGGTGGGGAAGAGTT 5276 TGA_ AG  A  _       II
                         GA  CC AGG GGGGAAGAGTT
                         II  II III IIIIIIIIIII
                         CT  GG TCC CCCCTTCTCAA
                         ACCC G_ C  A      II
GAM342 FGF5            GAGAAGGGGAGAGGGGAAGAG     5265      CCA            I
                         AGAAG  AGGGGGGAAGA
                         IIIII  IIIIIIIIIIII
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                    TCTTC  TCTCCCCTTCT
                     CCC            I
GAM342 FGF5          GAGAAGGGGAGAGGGGAAGAG    5265 TG   CCA        TT
                     AGAAG  AGGGGGGAAGAG
                     |||||  ||||||||||||
                     TCTTC  TCTCCCCTTCTC
                     __     CCC         TI
GAM342 FOSB          TGAGGGGCCAAGGGGTGGGAGAAGTT 5277   AA      __  AG   II
                     TGAG  GCCAAGGGG  GGA AGTT
                     ||||  |||||||||  |||  ||||
                     ACTC  CGGTTCCCC  CCT TCAA
                          CC      AC  CT   II
GAM342 FOSB          TGAGGGGCCAAGGGGTGGGAGAAGTT 5277 AGAA      _ A  TI
                     GCCAAGGGG GG AGAG
                     ||||||||| || ||||
                     CGGTTCCCC CC TCTT
                    CCC_       A C   CI
GAM342 GDI2          GCGAAGGAAAGGGGAAGAG      5269 C   ___      III
                     GC AAGG  GGGGAAGA
                     || ||||  ||||||||
                     CG TTCC  CCCCTTCT
                      C  TTT      CII
GAM342 GDI2          GCGAAGGAAAGGGGAAGAG      5269 TGAGAAGCCA       T
                         AGGGGGGAAGAG
                         ||||||||||||
                         TTTCCCCTTCTC
                    C_____     T
GAM342 GJA5         TGAACAGCCAAGGGAGAAAG     5279  A        AGT
                     TGAG AGCCAAGGGGGGAAG
                     |||| ||||||||||||||
                     ACTT TCGGTTCCCTCTTTC
                          G        III
GAM342 GJA5         TGAACAGCCAAGGGAGAAAG     5279  A         I
                     GAG AGCCAAGGGGGGAA
                     ||| |||||||||||||
                     CTT TCGGTTCCCTCTTT
                         G        I
GAM342 HD           TGACAGGCACATGGGGGAAGAG   5281  GA C AG_      TT
                     TGA AG CA  GGGGGAAGAG
                     ||| || ||  ||||||||||
                     ACT TC GT  CCCCCTTCTC
                      G_ C GTA         II
GAM342 HD           TGACAGGCACATGGGGGAAGAG   5281 GAGA C AG_     I
                     AG CA  GGGGGAAGA
                     || ||  |||||||||
                     TC GT  CCCCCTTCT
                     CTG_ C GTA       I
GAM342 HOXA4        TGAGCTGCCTTAATGGGGGAAGAG 5272   AA AAG__       TTI
                     TGAG GCC   GGGGGAAGAG
                     |||| |||   ||||||||||
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                        ACTC  CGG    CCCCCTTCTC
                          GA   AATTA       III
GAM342 HOXA4            TGAGCTGCCTTAATGGGGGAAGAG  5272 GAGAA  AAG__      I
                        GCC    GGGGGAAGA
                        III   IIIIIIIII
                        CGG    CCCCCTTCT
                       CGA__   AATTA       I
GAM342 MAP1A           GAGAAGCCAAGCAGGGGATGAG   5263 A     _    A I
                       GAAGCCAAG GGGGGA GA
                       IIIIIIIII IIIIII II
                       CTTCGGTTC TCCCCT CT
                       _     G   A I
GAM342 MAP1A           GAGAAGCCAAGCAGGGGATGAG   5263 TG      _    A TT
                       AGAAGCCAAG GGGGGA GAG
                       IIIIIIIIII IIIIII III
                       TCTTCGGTTC TCCCCT CTC
                       __        G   A TI
GAM342 MAPK14          GAGAAGCCAAAGTGGCAAAAG     5264        _ G  AI
                       AGAAGCCAAGG GG GAAG
                       IIIIIIIIIII II IIII
                       TCTTCGGTTTC CC TTTT
                         A   G   II
GAM342 MAPK14          GAGAAGCCAAAGTGGCAAAAG     5264 TG      G G    T
                       AGAAGCCAAGG GG AAGAGT
                       IIIIIIIIIII II IIIIII
                       TCTTCGGTTTC CC TTTTCG
                       __        A G   I
GAM342 MYCL2           TGAGAAGCCAAAGGTGCCAGA     5280         GGGA  GTT
                       TGAGAAGCCAAGGG   AGA
                       IIIIIIIIIIIII   III
                       ACTCTTCGGTTTCC   TCT
                         ACGG  III
GAM342 MYCL2           TGAGAAGCCAAAGGTGCCAGA     5280         GGGAAGI
                       GAGAAGCCAAGGG
                       IIIIIIIIIIIII
                       CTCTTCGGTTTCC
                       ACGGTCI
GAM342 NDP             TGAGA-GCCAAGGGGGAAA     5278    A        GAG
                       TGAGA GCCAAGGGGGAA
                       IIIII IIIIIIIIIIII
                       ACTCT CGGTTCCCCCTTT
                       _           III
GAM342 NDP             TGAGA-GCCAAGGGGGAAA     5278    A       I
                       TGAGA GCCAAGGGGGA
                       IIIII IIIIIIIIII
                       ACTCT CGGTTCCCCCTT
                       _         T
GAM342 NESH           GAAGCCAAGGTCGGGGCAG      5261       __   AAIII
                       GAAGCCAAGG GGGG
                       IIIIIIIII IIII
```

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                        CTTCGGTTCC CCCC
                           AG   GTCII
GAM342 NESH              GAAGCCAAGGTCGGGGCAG    5261 TGAGAA     __   A AGT
                           GCCAAGG  GGGG AG
                           IIIIIII  IIII II
                           CGGTTCC  CCCC TC
                        _____       AG   G GAC
GAM342 NONO             GAGAGGTGAAAGGGGGAAGAG    5266   AGCC          I
                           AGA   AAGGGGGGAAGA
                           III   IIIIIIIIIIII
                           TCT   TTTCCCCCTTCT
                            CCAC          I
GAM342 NONO             GAGAGGTGAAAGGGGGAAGAG    5266 T AAGCC          TT
                            GAG    AAGGGGGGAAGAG
                            III   IIIIIIIIIIIII
                            CTC    TTTCCCCCTTCTC
                           T CAC__          TI
GAM342 NRG1             AGATGC-AAGGGGGGAAGA     5258  A C        I
                           AGA GC AAGGGGGGAAG
                           III II IIIIIIIIIII
                           TCT CG TTCCCCCCTTC
                            A _       T
GAM342 NRG1             AGATGC-AAGGGGGGAAGA     5258 TGAGAA C
                              GC AAGGGGGGAAGAG
                              II IIIIIIIIIIIII
                              CG TTCCCCCCTTCTT
                           TA____   _
GAM342 PABPN1          TGAGCAGGCCCAAGGGGGTGAAG   5271    AA_  _     _   AGTTI
                           TGAG  GCC AAGGGGG GAAG
                           IIII  III IIIIIII IIII
                           ACTC  CGG TTCCCCC CTTC
                            GTC  G    A  IIITT
GAM342 PABPN1          TGAGCAGGCCCAAGGGGGTGAAG   5271 GAGAAG      _ I
                              CCAAGGGGG GAA
                              IIIIIIIII III
                              GGTTCCCCC CTT
                           GTCCG_      A I
GAM342 PAK1           TGAGAGTCCAAGGGGGAAGGCGT   5283    AG     G A TI
                           TGAGA  CCAAGGGGG AAG GT
                           IIIII  IIIIIIIIII III II
                           ACTCT  GGTTCCCCC TTC CG
                            CA      _ _ CA
GAM342 PAK1           TGAGAGTCCAAGGGGGAAGGCGT   5283    AG        AGAGI
                           GAGA  CCAAGGGGGGA
                           IIII  IIIIIIIIIII
                           CTCT  GGTTCCCCCTT
                            CA        CCGCI
GAM342 RECQL5         GAGAAGCCAAAGCGCTGGGAA     5262          ____   III
                           GAGAAGCCAAGG  GGGGA
                           IIIIIIIIII  IIIII
```

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                              CTCTTCGGTTTC   CCCTT
                                   GCGA    III
GAM342  RECQL5         GAGAAGCCAAAGCGCTGGGAA   5262 TG       G___      GAGTT
                          AGAAGCCAAGG   GGGAA
                          |||||||||||   |||||
                          TCTTCGGTTTC   CCCTT
                            __       GCGA    AIIIT
GAM342  SLC3A2         AGAAGCCAAAGGGCCTGGGAAG   5255          ____      IIIC
                          AGAAGCCAAGGGG   GGAA
                          |||||||||||||   ||||
                          TCTTCGGTTTCCC   CCTT
                             GGAC   CIII
GAM342  SLC3A2         AGAAGCCAAAGGGCCTGGGAAG   5255 TGAG       ____       AGTT
                           AAGCCAAGGGG   GGAAG
                           |||||||||||   |||||
                           TTCGGTTTCCC   CCTTC
                          ____       GGAC    CTII
GAM342  SNRPA          AGAAGGCCCCCAAGGGGGGA   5254   ____        IIIT
                           AGAAG   CCAAGGGGGG
                           |||||   ||||||||||
                           TCTTC   GGTTCCCCCC
                            CGGG       TIII
GAM342  SNRPA          AGAAGGCCCCCAAGGGGGGA   5254 TGAGAAG       AGAGT
                            CCAAGGGGGGA
                            |||||||||||
                            GGTTCCCCCCT
                          TTCCGGG       GAIII
GAM342  STX1A          TGAGAAGCCCCAAGGTGGTGAGGAG 5270        A_   _ _  A  TTII
                           TGAGAAGCC AGGG GG GA GAG
                           ||||||||| |||| || || |||
                           ACTCTTCGG TTCC CC CT CTC
                             GG   A  A  C   IIIT
GAM342  STX1A          TGAGAAGCCCCAAGGTGGTGAGGAG 5270 AG    A_   _ GA  AI
                            AAGCC AGGG GG AG
                            ||||| |||| || ||
                            TTCGG TTCC CC TC
                            __    GG   A AC  CI
GAM342  SURF6          AGAAGCCAAGAGAGCGGGGAGGAG   5257 __ _  CAA      AGI
                           AGA AGC  GGGGGGA
                           ||| |||  |||||||
                           TCT TCG  CCCTCCT
                           GT  C  C__     CII
GAM342  SURF6          AGAAGCCAAGAGAGCGGGGAGGAG   5257 TGAG      ____    A   I
                           AAGCCAAGG   GGGGA GAGTT
                           |||||||||   ||||| |||||
                           TTCGGTTCT   CCCCT CTCGG
                          ____       CTCG   C  I
GAM342  TAGLN2         AGAACAGGCCA--GGGGGAAGA   5253 TGAGAA  AG      T
                           GCCA GGGGGAAGAG
                           |||| ||||||||||
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                            CGGT CCCCCTTCTT
                       TTGTC_   __        C
GAM342  TAGLN2         AGAACAGGCCA--GGGGGAAGA   5253  ___   AG      II
                          AGAA  GCCA GGGGGAAG
                          ||||  |||| |||||||||
                          TCTT  CGGT CCCCCTTC
                             GTC   __        TI
GAM342  TMOD           GAGAAGCCAAATGGGGATG-GTT   5268        G   AGAGI
                          AGAAGCCAAG GGGGA
                          |||||||||| |||||
                          TCTTCGGTTT CCCCT
                              A   ACCAI
GAM342  TMOD           GAGAAGCCAAATGGGGATG-GTT   5268 TG      G   AGAGTT
                           AGAAGCCAAG GGGGA
                           |||||||||| |||||
                           TCTTCGGTTT CCCCT
                          __        A   ACCAAC
GAM342  XBP1           GATGCCAAAAAGGGGGAAGAG    5260 GAA   __        III
                           GCCAA GGGGGGAAGA
                           ||||| ||||||||||
                           CGGTT TCCCCCTTCT
                         CTA   TT      CII
GAM342  XBP1           GATGCCAAAAAGGGGGAAGAG    5260 TGAGAA   __        TT
                           GCCAA GGGGGGAAGAG
                           ||||| |||||||||||
                           CGGTT TCCCCCTTCTC
                       _____      TT        TT
GAM343  DYRK1A         AAACTG----CTTTAGTTTT    5286     TATC
                          AAACTG  CTTTAGTT
                          ||||||  ||||||||
                          TTTGAC  GAAATCAA
                          ____
GAM343  GRIN2A         TAAACTGTATCC-ACAGTTT     5290 _        TT   I
                           AAACTGTATCC TAGTT
                           ||||||||||| |||||
                           TTTGACATAGG GTCAA
                           A        T_   I
GAM343  GRIN2A         TAAACTGTATCC-ACAGTTT     5290 TGTA       TT    T
                            AACTGTATCC TAGTTT
                            |||||||||| ||||||
                            TTGACATAGG GTCAAA
                            ____       T_   C
GAM343  HMGN2          AAACTGTATCC---AGCTTTA    5288 TGTAAA     TTT
                           CTGTATCC AGTTT
                           |||||||| |||||
                           GACATAGG TCGAA
                         _____       _____
GAM343  HMGN2          AAACTGTATCC---AGCTTTA    5288          TTT  I
                           AAACTGTATCC AGTTT
                           ||||||||||| |||||
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                        TTTGACATAGG  TCGAA
                            ___      A
GAM343 MRE11A           TAAACTGTAAACTCTTAGCTT    5289 A      TC   _   I
                            AACTGTA CTTT AGTT
                            ||||||| |||| ||||
                            TTGACAT GAGA TCGA
                            _       TT   A   I
GAM343 MRE11A           TAAACTGTAAACTCTTAGCTT    5289 TGTA    TC   _   TA
                            AACTGTA CTTT AGTTT
                            ||||||| |||| |||||
                            TTGACAT GAGA TCGAA
                            ___     TT   A   CA
GAM343 PPP2R2C            TGTATCCTTCGGGCCTTTTA    5295       A_   III
                            TGTATCCTTT GTTTT
                            |||||||||| |||||
                            ACATAGGAAG CGGAA
                                CC     AAT
GAM343 PTPRG           TGTAATACAGAGTTATCCTTTATTTT 5292   _ TG___      GTTTTAII
                            TGTAA AC   TATCCTTTA
                            ||||| ||   |||||||||
                            ACATT TG   ATAGGAAAT
                            A TCTCA       AAAAIIIA
GAM343 PTPRG           TGTAATACAGAGTTATCCTTTATTTT 5292 GTAAACTG     GI
                                TATCCTTTA
                                |||||||||
                                ATAGGAAAT
                            GTCTCA__      AA
GAM343 SLA             TAGACTGTATCCATTTCTTTT    5291 AA       TTTAGTTI
                            ACTGTATCC
                            |||||||||
                            TGACATAGG
                            C_       TAAAGAAA
GAM343 SLA             TAGACTGTATCCATTTCTTTT    5291 TGTAA     _ AG   A
                            ACTGTATCC TTT TTTT
                            ||||||||| ||| ||||
                            TGACATAGG AAA AAAG
                            C____       T  GA  A
GAM343 YWHAG           TGTCACCTGTATCCTGTTA     5293 AAA       TTAGTTTT
                            TGT CTGTATCCT
                            ||| |||||||||
                            ACA GACATAGGA
                            GTG       CAATIIIA
GAM343 YWHAG           TGTCACCTGTATCCTGTTA     5293 AAA       TTII
                            TGT CTGTATCCT
                            ||| |||||||||
                            ACA GACATAGGA
                            GTG       CAAT
GAM343 YWHAG           TGTAAACTGCA--ATTTAGTGTTA 5294        TCC   TTI
                            TGTAAACTGTA TTTAGT
                            |||||||||| ||||||
```

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                            ACATTTGACGT  AAATCA
                              T__      CAA
GAM343  YWHAG         TGTAAACTGCA--ATTTAGTGTTA  5294          TCC     TTTA
                      TGTAAACTGTA  TTTAGT
                      |||||||||| ||||||
                            ACATTTGACGT  AAATCA
                              T__      CAAT
GAM343  ZNF189          AAACTGTATACTT--GTTTTA   5287        C  TAGTTTI
                        AAACTGTAT CTT
                        ||||||||| |||
                        TTTGACATA GAA
                            T  CAAAATI
GAM344  ADRA1A        GGGTGGGCTCTGAGTGGTTGGG   5303 TAG  T     T_     ATG
                         GG GCTCTGAGT TTGGG
                         || ||||||||| |||||
                         CC CGAGACTCA AACCC
                        CA_  _     CC    CAI
GAM344  AKAP4         GGGTGCTCTG-G--CTGGGATG   5304 TAGG     A  TT
                        GTGCTCTG GT TGGGAT
                        |||||||| || ||||||
                        CACGAGAC CG ACCCTA
                        ____       _  __
GAM344  ASGR2         AGGTTGCTCTGAGGGCTGGG    5299 TA  G     TT    AT
                        GG TGCTCTGAG TTGGG
                        || ||||||||| |||||
                        CC ACGAGACTC GACCC
                        __  A      CC    CI
GAM344  DLST          AGGCTGCTCTGAG-CTTGGGA   5300 TA  G      T   T
                        GG TGCTCTGAGTTT GGGA
                        || ||||||||||| ||||
                        CC ACGAGACTCGAA CCCT
                        __  G      _   C
GAM344  PCDHA12       AGGGC-CTCTGAG--TTGGGA   5301 TA   G     TT
                        GGGT CTCTGAGT TGGGA
                        |||| |||||||| |||||
                        CCCG GAGACTCA ACCCT
                        __    _    __
GAM344  PDE4B         GGTGCTCTG---CCTGGGATG   5305 TAGGGT    AGT
                         GCTCTG TTTGGGA
                         |||||| |||||||
                         CGAGAC GGACCCT
                        _____    __
GAM344  PIGA          AGGGTAGCAGCTG-GTTTGGGATG 5298 TA   _ T_ A       I
                         GGGT GC  CTG GTTTGGGATG
                         |||| || ||| |||||||||||
                         CCCA CG  GAC CAAAACCCTAC
                        __   T TC _        C
GAM344  RAD50         AGAGAGCTCTGAGTCT--GGATG   5302 TA  T      TG
                         GGG GCTCTGAGTTT GGATG
                         ||| |||||||||| |||||
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                         CTC CGAGACTCAGA  CCTAC
                          __    T            __
GAM345  ACCN1          CAGAGTGTGACTCATCTCT      5324 AGTACAGATC  TT
                          GT  CTCATCTCT
                          ||  |||||||||
                          CA  GAGTAGAGA
                       CA_____   CT
GAM345  ADAR          AAAAACCAACGAAGTCCCTTC  5309      ___      III
                         AAAAACCAA  AGTCTCTT
                         |||||||||  |||||||||
                         TTTTTGGTT  TCAGGGAA
                         GCT     GII
GAM345  BCL9          CAAAGACTAAAGTCTCTGCT     5323  A C     TCI
                          AAA AC AAAGTCTCT
                          ||| || |||||||||
                          TTT TG TTTCAGAGA
                           C A     CGI
GAM345  BCL9          CAAAGACTAAAGTCTCTGCT     5323 TGACAAAA  C      T
                          AC AAAGTCTCT CT
                          || ||||||||| ||
                          TG TTTCAGAGA GA
                       TC_____  A      C
GAM345  CAPZB         ACAAAAACCACACGGTCTCT     5316      AA__    III
                         ACAAAAACCA   GTCTC
                         ||||||||||   |||||
                         TGTTTTTGGT   CAGAG
                          GTGC   AII
GAM345  CAPZB         ACAAAAACCACACGGTCTCT      5316 TGAC     AA__   TCT
                          AAAAACCA   GTCTCT
                          ||||||||   ||||||
                          TTTTTGGT   CAGAGA
                          ____        GTGC    TAI
GAM345  CD36          TACAAGCTCTGGTTCCTCATCTCT  5329 AGTACAGATC       AI
                         GTTTCTCATCTCT
                         |||||||||||||
                         CAAGGAGTAGAGA
                       GTTCGAGAC_         GA
GAM345  CHRNA10       AGTACAGTTCAGTTTCTCAT     5320      A _     CTCT
                         AGTACAG TC GTTTCTCAT
                         ||||||| || |||||||||
                         TCATGTC AG CAAAGAGTA
                          A  T      IIIA
GAM345  CLECSF5       TACAGAAGCGGACCTCATCTCTA  5330 AGTA  T_ TT      I
                         CAGA CG TCTCATCTCTA
                         |||| || |||||||||||
                         GTCT GC GGAGTAGAGAT
                         ____     TC CT      A
GAM345  CNR1          CAGAAACCAAAGTACTCCT     5322 AA        _   I
                         AAACCAAAGT CTCTTC
                         |||||||||| ||||||
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```
                    TTTGGTTTCA GAGAGG
                      C_       T     I
GAM345  CNR1        CAGAAACCAAAGTACTCTCCT    5322 TGACAA        _       G
                      AAACCAAAGT CTCTTCT
                      |||||||||| |||||||
                      TTTGGTTTCA GAGAGGA
                      _____          T    A
GAM345  COIL        TGACAAAAAACCAAAGATCT     5332          __    _  CTTCTG
                      TGACAAAA  ACCAAAG TCT
                      ||||||||  ||||||| |||
                      ACTGTTTT  TGGTTTC AGA
                        TT    T   IIIGTC
GAM345  COIL        TGACAAAAAAACCAAAGATCT     5332          __    _  III
                      TGACAAAA  ACCAAAG TC
                      ||||||||  ||||||| ||
                      ACTGTTTT  TGGTTTC AG
                        TT      T  AII
GAM345  DMD        GACAAAAACCAAA---TCTTC    5326 TG        GTC
                     ACAAAAACCAAA  TCTTC
                     ||||||||||||  |||||
                     TGTTTTTGGTTT  AGAAG

                     __       ___
GAM345  DMD        GACAAAAACCAAA---TCTTC    5326          G  CI
                     GACAAAAACCAAA TCT
                     ||||||||||||| |||
                     CTGTTTTTGGTTT AGA
                            _  AG
GAM345  DNMT3B      GTAGCAGA-C--TTCTCATCT     5328 AGTA   CGT      C
                     CAGAT  TTCTCATCT
                     |||||  |||||||||
                     GTCTG  AAGAGTAGA
                   ATC_    ___      C
GAM345  EFNB2        AAAACCAAAGTGCTGTGCT     5313          _  CTTCII
                     AAAACCAAAGT CT
                     |||||||||| ||
                     TTTTGGTTTCA GA
                        C  CACGAI
GAM345  EGFL5       AAAAACC-AAG-CCCTTCTG     5312 _      A  T    I
                     AAAACCAA GTC CTTCT
                     |||||||| ||| |||||
                     TTTTGGTT CGG GAAGA
                     T     _  _    I
GAM345  FIGF      ACAGAAAACCAAATAATCAGTTCTG 5314 CA       __  TC   I
                     AAAACCAAA GTC TTCT
                     ||||||||| ||| ||||
                     TTTTGGTTT TAG AAGA
                     __        AT  TC   I
GAM345  FIGF      ACAGAAAACCAAATAATCAGTTCTG 5314 TGACA      __  TC   II
                     AAAACCAAA GTC TTCTG
                     ||||||||| ||| |||||
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```
                        TTTTGGTTT TAG AAGAC
                        TC___       AT  TC   TA
GAM345 FUT8        AAAAACCAAACGTCCATTCT    5310        _   C  II
                        AAAAACCAAA GTCT TTC
                        ||||||||| |||| |||
                        TTTTTGGTTT CAGG AAG
                              G   T  AI
GAM345 FUT8        AAAAACCAAACGTCCATTCT    5310 TGACAAAA    _   C
                          ACCAAA GTCT TTCT
                          |||||| |||| ||||
                          TGGTTT CAGG AAGA
                        _____       G   T
GAM345 GBP1       AAAAATCCCATATTCTCTTCTG    5308 AAAA  AAG      I
                          CCA  TCTCTTCT
                          ||| ||||||||
                          GGT  AGAGAAGA
                          TTAG  ATA      I
GAM345 GBP1       AAAAATCCCATATTCTCTTCTG    5308 TGACAAAAA  AAG
                            CCA  TCTCTTCTG
                            ||| |||||||||
                            GGT  AGAGAAGAC
                        TAG_____  ATA
GAM345 GPR44       GACAATAGACCAAAGTCCCT    5325    AA_        II
                          GACAA  ACCAAAGTCTC
                          ||||| ||||||||||||
                          CTGTT  TGGTTTCAGGG
                          ATC          AI
GAM345 GPR44       GACAATAGACCAAAGTCCCT    5325 TG  AA_        TCT
                          ACAA  ACCAAAGTCTCT
                          |||| |||||||||||||
                          TGTT  TGGTTTCAGGGA
                        __  ATC         CII
GAM345 HOXB7      AAAAACCAAAATTTCTCCT    5311          C   II
                          AAAAACCAAAGT TCTTC
                          ||||||||||| |||||
                          TTTTTGGTTTTA AGAGG
                               A   AI
GAM345 HOXB7      AAAAACCAAAATTTCTCCT    5311 TGACAAAA     C
                          ACCAAAGT TCTTCT
                          |||||||| ||||||
                          TGGTTTTA AGAGGA
                        _____       A
GAM345 IPF1      ACAAAAACCAATGGCTCTT    5317         AGT  II
                          ACAAAAACCAA  CTCT
                          |||||||||| ||||
                          TGTTTTTGGTT  GAGA
                             ACC   AI
GAM345 IPF1      ACAAAAACCAATGGCTCTT    5317 TGAC    AGT   CT
                          AAAAACCAA  CTCTT
                          ||||||||| |||||
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```
                              TTTTTGGTT  GAGAA
                              ____        ACC     AA
GAM345  JRKL        TATAAATC-TTTCTCATC-CTA   5331 AGTAC    G      CT
                              AGATC TTTCTCATCT
                              ||||| |||||||||||
                              TTTAG AAAGAGTAGG
                           A____      _        AT
GAM345  KIF5C       TGAGAAAAGCCCAAAGTCTCCCCTG 5334   C   A_         II
                           TGA AAAA  CCAAAGTCTCTTCTG
                           ||| |||| ||||||||||||||
                           ACT TTTT  GGTTTCAGAGGGGAC
                              C  CG         II
GAM345  KIF5C       TGAGAAAAGCCCAAAGTCTCCCCTG 5334 _  C  AA        I
                            GA AAA  CCAAAGTCTCTTCT
                            || ||| ||||||||||||||
                            CT TTT  GGTTTCAGAGGGGA
                           T _  CG          I
GAM345  PCDHA11       ACATGATCTATTCTCATCTCT    5315 AGTACA  GT     A
                              GATC  TTCTCATCTCT
                              ||||  |||||||||||
                              CTAG  AAGAGTAGAGA
                           A_____    AT         C
GAM345  PPARBP       CAAAATGACCAAAGTC-CTTC   5321    __        CTTII
                              CAAAA  ACCAAAGTCT
                              ||||| ||||||||||
                              GTTTT  TGGTTTCAGG
                            AC         AAGII
GAM345  PPARBP       CAAAATGACCAAAGTC-CTTC   5321 TGACAAAA     T  T
                              ACCAAAGTC CTTC
                              ||||||||| ||||
                              TGGTTTCAG GAAG
                           TTAC____       _  T
GAM345  PTPN1       AGCAGAGATCAAAGTTTCTCATTTC 5319   C   ___      C  TAII
                           AGTA AGATC  GTTTCTCAT TC
                           |||| |||||  ||||||||| ||
                           TCGT TCTAG  CAAAGAGTA AG
                            C    TTT      A  IIIA
GAM345  RAG1        ACAGATCTTTGCTCATCTCT    5318 AGTACA   GTTT
                              GATC   CTCATCTCT
                              ||||   |||||||||
                              CTAG   GAGTAGAGA
                            _____      AAAC
GAM345  RET        TGATGAAAACCAAA-TGTCTTC   5336 _  CA      _   CTTI
                            GA  AAAACCAAA GTCT
                            ||  |||||||||| ||||
                            CT  TTTTGGTTT CAGA
                           A  AC      A  AIII
GAM345  RET        TGATGAAAACCAAA-TGTCTTC   5336   CA      GTC   TG
                            TGA  AAAACCAAA  TCTTC
                            |||  |||||||||  |||||
```

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                              ACT TTTTGGTTT AGAAG
                               AC     AC_   II
GAM345 SET7           GAAAAAAACCAAAG-CCATTCT   5327 AC        TCTI
                         AAAAACCAAAGTC
                         IIIIIIIIIIII
                         TTTTTGGTTTCGG
                         T_        TAAG
GAM345 SET7           GAAAAAAACCAAAG-CCATTCT   5327 TGAC       TC
                         AAAAACCAAAGTC TTCTG
                         IIIIIIIIIIII IIIII
                         TTTTTGGTTTCGG AAGAT
                        TT__       T_
GAM345 SLC22A1LS        TGACAAAAAAAAAGGTCTCT     5335      CC A  TCT
                        TGACAAAAA AA GTCTCT
                        IIIIIIIII II IIIIII
                        ACTGTTTTT TT CAGAGA
                          TT C    III
GAM345 SLC22A1LS        TGACAAAAAAAAAGGTCTCT     5335      CC A  I
                         GACAAAAA AA GTCTC
                         IIIIIIII II IIIII
                         CTGTTTTT TT CAGAG
                          TT C   I
GAM345 YWHAG          TGACAAAAAGCACAAAGGCTCATTC 5333     C__  T _ TGII
                       TGACAAAAA  CAAAG CTC TTC
                       IIIIIIIII  IIIII III III
                       ACTGTTTTT  GTTTC GAG AAG
                         CGT    C  T  IIIG
GAM346 ADD2          TCCAAGGCT---CCTTCTGT     5346     GTC A  G
                     TCCAAGGCT  CCT CTGT
                     IIIIIIIII  III IIII
                     AGGTTCCGA  GGA GACA
                         ___  A  I
GAM346 ATSV          TCCAAGGTGGCTGTCCCTGCCCTGCC 5344    ___     A G  III
                     TCCAA GGCTGTCCCT CT TGCC
                     IIIII IIIIIIIIII II IIII
                     AGGTT CCGACAGGGA GG ACGG
                       CCA      C G  III
GAM346 DEC1          CCAAGGCTGT-TCTAGCTG     5343 TC     CC _ TGC
                      CAAGGCTGT CTA CTG
                      IIIIIIIII III III
                      GTTCCGACA GAT GAC
                       __     A_  C TII
GAM346 DMPK          TCCCTGGCTGTCCC--CTGGGCC  5347 AA     TA T
                      TCC GGCTGTCCC CTG GCC
                      III IIIIIIIII III III
                      AGG CCGACAGGG GAC CGG
                       GA      __  C
GAM346 FXYD1         CCAATCGGGCTGTCCCCTGCTG  5342 TCCAA_     TA  GCCI
                       GGCTGTCCC CTGT
                       IIIIIIIII IIII
```

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                      CCGACAGGG GACG
                    GTTAGC       __   ACTI
GAM346 MEN1         TCCCAGGCATCTCCCTACTGT   5345  A  TG_        GCC
                    TCC AGGC  TCCCTACTGT
                    ||| ||||  ||||||||||
                    AGG TCCG  AGGGATGACA
                      G   TAG        |||
GAM346 SIM2         CAGGGCAGGTCCCTACTGTG    5340 TCCAA  T_       CC
                    GGC GTCCCTACTGTG
                    ||| ||||||||||||
                    CCG CAGGGATGACAC
                      C____  TC       AC
GAM346 UBE2I        CAAGGCTGTCTCGCACTGGGC   5341 TCCA     CC_   T C
                    AGGCTGTC  TACTG GC
                    ||||||||  ||||| ||
                    TCCGACAG  GTGAC CG
                      ____       AGC   C A
GAM346 WHSC1        AAGGCTGTCCCGTCCTGGTGC   5339 TCCAAG    TA_ _ C
                    GCTGTCCC  CTG TGC
                    ||||||||  ||| |||
                    CGACAGGG  GAC ACG
                      _____       CAG  C A
GAM347 ADAMTS5      CACAGACAAATGGCACTGGGATT  5352 TGAC   C _     GCI
                    ACAGA GG ACTGGGATTG
                    ||||| || |||||||||||
                    TGTTT CC TGACCCTAAT
                      TC__   A G      AAI
GAM347 ANGPT4       TGTCACAGACGGA-GGGGAGTTGG  5358 TGA      CT _  CI
                    CACAGACGGA GGGA TTGG
                    |||||||||| |||| ||||
                    GTGTCTGCCT CCCT AACC
                      ACA       C_  C II
GAM347 AXL          ACTCAGAAGGTGAGGGATTGGC   5350 TGACA  C ACT
                    CAGA GG  GGGATTGGC
                    |||| ||  |||||||||
                    GTCT CC  CCCTAACCG
                      A____   T ACT
GAM347 IL1B         ACAAAAGGGCTGGGGATTGGC    5351 TGACACAGAC A   _
                    GG CTGGG ATTGGC
                    || ||||| |||||||
                    CC GACCC TAACCG
                      TT_____ C  C
GAM347 PDGFB        GAGACAGACGGACGAGGGA     5355 TGAC     T_ TTGG
                    ACAGACGGAC GGGA
                    |||||||||| ||||
                    TGTCTGCCTG CCCT
                      TC__      CT TIII
GAM347 RANBP3       TGACACAGAGGGCACAGTGGAGGGGC 5357     C _ TG_ TT II
                    TGACACAGA GG AC  GGA GGC
                    ||||||||| || || ||| |||
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                    ACTGTGTCT CC TG  CCT CCG
                      C  G  TCA  CC  II
GAM347 SIRT7        TGACACAGA-GGCC--GGATGGGC 5359      C  A   G  T
                    TGACACAGA GG CTGG AT GGC
                    ||||||||| || |||| || |||
                    ACTGTGTCT CC GGCC TA CCG
                      _  _   _ C
GAM347 SLC7A5       GACACAGACAGGGAGCAGGCA-TGGC 5354 TG      __  CT  AT   II
                    ACACAGAC GGA GGG TGGC
                    |||||||| ||| ||| ||||
                    TGTGTCTG CCT TCC ACCG
                     __     TC  CG  GT  TI
GAM347 TMPRSS2      CACAGACGGATCCTGCAAATGG    5353 TGACAC    __  G  T  C
                    AGACGGA CTG GA TGG
                    ||||||| ||| || |||
                    TCTGCCT GAC TT ACC
                    _____      AG  G  T  C
GAM347 TPM2        GAC-CGGACGGACTGGGCTGGG   5356 TGACACA      A  C
                    GACGGACTGGG TTGG
                    |||||||||| ||||
                    CTGCCTGACCC GACC
                 TGGC___       _ C
GAM348 CKMT2       TCAGAGTAGAGATTTATGTCTGTT 5367      _TA_  A TTTTTI
                    TCAGAGTAG G  TATG CT
                    ||||||||| |  |||| ||
                    AGTCTCATC C  ATAC GA
                     T TAA   A  CAAIII
GAM348 CSNK1G3      AGAGAATGTTAATATGACTT     5362 TC   AGGT     TTT
                    AGAGT  ATATGACTT
                    |||||  |||||||||
                    TCTTA  TATACTGAA
                    __   CAAT      TAI
GAM348 DTNA        CAAATTAG---TATGACTTTTTT  5365 TCA  A  TA
                    GAGT GGTA TGACTTTT
                    |||| |||| |||||||||
                    TTTA TCAT ACTGAAAAA
                    ___   A  __
GAM348 EDNRA        TCAAAGT--GTA-ATGACTTTT   5368      AG  T     T
                    TCAGAGT GTA ATGACTTTT
                    ||||||| ||| |||||||||
                    AGTTTCA CAT TACTGAAAA
                     __  _     I
GAM348 SFRS2IP      TCTGAGTA---ATATGACTTATT  5369 TCA   GGT     TTT
                    GAGTA ATATGACTT
                    ||||| |||||||||
                    CTCAT TATACTGAA
                    AGA   ___     TAA
GAM348 SLC4A10      CAAACTAGGTGTATATGACTT    5364 TC G  __      TTTT
                    AGA TAGGT ATATGACTT
                    ||| ||||| |||||||||
```

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                              TTT ATCCA  TATACTGAA
                              __  G   CA       TIII
GAM348  SLC4A4      CACAGTAGAGAAGATGACTTTT   5363 TCAG    _ TAT       TT
                            AGTAG G  ATGACTTTT
                            |||||| |  |||||||||
                            TCATC C  TACTGAAAA
                            TG__  T TTC       TI
GAM348  ZNF141      GAGGAG--ATATGACTTTT      5366 TCAGAGTA  T
                            GG ATATGACTTTT
                            || |||||||||||
                            TC TATACTGAAAA
                       C_____ _
GAM349  CAPN5      GCGGGTCCAGCCGGGCTCCCGGGA 5372 TG   A   A__      CI
                            CGGGT CAGTT  CTCCCGGGA
                            ||||| |||||  |||||||||
                            GCCCA GTCGG  GAGGGCCCT
                            __   G   CCC      AI
GAM349  CTLA1      GGGTACAGTAACCTCAGAGAC    5374 TGCGGG    TA_  CC
                            TACAGT  CTC  GGGAC
                            |||||| |||  |||||
                            ATGTCA  GAG  CTCTG
                            _____    TTG  T_
GAM349  GGA3      TGGGGGTCCATGT--TCCCGGGAC  5377  C   A GTTAC
                            TG GGGT CA   TCCCGGGAC
                            || |||| ||   |||||||||
                            AC CCCA GT   AGGGCCCTG
                             C  G ACA__
GAM349  IGHMBP2       TGTGGGG-CAGCTTTTCCCGGGAC 5378  C  TA   AC     I
                            TG GGG  CAGTT  TCCCGGGAC
                            || ||| |||||  |||||||||
                            AC CCC  GTCGA  AGGGCCCTG
                             A  C_   AA      I
GAM349  TXNRD1      TGCAGG-ACAGTTCTCTTTCCCGGGAC5375    T    AC___      II
                            TGCGGG ACAGTT   TCCCGGGAC
                            |||||| ||||||   |||||||||
                            ACGTCC TGTCAA   AGGGCCCTG
                             _      GAGAA      II
GAM349  VENTX2      TGTGGGTACAG----TCCCGG    5376  C    TTAC    G
                            TG GGGTACAG  TCCCGG
                            || |||||||||  ||||||
                            AC CCCATGTC  AGGGCC
                            A      ____    I
GAM349  WISP3      GCGAGCACT-TTCCTCCCGGGAC   5373 TG    AG  A
                            CGGGTAC TT CTCCCGGGAC
                            ||||||| || |||||||||||
                            GCTCGTG AG GAGGGCCCTG
                            __    AA _
GAM350  NT5M      AGCGCGC-TGGCCCGTCGTGG     5382 TA    CATC       T
                            GCGTT  GCCCGTCGTGG
                            |||||  ||||||||||||
```

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                        CGCGA   CGGGCAGCACC
                        CG    C___        C
GAM350  SLC15A1         TAGCGTTCACGGCCGGGCGCGGT   5383      C  CGT    CI
                        TAGCGTTCAT GCC  CGTGGT
                        IIIIIIIII III  IIIIII
                        ATCGCAAGTG CGG  GCGCCA
                              C  CCC     II
GAM350  TP53            AGCGTGTCA----CCGTCGTGG   5381 TA   TCA    C
                           GCGT  TCGCC GTCGTGG
                           IIII  IIIII IIIIIII
                           CGCA  AGTGG CAGCACC
                           __    C__    _
GAM351  BAALC           TGCCATGGGCAGTGGGTTGG     5398 GACAAGT      TGI
                             GCCGTGGGT
                             IIIIIIIII
                             CGGTACCCG
                             _____          TCA
GAM351  BAALC           TGCCATGGGCAGTGGGTTGG     5398 TGACAAG      __   CT
                             TGCCGTGGGT TGGG
                             IIIIIIIIII IIII
                             ACGGTACCCG ACCC
                             _____         TC  AA
GAM351  BCL9            GAAAATGTGCCAGTGGGTTGG    5395 GACAA_   _       III
                             GTGCC GTGGGTTG
                             IIIII IIIIIIII
                             CACGG CACCCAAC
                        CTTTTA    T     CII
GAM351  BCL9            GAAAATGTGCCAGTGGGTTGG    5395 TGACAA    _      GCTT
                             GTGCC GTGGGTTGG
                             IIIII IIIIIIIII
                             CACGG CACCCAACC
                        TTTTA_    T      AIII
GAM351  BRCA1           AGTGCCGTGGTATGATCTT      5393          GT GG II
                             AGTGCCGTGG TG CT
                             IIIIIIIIII II II
                             TCACGGCACC AC GA
                              AT  TA  AI
GAM351  BRCA1           AGTGCCGTGGTATGATCTT      5393 TGACAA CC   GTTG
                             GTG GTGG  GGCT
                             III IIII  IIII
                             CAC TACT  CCGA
                        G_____   CA  AGAA
GAM351  CDO1            TGGCAGAGTGCCGTGAGTT      5397 A _        GGGCT
                             TG CA AGTGCCGTGGGTT
                             II II IIIIIIIIIIII
                             AC GT TCACGGCACTCAA
                              C  C         IIITT
GAM351  CDO1            TGGCAGAGTGCCGTGAGTT      5397 A _        II
                             TG CA AGTGCCGTGGGT
                             II II IIIIIIIIIIII
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                          AC GT TCACGGCACTCA
                           C  C          AI
GAM351  FOXE1         AAGTGATCCCTGGGTTGGG      5386  __ G      III
                          AAGTG  CC TGGGTTGG
                          ||||| || |||||||||
                          TTCAC  GG ACCCAACC
                           TA  G      CII
GAM351  FOXE1         AAGTGATCCCTGGGTTGGG      5386 TGACAAGTG  G     CT
                             CC TGGGTTGGG
                             || |||||||||
                             GG ACCCAACCC
                           CTA_____ G     CA
GAM351  GBF1          AAGTGCAGAGTGGTTGGGCTT    5387 A    CGTG_       I
                            GTGC  GGTTGGGCT
                            ||||    |||||||||
                            CACG    CCAACCCGA
                            _   TCTCA       I
GAM351  GBF1          AAGTGCAGAGTGGTTGGGCTT    5387 TGACAAGTGCC   G
                             GTGG TTGGGCTT
                             |||| ||||||||
                             CACC AACCCGAA
                            CGTCT_____  _
GAM351  HLA-A         GACATGAGG-GTGGGTTGGTCT   5396 CAA  CC_       GI
                             GTG  GTGGGTTGG
                             |||  |||||||||
                             TAC  CACCCAACC
                            TG_  TCC       AI
GAM351  HLA-A         GACATGAGG-GTGGGTTGGTCT   5396 TGACAA  CC_      G
                             GTG  GTGGGTTGG CTT
                             |||  ||||||||| |||
                             TAC  CACCCAACC GAG
                            TG____ TCC      A
GAM351  MAP3K14       ACAGGTCAGCCTTGGGTTGGG    5390 TGACAAGT  G     CTT
                             GCC TGGGTTGGG
                             ||| |||||||||
                             CGG ACCCAACCC
                            TCCAGT__ A      CCI
GAM351  MAP3K14       ACAGGTCAGCCTTGGGTTGGG    5390 A __ G       III
                            ACA GT GCC TGGGTTGG
                            ||| || ||| |||||||||
                            TGT CA CGG ACCCAACC
                             C  GT  A        CII
GAM351  PLAT          TGACAGGT-CAGGAGGTTGGGCTT 5400     A GCCGT        I
                            TGACA GT    GGGTTGGGCTT
                            ||||| ||    |||||||||||
                            ACTGT CA    TCCAACCCGAA
                             C  GTCC_      I
GAM351  PLAT          TGACAGGT-CAGGAGGTTGGGCTT 5400 _  A GCCGT        I
                             GACA GT    GGGTTGGGCT
                             |||| ||    |||||||||||
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                       CTGT CA    TCCAACCCGA
                       A   C GTCC_           I
GAM351  RS1            AACTCCCCTACGTTGGGCTT    5389 AGTG G  G       I
                           CC TG GTTGGGCT
                           || || ||||||||
                           GG AT CAACCCGA
                       TGAG G  G       I
GAM351  RS1            AACTCCCCTACGTTGGGCTT    5389 TGACAAGTG G  G
                            CC TG GTTGGGCT
                            || || ||||||||
                            GG AT CAACCCGA
                       G_____ G G
GAM351  SIAT4C         AGTGCCGTGTCTAGGCCTT     5394       GG    II
                       AGTGCCGTG TTGGGCT
                       ||||||||| |||||||
                       TCACGGCAC GATCCGG
                            A_    AA
GAM351  SLC12A7        AGTGCCGTGATGCTGTTGGGC   5391        ____    IIIG
                       AGTGCCGTGG  GTTGGG
                       ||||||||||  ||||||
                       TCACGGCACT  CAACCC
                            ACGA    GIII
GAM351  SOX12          AAGGGGTGGGGGTTGGGCT     5388 AA___   CCGT      II
                           GTG  GGGTTGGGC
                           |||  |||||||||
                           CAC  CCCAACCCG
                       TTCCC  C___      AI
GAM351  SOX12          AAGGGGTGGGGGTTGGGCT     5388 TGACAA  CCGT
                            GTG  GGGTTGGGCT
                            |||  ||||||||||
                            CAC  CCCAACCCGA
                       C_____  C___
GAM351  UCP2          TGACAAGTGGGCTAGGCTGGGCT  5399       CCG      TI
                       TGACAAGTG TGGGTTGGGCT
                       ||||||||| ||||||||||||
                       ACTGTTCAC ATCCGACCCGA
                            CCG        II
GAM351  UCP2          TGACAAGTGGGCTAGGCTGGGCT  5399       CCG      I
                       GACAAGTG TGGGTTGGGC
                       |||||||| ||||||||||
                       CTGTTCAC ATCCGACCCG
                            CCG        I
GAM351  WNT6          AGAGCCCTGGGAGTTGGGCTT    5392 T  G  __      III
                       AG GCC TGGG TTGGGCT
                       || ||| |||| |||||||
                       TC CGG ACCC AACCCGA
                        T  G  TC    AII
GAM352  CAPN10         CTGACGGAGGCTTCCCGTGG     5409  _    G III
                       CTGA GGAGGCTTC TG
                       |||| |||||||||| ||
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```
                              GACT CCTCCGAAG GC
                               G      G ACC
GAM352 EHD2          AGCTGTGGGGAGGCTTCCAGGG   5406 GAT  A__       GT I
                        CTG  GGAGGCTTC GG
                        ||| ||||||||| ||
                        GAC  CCTCCGAAG CC
                          C__ ACC       GT I
GAM352 EHD2          AGCTGTGGGGAGGCTTCCAGGG   5406 TGAGATC A      GT
                           TG GGAGGCTTC GGG
                           || ||||||||| |||
                           AC CCTCCGAAG CCC
                        GAC____ C      GT
GAM352 GJA5          TGAGTAATCTGAA-AGGCTTCGT   5414  __     G      GGG
                        TGAG ATCTGAG AGGCTTCGT
                        |||| ||||||| |||||||||
                        ACTC  TAGACTT TCCGAAGCA
                          AT    _      |||
GAM352 GJA5          TGAGTAATCTGAA-AGGCTTCGT   5414 GA_     G     I
                          GATCTGAG AGGCTTCG
                          |||||||| |||||||||
                          TTAGACTT TCCGAAGC
                          TCA     _     I
GAM352 ITGB4         GAGTAGCTGAGGAGGCTCCG      5410  AT_          II
                        GAG  CTGAGGAGGCTTC
                        |||  ||||||||||||
                        CTC  GACTCCTCCGAGG
                          ATC        CI
GAM352 ITGB4         GAGTAGCTGAGGAGGCTCCG      5410 TGAGAT        TGG
                           CTGAGGAGGCTTCG
                           ||||||||||||||
                           GACTCCTCCGAGGC
                        TCATC_         CII
GAM352 JAM2          TCTGAGGAGG--TCGAGGG        5413     CT  T I
                        TCTGAGGAGG TCG GG
                        |||||||||| ||| ||
                        AGACTCCTCC AGC CC
                           __ T C
GAM352 LAMC1          TGAGA-CTGAGGAGG-TTC       5415   T    C GTG
                        TGAGA CTGAGGAGG TTC
                        ||||| ||||||||| |||
                        ACTCT GACTCCTCC AAG
                           _    _ |||
GAM352 LAMC1          TGAGA-CTGAGGAGG-TTC       5415   T    CTTI
                        TGAGA CTGAGGAGG
                        ||||| |||||||||
                        ACTCT GACTCCTCC
                           _     AAGI
GAM352 LZTR1         GATTTGGAGGAGGCTGCCCTGTGGG 5412 ATCT      __ _  I
                        GAGGAGGCT TC GTGG
                        ||||||||| || ||||
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```
                        CTCCTCCGA GG CACC
                        C___        CG A   I
GAM352  LZTR1           GATTTGGAGGAGGCTGCCCTGTGGG 5412 TGAGATCT       __ _     II
                          GAGGAGGCT  TC GTGGG
                          |||||||| || |||||
                          CTCCTCCGA GG CACCC
                        AAC_____        CG A   AC
GAM352  MEF2A           AGATCTGAGGTCCAGAGTTCG   5403       ___ GC   III
                          AGATCTGAGG  AG TTC
                          ||||||||| || |||
                          TCTAGACTCC  TC AAG
                           AGG TC  CII
GAM352  MEF2A           AGATCTGAGGTCCAGAGTTCG     5403 TGAG      ___ GC   T G
                          ATCTGAGG  AG TTCG GG
                          |||||||| || |||| ||
                          TAGACTCC  TC AAGC TC
                          ____        AGG  TC  _ I
GAM352  MEIS1           ATGTAAGGAGGCTTC-TGG      5408 ATC       GTGI
                          TGAGGAGGCTTC
                          ||||||||||||
                          ATTCCTCCGAAG
                        TAC        ACCI
GAM352  MEIS1           ATGTAAGGAGGCTTC-TGG      5408 TGAGATCT       G
                          GAGGAGGCTTC TG
                          ||||||||||| ||
                          TTCCTCCGAAG AC

                        _____       _
GAM352  NGB             TGA-ATCTGAGGA-GCT--GTGG   5417    A      G TC
                          TGAG TCTGAGGAG CT GTGG
                          |||| |||||||| || ||||
                          ACTT AGACTCCTC GA CACC
                          _        _ __
GAM352  NGB             TGA-ATCTGAGGA-GCT--GTGG   5417 A        G TC
                          G GATCTGAGGAG CT GTG
                          | |||||||||| || |||
                          A TTAGACTCCTC GA CAC
                          C        _ __
GAM352  NOS2A           TGAGA---GAGGAGGCTCCG      5416    TCT       TG
                          TGAGA GAGGAGGCTTCG
                          ||||| ||||||||||||
                          ACTCT CTCCTCCGAGGC
                                     ||
GAM352  NOS2A           TGAGA---GAGGAGGCTCCG      5416 _  TCT
                          GAGA  GAGGAGGCTTC
                          |||| |||||||||||
                          CTCT  CTCCTCCGAGG
                          A ___
GAM352  PCDHGA1         AGAACT-AGGAGGCTT-GTAGG    5405 _ T G      C I
                          GA CT AGGAGGCTT GTGG
                          || || |||||||| ||||
```

```
                           CT GA TCCTCCGAA CATC
                            T T _      _   I
GAM352 PCDHGA1      AGAACT-AGGAGGCTT-GTAGG    5405 TGAGATCTG      C
                           AGGAGGCTT GTGG

                           |||||||| ||||
                           TCCTCCGAA CATC

                        TTGA_____      _
GAM352 PCDHGA10     AGAACT-AGGAGGCTT-GTAGG    5405 _ T G      C  I
                         GA CT AGGAGGCTT GTGG

                         || || |||||||| ||||
                         CT GA TCCTCCGAA CATC
                          T T _      _   I
GAM352 PCDHGA10     AGAACT-AGGAGGCTT-GTAGG    5405 TGAGATCTG      C
                           AGGAGGCTT GTGG

                           |||||||| ||||
                           TCCTCCGAA CATC

                        TTGA_____        _
GAM352 PCDHGA11     AGAACT-AGGAGGCTT-GTAGG    5405 _ T G      C  I
                         GA CT AGGAGGCTT GTGG

                         || || |||||||| ||||
                         CT GA TCCTCCGAA CATC
                          T T _      _   I
GAM352 PCDHGA11     AGAACT-AGGAGGCTT-GTAGG    5405 TGAGATCTG      C
                           AGGAGGCTT GTGG

                           |||||||| ||||
                           TCCTCCGAA CATC

                        TTGA_____        _
GAM352 PCDHGA12     AGAACT-AGGAGGCTT-GTAGG    5405 _ T G      C  I
                         GA CT AGGAGGCTT GTGG

                         || || |||||||| ||||
                         CT GA TCCTCCGAA CATC
                          T T _      _   I
GAM352 PCDHGA12     AGAACT-AGGAGGCTT-GTAGG    5405 TGAGATCTG      C
                           AGGAGGCTT GTGG

                           |||||||| ||||
                           TCCTCCGAA CATC

                        TTGA_____        _
GAM352 PCDHGA2      AGAACT-AGGAGGCTT-GTAGG    5405 _ T G      C  I
                         GA CT AGGAGGCTT GTGG

                         || || |||||||| ||||
                         CT GA TCCTCCGAA CATC
                          T T _      _   I
GAM352 PCDHGA2      AGAACT-AGGAGGCTT-GTAGG    5405 TGAGATCTG      C
                           AGGAGGCTT GTGG

                           |||||||| ||||
                           TCCTCCGAA CATC

                        TTGA_____        _
GAM352 PCDHGA3      AGAACT-AGGAGGCTT-GTAGG    5405 _ T G      C  I
                         GA CT AGGAGGCTT GTGG

                         || || |||||||| ||||
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                                        CT GA TCCTCCGAA CATC
                                        T  T  _       _   I
GAM352  PCDHGA3          AGAACT-AGGAGGCTT-GTAGG    5405 TGAGATCTG       C
                                AGGAGGCTT GTGG
                                |||||||||| ||||
                                TCCTCCGAA CATC
                             TTGA_____        _
GAM352  PCDHGA4          AGAACT-AGGAGGCTT-GTAGG    5405 _ T  G      C  I
                            GA CT AGGAGGCTT GTGG
                            || || |||||||||| ||||
                            CT GA TCCTCCGAA CATC
                            T  T  _       _   I
GAM352  PCDHGA4          AGAACT-AGGAGGCTT-GTAGG    5405 TGAGATCTG       C
                                AGGAGGCTT GTGG
                                |||||||||| ||||
                                TCCTCCGAA CATC
                             TTGA_____          _
GAM352  PCDHGA5          AGAACT-AGGAGGCTT-GTAGG    5405 _ T  G      C  I
                            GA CT AGGAGGCTT GTGG
                            || || |||||||||| ||||
                            CT GA TCCTCCGAA CATC
                            T  T  _       _   I
GAM352  PCDHGA5          AGAACT-AGGAGGCTT-GTAGG    5405 TGAGATCTG       C
                                AGGAGGCTT GTGG
                                ||||||||| ||||
                                TCCTCCGAA CATC
                             TTGA_____        _
GAM352  PCDHGA6          AGAACT-AGGAGGCTT-GTAGG    5405 _ T  G      C  I
                            GA CT AGGAGGCTT GTGG
                            || || |||||||||| ||||
                            CT GA TCCTCCGAA CATC
                            T  T  _       _   I
GAM352  PCDHGA6          AGAACT-AGGAGGCTT-GTAGG    5405 TGAGATCTG       C
                                AGGAGGCTT GTGG
                                ||||||||| ||||
                                TCCTCCGAA CATC
                             TTGA_____        _
GAM352  PCDHGA7          AGAACT-AGGAGGCTT-GTAGG    5405 _ T  G      C  I
                            GA CT AGGAGGCTT GTGG
                            || || |||||||||| ||||
                            CT GA TCCTCCGAA CATC
                            T  T  _       _   I
GAM352  PCDHGA7          AGAACT-AGGAGGCTT-GTAGG    5405 TGAGATCTG       C
                                AGGAGGCTT GTGG
                                ||||||||| ||||
                                TCCTCCGAA CATC
                             TTGA_____        _
GAM352  PCDHGA8          AGAACT-AGGAGGCTT-GTAGG    5405 _ T  G      C  I
                            GA CT AGGAGGCTT GTGG
                            || || |||||||||| ||||
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                        CT GA TCCTCCGAA CATC
                        T  T _      _   I
GAM352  PCDHGA8         AGAACT-AGGAGGCTT-GTAGG     5405 TGAGATCTG       C
                            AGGAGGCTT GTGG
                            ||||||||| ||||
                            TCCTCCGAA CATC
                        TTGA_____        _
GAM352  PCDHGA9         AGAACT-AGGAGGCTT-GTAGG     5405 _ T G       C   I
                          GA CT AGGAGGCTT GTGG
                          || || ||||||||| ||||
                          CT GA TCCTCCGAA CATC
                          T  T _      _   I
GAM352  PCDHGA9         AGAACT-AGGAGGCTT-GTAGG     5405 TGAGATCTG       C
                            AGGAGGCTT GTGG
                            ||||||||| ||||
                            TCCTCCGAA CATC
                        TTGA_____        _
GAM352  PCDHGB1         AGAACT-AGGAGGCTT-GTAGG     5405 _ T G       C   I
                          GA CT AGGAGGCTT GTGG
                          || || ||||||||| ||||
                          CT GA TCCTCCGAA CATC
                          T  T _      _   I
GAM352  PCDHGB1         AGAACT-AGGAGGCTT-GTAGG     5405 TGAGATCTG       C
                            AGGAGGCTT GTGG
                            ||||||||| ||||
                            TCCTCCGAA CATC
                        TTGA_____        _
GAM352  PCDHGB2         AGAACT-AGGAGGCTT-GTAGG     5405 _ T G       C   I
                          GA CT AGGAGGCTT GTGG
                          || || ||||||||| ||||
                          CT GA TCCTCCGAA CATC
                          T  T _      _   I
GAM352  PCDHGB2         AGAACT-AGGAGGCTT-GTAGG     5405 TGAGATCTG       C
                            AGGAGGCTT GTGG
                            ||||||||| ||||
                            TCCTCCGAA CATC
                        TTGA_____        _
GAM352  PCDHGB3         AGAACT-AGGAGGCTT-GTAGG     5405 _ T G       C   I
                          GA CT AGGAGGCTT GTGG
                          || || ||||||||| ||||
                          CT GA TCCTCCGAA CATC
                          T  T _      _   I
GAM352  PCDHGB3         AGAACT-AGGAGGCTT-GTAGG     5405 TGAGATCTG       C
                            AGGAGGCTT GTGG
                            ||||||||| ||||
                            TCCTCCGAA CATC
                        TTGA_____        _
GAM352  PCDHGB4         AGAACT-AGGAGGCTT-GTAGG     5405 _ T G       C   I
                          GA CT AGGAGGCTT GTGG
                          || || ||||||||| ||||
```

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                                    CT GA TCCTCCGAA CATC
                                    T  T  _       _    I
GAM352  PCDHGB4        AGAACT-AGGAGGCTT-GTAGG    5405 TGAGATCTG       C
                            AGGAGGCTT GTGG
                            ||||||||| ||||
                            TCCTCCGAA CATC
                        TTGA_____        _
GAM352  PCDHGB5        AGAACT-AGGAGGCTT-GTAGG    5405 _  T  G       C   I
                         GA CT AGGAGGCTT GTGG
                         || || ||||||||| ||||
                         CT GA TCCTCCGAA CATC
                         T  T  _       _    I
GAM352  PCDHGB5        AGAACT-AGGAGGCTT-GTAGG    5405 TGAGATCTG       C
                            AGGAGGCTT GTGG
                            ||||||||| ||||
                            TCCTCCGAA CATC
                        TTGA_____        _
GAM352  PCDHGB6        AGAACT-AGGAGGCTT-GTAGG    5405 _  T  G       C   I
                         GA CT AGGAGGCTT GTGG
                         || || ||||||||| ||||
                         CT GA TCCTCCGAA CATC
                         T  T  _       _    I
GAM352  PCDHGB6        AGAACT-AGGAGGCTT-GTAGG    5405 TGAGATCTG       C
                            AGGAGGCTT GTGG
                            ||||||||| ||||
                            TCCTCCGAA CATC
                        TTGA_____        _
GAM352  PCDHGB7        AGAACT-AGGAGGCTT-GTAGG    5405 _  T  G       C   I
                         GA CT AGGAGGCTT GTGG
                         || || ||||||||| ||||
                         CT GA TCCTCCGAA CATC
                         T  T  _       _    I
GAM352  PCDHGB7        AGAACT-AGGAGGCTT-GTAGG    5405 TGAGATCTG       C
                            AGGAGGCTT GTGG
                            ||||||||| ||||
                            TCCTCCGAA CATC
                        TTGA_____        _
GAM352  PCDHGC3        AGAACT-AGGAGGCTT-GTAGG    5405 _  T  G       C   I
                         GA CT AGGAGGCTT GTGG
                         || || ||||||||| ||||
                         CT GA TCCTCCGAA CATC
                         T  T  _       _    I
GAM352  PCDHGC3        AGAACT-AGGAGGCTT-GTAGG    5405 TGAGATCTG       C
                            AGGAGGCTT GTGG
                            ||||||||| ||||
                            TCCTCCGAA CATC
                        TTGA_____        _
GAM352  PCDHGC4        AGAACT-AGGAGGCTT-GTAGG    5405 _  T  G       C   I
                         GA CT AGGAGGCTT GTGG
                         || || ||||||||| ||||
```

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                    CT GA TCCTCCGAA CATC
                     T T _      _    I
GAM352 PCDHGC4      AGAACT-AGGAGGCTT-GTAGG    5405 TGAGATCTG      C
                        AGGAGGCTT GTGG
                        |||||||| ||||
                        TCCTCCGAA CATC
                    TTGA_____        _
GAM352 PCDHGC5      AGAACT-AGGAGGCTT-GTAGG    5405 _ T G      C   I
                      GA CT AGGAGGCTT GTGG
                      || || ||||||||| ||||
                      CT GA TCCTCCGAA CATC
                       T T _    _   I
GAM352 PCDHGC5      AGAACT-AGGAGGCTT-GTAGG    5405 TGAGATCTG      C
                        AGGAGGCTT GTGG
                        ||||||||| ||||
                        TCCTCCGAA CATC
                    TTGA_____       _
GAM352 SACM2L      AGAGCTGAGGAGGCTTCATG    5404  T          I
                      GA CTGAGGAGGCTTCGT
                      || |||||||||||||||
                      CT GACTCCTCCGAAGTA
                       C           I
GAM352 SACM2L      AGAGCTGAGGAGGCTTCATG    5404 TGAGAT         G
                         CTGAGGAGGCTTCGTG
                         ||||||||||||||||
                         GACTCCTCCGAAGTAC
                    TC____           G
GAM352 SLA2       GAGATCTGAGAGCTAGGCTGGGTG  5411 GA     ___    TCGTI
                      TCTGAGG  AGGCT
                      |||||||  |||||
                      AGACTCT  TCCGA
                      __     CGA    CCCII
GAM352 SLA2       GAGATCTGAGAGCTAGGCTGGGTG  5411 TG       ___   TC  GGI
                      AGATCTGAGG  AGGCT GTG
                      ||||||||||  ||||| |||
                      TCTAGACTCT  TCCGA CAC
                      __      CGA    CC  GII
GAM352 STIM1      ATCTGAGGAGGTTTGGGGG     5407        CTTCGTGII
                      ATCTGAGGAGG
                      |||||||||||
                      TAGACTCCTCC
                          AAACCCCCI
GAM353 ADRA2A      GGGAGGGCA-GG--C-AGGGC   5435 TG    TG  CA
                      GGAGGGCA GGT AGGGC
                      |||||||| ||| |||||
                      CCTCCCGT CCG TCCCG
                           __     __
GAM353 AGXT       GGGTGGGCATGGGACAGGTGTGT  5440 TG A    T  A GCGTI
                      GG GGGCATGGG CA GG
                      || ||||||||| || ||
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                              CC CCCGTACCC GT CC
                              __   A       T _ ACACA
GAM353 ALPPL2        AGGGCGTGGTGTCAAGGGC    5420 TGGGAGGGCA _      G
                              TGG GTCAAGGGC
                              ||| ||||||||
                              ACC CAGTTCCCG
                              GC_____  A      A
GAM353 CALU          TGGGGTGTGATGGGTCAAAGGC  5455    AGGGC        GT
                              TGGG   ATGGGTCAAGGGC
                              ||||   |||||||||||
                              ACCC   TACCCAGTTTCCG
                              CACAC          ||
GAM353 COL4A6        GGGAGGGCAAGGGGCAGAGTGGC  5429 TG     T_  CA _ TI
                              GGAGGGCA GGGT AG GGCG
                              |||||||| |||| || ||||
                              CCTCCCGT CCCG TC CCGT
                              __     TC  TC A  ||
GAM353 CYBA          GGGAGGGCA--GGTCCGGGGCG   5437 TG    TG AA
                              GGAGGGCA GGTC GGGCG
                              |||||||| |||| |||||
                              CCTCCCGT CCAG CCCGC
                              __     __  GC
GAM353 DPH2L1        TGGGAGGGCATGGATGACGG     5450         CAAG
                              TGGGAGGGCATGGGT  GGCG
                              |||||||||||||||  ||||
                              ACCCTCCCGTACCTA  CTGC
                                        ___
GAM353 EHD2          GGGAGGGCA-GG--C-AGGGCGT  5439 TG    TG CA
                              GGAGGGCA GGT AGGGCG
                              |||||||| ||| ||||||
                              CCTCCCGT CCG TCCCGC
                              __     __  __
GAM353 EPB49         TGGGAGGGC-TGGGT---GGGCG  5457      A   CAA
                              TGGGAGGGC TGGGT  GGGCG
                              ||||||||| |||||  |||||
                              ACCCTCCCG ACCCA  CCCGC
                              __     _  ___
GAM353 ERBB2         TGGGAGGGCGCGGGGCGCGGG    5451      A  TCAA CGT
                              TGGGAGGGC TGGG  GGG
                              ||||||||| ||||  |||
                              ACCCTCCCG GCCC  CCC
                              C   CGCG  |||
GAM353 GNB2          TGGGAGGGCAGGGACCCAAGGC   5453     T GT A  GT
                              TGGGAGGGCA GG  C AGGGC
                              |||||||||| || | |||||
                              ACCCTCCCGT CC  G TTCCG
                              C TG G     ||
GAM353 GRM4          TGGGTGGGCATGGG-C-AGGGC   5456  A     CA  G
                              TGGG GGGCATGGGT AGGGC
                              |||| |||||||||| |||||
```

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                              ACCC CCCGTACCCG  TCCCG
                                A       __    I
GAM353  ID3              GGGAGGGCA-GGGCCCAGG      5431 TG      T   AA
                              GGAGGGCA GGGTC  GGGC
                              |||||||| |||||  ||||
                              CCTCCCGT CCCGG  TCCG
                                __       _    G_
GAM353  IL24          TGGGACC-CATGGC-CAAGGGCGT  5458    GGG    G
                              TGGGA  CATGG TCAAGGGCGT
                              |||||  ||||| ||||||||||
                              ACCCT  GTACC GGTTCCCGCA
                                GG_    _
GAM353  JUNB          GGGAGGGCAGGGGGCGGGGG       5434 TG      T  TCAA  C
                              GGAGGGCA GGG   GGG G
                              |||||||| |||   ||| |
                              CCTCCCGT CCC   CCC C
                                __        C  CG__  C
GAM353  KCNAB2          GGGTGGGTGGGGGTCAAGGGC     5436 __   A  CATG      GT
                              TGGG GGG   GGTCAAGGGC
                              |||| |||   ||||||||||
                              ACCC CCC   CCAGTTCCCG
                                CC   A   ____        GI
GAM353  KCNMB1          TGGGAGGGCAGGTGGAGAAGG     5445        TG_  TC   GCGT
                              TGGGAGGGCA  GG AAGG
                              ||||||||||  || ||||
                              ACCCTCCCGT  CC TTCC
                                  CCA  TC   IIIT
GAM353  KLK13           GGGAGGGCA-GGG-C--GGGCG    5438 TG      T  CAA
                              GGAGGGCA GGGT  GGGC
                              |||||||| ||||  ||||
                              CCTCCCGT CCCG  CCCG
                                __      _   ___
GAM353  MEOX1           GGAAGG--TGGG-CAAGGGCGT    5423 TGG    GCA   T
                              GAGG   TGGG CAAGGGCG
                              ||||   |||| ||||||||
                              TTCC   ACCC GTTCCCGC
                                ___    ___   _
GAM353  MGAT1           GGGAGGGCA--GGCCAGGGG      5433 TG      TG   A  C
                              GGAGGGCA GGTCA GGG
                              |||||||| ||||| |||
                              CCTCCCGT CCGGT CCC
                                __      __   C  T
GAM353  MSX1            GGGCATGGGCTC-CGGGCG       5441 TGGGA   A_   CAA
                              GGGC TGGGT GGGC
                              |||| ||||| ||||
                              CCCG GCCCG CCCG
                                A____   AG   ___
GAM353  NEFH            GGGAGGGCATGGGGGCAGGGGC    5425 TG        T_  A  GT
                              GGAGGGCATGGG CA GGGC
                              ||||||||||| || ||||
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                     CCTCCCGTACCC GT CCCG
                        __      CC C  GI
GAM353 OPCML         GGAAAGGGAAGGGTCAAGG      5430 T GG   CAT      GCG
                        G AGGG  GGGTCAAGG
                        | ||||  |||||||||
                        C TCCC  CCCAGTTCC
                        _ TT  TT_     AII
GAM353 PLD2          TGGGAGGGCCCTGGGACAGGGAGGGGGT5442      A_  T ___  C III
                        TGGGAGGGC TGGG CA  AGGG GT
                        ||||||||| |||| ||  |||| ||
                        ACCCTCCCG ACCC GT  TCCC CA
                           GG   T CCC   C III
GAM353 PML          GGAGGGCATGG--CGAAGGCG    5421 TGGG      GTCA
                        AGGGCATGG   AGGGCG
                        |||||||||   ||||||
                        TCCCGTACC   TTCCGC
                        ____        GC__
GAM353 PPT2         TGGGAGGGC-TGATGTCAGGGG    5446      A _  A CGT
                        TGGGAGGGC TGG GTCA GGG
                        ||||||||| ||| |||| |||
                        ACCCTCCCG ACT CAGT CCC
                          _  A  C III
GAM353 PRKCN        TGGGAGGGCTAAGGGT-AAG     5444      AT_  C GGCG
                        TGGGAGGGC  GGGT AAG
                        |||||||||  |||| |||
                        ACCCTCCCG  CCCA TTC
                          ATT  _  IIIT
GAM353 RARA         GGGAGGGCAGGTGGGGGCAGGGC  5424 TG      __  TCA   GTI
                        GGAGGGCA TGGG  AGGGC
                        ||||||||| |||| |||||
                        CCTCCCGT ACCC  TCCCG
                          __       CC  CCG   AII
GAM353 RHCG         GGGAGGGCAGGGGTGGAGG      5432 TG    T  CAA   G
                        GGAGGGCA GGGT  GGGC
                        ||||||||| |||| ||||
                        CCTCCCGT CCCA  TCCG
                          __    C  CC_   I
GAM353 RNF4         TGGGAGGGCCCTGGGTCCAGCGC  5443      A_   A G GTI
                        TGGGAGGGC TGGGTC AG GC
                        ||||||||| |||||| || ||
                        ACCCTCCCG ACCCAG TC CG
                           GG    G G III
GAM353 SLC7A4       TGGGAGGGC--GGGGCAAG      5447      AT T GGC
                        TGGGAGGGC GGG CAAG
                        ||||||||| ||| ||||
                        ACCCTCCCG CCC GTTC
                          C_  _  III
GAM353 SORCS2       TGGGAGGGCCTGGCACCCGGGC   5454      ATG CAA_ GT
                        TGGGAGGGC GGT  GGGC
                        ||||||||| |||  ||||
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                              ACCCTCCCG  CCG   CCCG
                                  GA_  TGGG  II
GAM353 SOX13          GGGAGGGCAGGAGGAGGTCA   5426 TG      T____      AGGGCG
                              GGAGGGCA   GGGTCA
                              ||||||||   ||||||
                              CCTCCCGT   TCCAGT
                                  __   CCTCC    CIIITG
GAM353 SOX13          GGGAGGGCAGGCAGGTGAGGGGC   5427 TG      __   CAA   TI
                              GGAGGGCA TGGGT GGGCG
                              |||||||| ||||| |||||
                              CCTCCCGT GTCCA CCCGT
                                  __      CC   CTC   II
GAM353 SREBF2          GGGAGGGCATGCTGGGCACAGGC   5428 TG      ___   T A  GTI
                              GGAGGGCA  TGGG CA GGGC
                              ||||||||  |||| || ||||
                              CCTCCCGT  ACCC GT TCCG
                                  __       ACG  _ G  GII
GAM353 TAGLN2          TGGGAGGGCA-GGGGCAAGG      5449      T T   GCG
                              TGGGAGGGCA GGG CAAGG
                              |||||||||| ||| |||||
                              ACCCTCCCGT CCC GTTCC
                                      C  _   III
GAM353 TFAP4          GGCGGGCATGGG--AGGGGCG   5422 TGGGA    TCAA
                              GGGCATGGG   GGGCG
                              |||||||||   |||||
                              CCCGTACCC   CCCGC
                              G____         TC__
GAM353 THRA          TGGGAGGGCTGGGGGCAAG      5448      A  TCAAG
                              TGGGAGGGC TGGG    GGCG
                              ||||||||| ||||    ||||
                              ACCCTCCCG ACCC    CCGT
                                      _   _____
GAM353 ZNF76          TGGGAGGGCA--GGAC-AGGGC   5452      T T A  G
                              TGGGAGGGCA GGG CA GGGC
                              |||||||||| ||| || ||||
                              ACCCTCCCGT CCT GT CCCG
                                      _  _ _   I
GAM354 BGN          GGGAACATGTGATGGGGGCC      5466          CGCTGCI
                              GGAACATGTGGT
                              ||||||||||||
                              CCTTGTACACTA
                                      CCCCCGI
GAM354 BGN          GGGAACATGTGATGGGGGCC   5466 TGCGGG      CGCT
                              AACATGTGGT   GCC
                              ||||||||| |||
                              TTGTACACTA   CGG
                              _____         CCCC
GAM354 DDX20          TGAGGCAACTGGTGAGTCGCTGCC   5467 C G  AT _      II
                              TG GG AAC  GTG GTCGCTGCC
                              II II III  III IIIIIIIII
```

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                              AC CC TTG  CAC CAGCGACGG
                                T  G  AC  T       II
GAM354  DDX20          TGAGGCAACTGGTGAGTCGCTGCC  5467 GC  G  AT  _      I
                            GG AAC  GTG GTCGCTGC
                            II III  III IIIIIIII
                            CC TTG  CAC CAGCGACG
                            T_ G  AC  T      I
GAM354  EGFL5          GCCGGTACG-GTGGTCGCT      5462  G  A  AT      I
                            GC GG AC  GTGGTCGC
                            II II II  IIIIIIII
                            CG CC TG  CACCAGCG
                             G  A  C_      A
GAM354  EGFL5          GCCGGTACG-GTGGTCGCT        5462 TG  GA  AT        C
                            CGG AC  GTGGTCGCTG
                            III II  IIIIIIIIII
                             GCC  TG  CACCAGCGAT
                            G_  A_  C_      I
GAM354  GGA3          GGGAACA--TGGTCTGTGCC      5465     TG  ___  GI
                            GGGAACA TGGTC  GCT
                            IIIIIII IIIII  III
                            CCCTTGT ACCAG  CGG
                                 __  ACA  II
GAM354  GUCY2C          GGACACTTGAGGTCGCTGCC      5464   _  A  T       II
                            GGA AC TG GGTCGCTGC
                            III II II IIIIIIIII
                            CCT TG AC CCAGCGACG
                             G  A  T       GI
GAM354  GUCY2C          GGACACTTGAGGTCGCTGCC      5464 TGCGGGA  A  T
                              AC TG GGTCGCTGCC
                              II II IIIIIIIIII
                              TG AC CCAGCGACGG
                              _____  A  T
GAM354  KCNAB2          GCGGGAACA-GAGGTGCCTGC      5463 _      TGT  C  GI
                             CGGGAACA  GGT GCT
                             IIIIIIII  III III
                             GCCCTTGT  CCA CGG
                              C      CT_  _  AC
GAM354  KCNAB2          GCGGGAACA-GAGGTGCCTGC      5463 TG      TGT  C  _  C
                             CGGGAACA  GGT GC TGC
                             IIIIIIII  III II III
                             GCCCTTGT  CCA CG ACG
                              __      CT_  _  G  T
GAM354  KIF5B          TGAGGG--CTTGTGGTCGC      5468  C  AACA      TG
                            TG GGG  TGTGGTCGC
                            II III  IIIIIIIII
                            AC CCC  ACACCAGCG
                             T  GA__      II
GAM354  KIF5B          TGAGGG--CTTGTGGTCGC      5468  C  AACA      I
                            TG GGG  TGTGGTCG
                            II III  IIIIIIII
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```
                      AC CCC   ACACCAGC
                       T GA__       G
GAM354 TLL1        CGGAAACATGTGGATGCCGCC   5461          TC   I
                    GGGAACATGTGG GCTGC
                    |||||||||||| |||||
                    CCTTTGTACACC CGGCG
                           TA    I
GAM354 TLL1        CGGAAACATGTGGATGCCGCC   5461 TGCG       TC
                     GGAACATGTGG GCTGCC
                     ||||||||||| ||||||
                     CTTTGTACACC CGGCGG
                     ____             TA
GAM355 ADAM19        GCTCGGCGCTCACACGCCCTCAGCC 5489 TGCC  _  C__       II
                     CGG GCTC  CGCCCTCAGCC
                     ||| ||||  |||||||||||
                     GCC CGAG  GCGGGAGTCGG
                      GA__  G   TGT      TI
GAM355 AGTR1         CGGGTCTCCCGCCCGCCGCC    5487 TGCCCGGG     TCA
                      CTCCCGCCC  GCC
                      |||||||||  |||
                      GAGGGCGGG  CGG
                     A_____         CGG
GAM355 BMPR1B        CCCGGCTCCCGCGTCCTCAGC   5483 TGCCCG     __   C
                      GGCTCCCGC CCTCAGC
                      ||||||||| |||||||
                      CCGAGGGCG GGAGTCG
                      _____      CA   C
GAM355 C18orf1       CCGGGCTCCCTGCGCCCACAGC  5481 TGCCCG     ___ T CI
                      GGCTCCC  GCCC CAGC
                      |||||||  |||| ||||
                      CCGAGGG  CGGG GTCG
                      _____    ACG  T  TC
GAM355 CDR2          CCCGGCCCCTCCGCCCTCAGCC  5475 TGCC  G  _       I
                      CGG CTC CCGCCCTCAGCC
                      ||| ||| ||||||||||||
                      GCC GGG GGCGGGAGTCGG
                      ____  G  A      T
GAM355 CDS1          TGCCCGGGCCTCCCGCAC-CAG  5501        _   _ TCAGCC
                      TGCCCGGGC TCCCGC CC
                      ||||||||| |||||| ||
                      ACGGGCCCG AGGGCG GG
                         G    T TCIIIC
GAM355 CEBPA          CCGGGCTCCC-AGCTCAGCC   5485 TGCCCG       CC
                      GGCTCCCG CTCAGC
                      |||||||| ||||||
                      CCGAGGGT GAGTCG
                      _____      C_
GAM355 CLDN5         CCCGGGCTCTGCATCCGCCC    5474 TGCC     _____     CAGCC
                      CGGGCTC  CCGCCCT
                      |||||||  |||||||
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                          GCCCGAG     GGCGGGG
                          ____      ACGTA     AIIIC
GAM355  CLTCL1          TGCCTGCTCTGCAGCCCTCAGC   5506   CGG   CC__        CI
                          TGCC  GCTC   GCCCTCAGC
                          IIII  IIII   IIIIIIIII
                          ACGG  CGAG   CGGGAGTCG
                            A__   ACGT       II
GAM355  EN2             CCCGGGCTCCCCGCTCCTC      5473 TGCC       _ _    AGC
                          CGGGCTCCC GC CCTC
                          IIIIIIIII II IIII
                          GCCCGAGGG CG GGAG
                            ____       G A  AGI
GAM355  ENPP1           GCCGCGGCTCCCGCCCCCGC     5495 TGC  _        A  C
                          CCG GGCTCCCGCCCTC GC
                          III IIIIIIIIIIIII II
                          GGC CCGAGGGCGGGGG CG
                            ___  G       G C
GAM355  FKBP10          TGCCCTCCCTCCCACCCCTCAGCC  5504     GGG      _   II
                          TGCCC  CTCCCGCCC TCAGCC
                          IIIII  IIIIIIIII IIIIII
                          ACGGG  GAGGGTGGG AGTCGG
                            AGG       G     II
GAM355  GALR1           TGCCCGGGCGCCTCCGCCCGCTGC  5502         _ _    TCA CII
                          TGCCCGGGC TC CCGCCC  GC
                          IIIIIIIII II IIIIII  II
                          ACGGCCCG GG GGCGGG  CG
                             C A    CGA III
GAM355  GNL1            CCGAGCTCCCGCCGCCTCA       5482 TGCCCG       __
                          GGCTCCCGCC CTCAGC
                          IIIIIIIIII IIIIII
                          TCGAGGGCGG GAGTTG
                            _____      CG
GAM355  GORASP1         GCCCGGGCTGCCTGCCCACA      5491 TG   _ C   T GCC
                          CCCGGGCT CC GCCC CA
                          IIIIIIII II IIII II
                          GGGCCCGA GG CGGG GT
                            __    C  A  T AII
GAM355  GYPC            CCCGGGCTCCTGACCCTCGGC     5478 TGCC     C_    A C
                          CGGGCTCC GCCCTC GC
                          IIIIIIII IIIIII II
                          GCCCGAGG TGGGAG CG
                            ____    AC    C C
GAM355  HNF4A           CCCGAAGGCCCCCGCCCTCCGCC   5471 TGCCC            A  I
                          GGGCTCCCGCCCTC GCC
                          IIIIIIIIIIIIII III
                          TCCGGGGGCGGGAG CGG
                          GCT__       G  G
GAM355  HRMT1L1         GCCTGAGCCACCGCCCTCAACC    5497 TG C  TC          I
                          CC GGGC CCGCCCTCAGCC
                          II IIII IIIIIIIIIIII
```

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                      GG CTCG  GGCGGGAGTTGG
                    __  A   GT         G
GAM355 IKBKAP       TGTCCGCGGCTCCCGCTCTC    5499  C  _       C  AGCC
                    TG CCG GGCTCCCGC CTC
                    II III IIIIIIIII III
                    AC GGC CCGAGGGCG GAG
                     A    G      A  IIIC
GAM355 KCNK1        CCTGGCTCCCGCCCGCCGCC    5486 TGCCCG       TCA
                      GGCTCCCGCCC  GCC
                      IIIIIIIIIII  III
                      CCGAGGGCGGG  CGG
                    _____           CGG
GAM355 KIF5C        CCCGGGCTCCTGCGCGCTCAGCC   5477 TGCC    __  C    I
                      CGGGCTCC CGC CTCAGCC
                      IIIIIIII III IIIIIII
                      GCCCGAGG GCG GAGTCGG
                     ____      AC  C    T
GAM355 MAP3K11      CCGGGCCCTGGCCCTCAGCC     5484 TGCCCG    CC
                       GGCTC GCCCTCAGCC
                       IIIII IIIIIIIIII
                       CCGGG CGGGAGTCGG
                      _____    AC
GAM355 MAPT         CCCGTGGCCTCCCGCCC-CACCC   5472 TGCCC G     T G  I
                      GG CTCCCGCCC CA CC
                      II IIIIIIIII II II
                      CC GAGGGCGGG GT GG
                    GCA__ G    _ G G
GAM355 MUCDHL       CGGGCTCCCGGCCGCAGCC     5488 TGCCCGGG    C T
                       CTCCCG CC CAGC
                       IIIIII II IIII
                       GAGGGC GG GTCG
                      _____    C C
GAM355 MYO5A        CCCGGGCTCGCCGCGAGCAGCC   5476 TGCC    _  CCT   I
                      CGGGCTC CCGC  CAGCC
                      IIIIIII IIII  IIIII
                      GCCCGAG GGCG  GTCGG
                     ____      C  CTC   C
GAM355 NAGA         TGCCTGGCTAGCTCGGCCGCCCTCAACC5500  C ___  __        III
                     TGCC GG  GCTC CCGCCCTCAGCC  G
                     IIII II  IIII IIIIIIIIIII  I
                     ACGG CC  CGAG GGCGGGAGTTGG  C
                      A GAT   CC         III
GAM355 NEUROD2      GCCCGGGCTCCGGCGCCCT     5492 TG        __    CAGC
                     CCCGGGCTCC CGCCCT
                     IIIIIIIIII IIIIII
                     GGGCCCGAGG GCGGGA
                    __           CC   TIII
GAM355 PACSIN1      GCCCGGGCTGAGGGCCTGCATGCC   5493 TG      CCC_ CT _ II
                     CCCGGGCT  GCC CA GCC
                     IIIIIIII   III II III
```

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                         GGGCCCGA   CGG  GT CGG
                     __   CTCC   AC  A  GI
GAM355  PITPN        GCCCGGCCTCCCGCCCGCTGCC   5496 TG    G      TCA   I
                     CCCGG CTCCCGCCC  GCC
                     ||||| |||||||||  |||
                     GGGCC GAGGGCGGG  CGG
                     __   G     CGA  G
GAM355  PLXNA1       GCCCTGGCCTCAC-CCCTCAGCC   5490 TG  _  G  CCG       I
                     CCC GG CTC  CCCTCAGCC
                     ||| || |||  |||||||||
                     GGG CC GAG  GGGAGTCGG
                     __  A G  TG_     G
GAM355  POLH         TGCCCGGGCAACCGTCCCCAGC    5505       TC  C    CI
                     TGCCCGGGC CCG CCTCAGC
                     ||||||||| ||| ||||||||
                     ACGGGCCCG GGC GGGGTCG
                          TT  A    II
GAM355  PVRL2        CCCGGGCTCCC-CATGCAGCC     5480 TGCC      GCCCT
                     CGGGCTCCC   CAGCC
                     |||||||||   |||||
                     GCCCGAGGG   GTCGG
                     ____        GTAC_
GAM355  RASGRP2       GCCCTGGC-CCTGCCCTCAGC    5494 TG  G  T C      C
                     CCC GGC CC GCCCTCAGC
                     ||| ||| || |||||||||
                     GGG CCG GG CGGGAGTCG
                     __  A _ A       A
GAM355  SIAT4C       TGGCCGGGCTCCCACGGCTCCAGC  5503 C        C_ _ CII
                     TG CCGGGCTCCCGC CTC AGC
                     || ||||||||||| ||| |||
                     AC GGCCCGAGGGTG GAG TCG
                     C        CC G  III
GAM355  SLC19A1      TGCCCTGGGGCTCCCGGACCCGGCC 5498   __     CC  A  II
                     TGCCC GGGCTCCCG CTC GCC
                     ||||| ||||||||| ||| |||
                     ACGGG CCCGAGGGC GGG CGG
                          AC    CT C II
GAM355  TP53BP2      CCCGGGCTCCCCCGCCCCGGCC    5479 TGCC      __   CA   I
                     CGGGCTCCC GCCCT GCC
                     ||||||||| ||||| |||
                     GCCCGAGGG CGGGG CGG
                     ____      GG  C_ C
GAM356  CTH          GAAGAAGAGAG-GAAAAGAAC     5510 T_  AT A T     CT
                     GAA GA AG GAAAAGAAC
                     ||| || || |||||||||
                     CTT CT TC CTTTTCTTG
                     TT __ C _    TI
GAM356  DMPK         ATGAATTTCAAGAAGAACCTG     5509 TGAAATGAAAGT A
                     GA AAGAACCTG
                     || |||||||||
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                         TT TTCTTGGAC
                   TAAAG_____  C
GAM356  DRD3       TGAAATGAACAG---AAAGAA    5511       AGT  A  CC
                   TGAAATGAA  GAAA GAA
                   |||||||||  |||| |||
                   ACTTTACTT  CTTT CTT
                     GT_  _  II
GAM356  MELK       TGGAATTAGA---AAAAGAACCTG  5513 TGAAATGAA  T
                     AG GAAAAGAACCTG
                     || |||||||||||
                     TC TTTTTCTTGGAC
                   ACCTTAA__  _
GAM356  NR1I2      TGATGTGAAAGTGAGCAAAG     5512  AA       AA  ACCT
                    TGA TGAAAGTGA AGA
                    ||| ||||||||| |||
                    ACT ACTTTCACT TTT
                     AC     CG  CIII
GAM357  B4GALT5     ACAGCA--TGAACAAACGGGGAC  5517 TA    CC   A
                    CAGTA TGGA AAACGGGGAC
                    ||||| |||| ||||||||||
                    GTCGT ACTT TTTGCCCCTG
                     __   __  G
GAM357  FBXO7       GTAGCTGAGGCGAAACGGGGA   5520 TACAGTACCT AA      C
                      GG AAACGGGGA
                      || |||||||||
                      CC TTTGCCCCT
                   GACT_____  GC      T
GAM357  PIK3CG      AGTACCTGGGACTACAGGCAC   5518 TACAGT    AAAA  G
                      ACCTGG   ACGGG AC
                      ||||||   ||||| ||
                      TGGACC   TGTCC TG
                   _____  CTGA   G
GAM357  SERPINB5     ACAGTTATCCTGGAAAATGCGTGGA 5516 TA  A__      A_ G CII
                     CAGT  CCTGGAAAA CG GGA
                     ||||  ||||||||| || |||
                     GTCA  GGACCTTTT GC CCT
                     __  ATA     AC A TII
GAM357  SLC1A4      GTAATTGGAAAAACATGGAC    5521 TACAGTACC      G
                      TGGAAAAACG GGA
                      |||||||||| |||
                      ACCTTTTTGT CCT
                   A_____      A
GAM357  TNFAIP2     CAGTACCTGGGAAAA-GGGGAC  5519 TACA     A  C
                      GTACCTGG AAAA GGGGAC
                      |||||||| |||| ||||||
                      CATGGACC TTTT CCCCTG
                      ____     C  _
GAM358  ADAM11      TGACAGGGACAGCAGGACG     5538        C C _ CII
                    TGACAGGGAC GC GG C
                    |||||||||| || || |
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                        ACTGTCCCTG CG CC G
                          T  T  T CII
GAM358 ADAM11          TGACAGGGACAGCAGGACG      5538      C  C  C CCCC
                         TGACAGGGAC GC GG CG
                         ||||||||| || || ||
                         ACTGTCCCTG CG CC GC
                          T  T  T IIIG
GAM358 ANK1          GACAAG---CGCCTAGGCCGCCCCG 5530 _    GAC    __        I
                         ACAGG  CGCC GGCCGCCCC
                         |||||  |||| |||||||||
                         TGTTC  GCGG CCGGCGGGG
                           C    ___  AT       I
GAM358 ANK1          GACAAG---CGCCTAGGCCGCCCCG 5530 TG   GAC    __
                         ACAGG  CGCC GGCCGCCCCG
                         |||||  |||| ||||||||||
                         TGTTC  GCGG CCGGCGGGGC
                           __    ___    AT
GAM358 ANK1          GACAAGG--CGCCTAGGCCGCCCCG 5531     AC   __        I
                         ACAGGG CGCC GGCCGCCCC
                         |||||| |||| |||||||||
                         TGTTCC GCGG CCGGCGGGG
                             __   AT      I
GAM358 ANK1          GACAAGG--CGCCTAGGCCGCCCCG 5531 TG    AC   __         I
                         ACAGGG CGCC GGCCGCCCCG
                         |||||| |||| ||||||||||
                         TGTTCC GCGG CCGGCGGGGC
                           __   __  AT       C
GAM358 BRF1          TGACAGGGAGCGCC-ACTGCCC    5539     C  G C  CG
                        TGACAGGGA CGCCG C GCCC
                        ||||||||| ||||| | ||||
                        ACTGTCCCT GCGGT G CGGG
                             C  _A  II
GAM358 BRF1          TGACAGGGAGCGCC-ACTGCCC     5539 _     C   __  GCCI
                         GACAGGGA CGCCG GCC
                         |||||||| ||||| |||
                         CTGTCCCT GCGGT CGG
                          A    C  GA  IIIC
GAM358 CACNA1A         GGGAGTCGCCGGCCGTGCCG     5536  C_      CC II
                         GGGA CGCCGGCCG CC
                         |||| ||||||||| ||
                         CCCT GCGGCCGGC GG
                           CA    AC CI
GAM358 CACNA1A         GGGAGTCGCCGGCCGTGCCG      5536 TGACAGGGAC     CC
                          CGCCGGCCG CC
                          ||||||||| ||
                          GCGGCCGGC GG
                          A_____      AC
GAM358 CDC34          GACAGGTGG-GCCGGCCGCTCC    5534  GACC     CI
                         ACAGG  GCCGGCCGC
                         |||||  |||||||||
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                              TGTCC   CGGCCGGCG
                               ACC_        AG
GAM358 CDC34              GACAGGTGG-GCCGGCCGCTCC    5534 TG    GACC      _  G
                               ACAGG   GCCGGCCGC CCC
                               |||||   ||||||||| |||
                               TGTCC   CGGCCGGCG GGG
                                __   ACC_      A  I
GAM358 COL18A1            CAGGGGCTGGCCGGCCGCTCC    5525 A  ACC      CCI
                               GGG   GCCGGCCGC
                               |||   |||||||||
                               CCC   CGGCCGGCG
                                C  GAC      AGI
GAM358 COL18A1            CAGGGGCTGGCCGGCCGCTCC    5525 TGACA  ACC      _  G
                               GGG   GCCGGCCGC CCC
                               |||   ||||||||| |||
                               CCC   CGGCCGGCG GGG
                               _____  GAC      A  A
GAM358 FCN2              GACAGGGAC--ACGGCCCCC    5532      CGC    GI
                               GACAGGGAC  CGGCC
                               |||||||||  |||||
                               CTGTCCCTG  GCCGG
                                 T__    GG
GAM358 FCN2              GACAGGGAC--ACGGCCCCC    5532 TG    CGC    G
                                 ACAGGGAC  CGGCC CCC
                                 ||||||||  ||||| |||
                                 TGTCCCTG  GCCGG GGG
                                __       T__   _
GAM358 GPC1              CAGAG-CCGCCGGCCCTCCC     5529 _  A      G_ CI
                                 AGGG CCGCCGGCC  CC
                                 |||| ||||||||| ||
                                 TCTC GGCGGCCGG  GG
                                G   _     GA II
GAM358 GPC1              CAGAG-CCGCCGGCCCTCCC     5529 TGACAG  A      GC
                                 GG CCGCCGGCC  CCC
                                 || ||||||||| |||
                                 TC GGCGGCCGG  GGG
                               _____ _       GA
GAM358 HDAC4             ACAGGGACCGCCGGGCTGCAGCCCC 5524 CAGG      _ C___    I
                               GACCGCCGG C   GCCC
                               ||||||||| |   ||||
                               CTGGCGGCC G   CGGG
                                  ____    C ACGT   I
GAM358 HDAC4             ACAGGGACCGCCGGGCTGCAGCCCC 5524 TGAC        _ C___    GII
                               AGGGACCGCCGG C   GCCCC
                               |||||||||| |   |||||
                               TCCCTGGCGGCC G   CGGGG
                                  ____      C ACGT   ACI
GAM358 MAD1L1            GAGAGGGT--GCTGGCCGCCCC    5535 AC_   ACC  C        I
                               AGGG   GC GGCCGCCC
                               ||||   || |||||||
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                         TCCC  CG CCGGCGGG
                         CTC   A__  A       I
GAM358 MAD1L1        GAGAGGGT--GCTGGCCGCCCC   5535 TGAC    ACC  C
                         AGGG  GC GGCCGCCCC
                         |||| || |||||||||
                         TCCC  CG CCGGCGGGG
                         TC__  A__  A
GAM358 MAPRE3        CAGGG-CTGC-GGCCGCCC      5527      ACC  C      I
                         CAGGG  GC GGCCGCC
                         |||||  || ||||||||
                         GTCCC  CG CCGGCGG
                          GA_  _      G
GAM358 MLC1         TGGCAGGGTCTGCAGGCCGCCCC  5540 A    ACC  C       GI
                         TG CAGGG  GC GGCCGCCCC
                         || |||||  || ||||||||||
                         AC GTCCC  CG CCGGCGGGG
                          C   AGA  T        II
GAM358 MLC1         TGGCAGGGTCTGCAGGCCGCCCC  5540 GA    ACC  C      I
                         CAGGG  GC GGCCGCCC
                         |||||  || |||||||||
                         GTCCC  CG CCGGCGGG
                         CC   AGA  T       I
GAM358 PAK4        GACAGGGACCATCTGTCCCCC     5533        CCGG_ G I
                         ACAGGGACCG   CC CC
                         ||||||||||   || ||
                         TGTCCCTGGT   GG GG
                           AGACA _  I
GAM358 PAK4        GACAGGGACCATCTGTCCCCC     5533 TG       CCGGCCG  G
                         ACAGGGACCG    CCCC
                         ||||||||||    ||||
                         TGTCCCTGGT    GGGG
                          __       AGACA__   G
GAM358 PPP5C       GGGAT-GCAGGCCGCCCG        5537    CC C       I
                         GGGA  GC GGCCGCCCC
                         ||||  || |||||||||
                         CCCT  CG CCGGCGGGG
                          A_   T       C
GAM358 PPP5C       GGGAT-GCAGGCCGCCCG        5537 TGA  GA   GG
                         CAGG  CCGCC  CCGCCC
                         ||||  |||||  ||||||
                         GTCC  GGCGG  GGCGGG
                         C__   __    __
GAM358 TBX2        CAGGGACCGCTGG--GCCC       5528       C_  GCCI
                         CAGGGACCGC  GGCC
                         ||||||||||  ||||
                         GTCCCTGGCG  CCGG
                          AC   GIII
GAM358 TBX2        CAGGGACCGCTGG--GCCC       5528 TGACAG    C CC
                         GGACCGC GG GCCC
                         ||||||| || ||||
```

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                          CCTGGCG CC  CGGG
                          _____      A __
GAM358 WHSC1        CAGGCAGGGCCGGCCGCCC    5526   GACC        II
                        CAGG   GCCGGCCGCC
                        ||||   ||||||||||
                        GTCC   CGGCCGGCGG
                          GTCC      GI
GAM358 WHSC1        CAGGCAGGGCCGGCCGCCC    5526 TGA  GACC        C
                        CAGG   GCCGGCCGCCC
                        ||||   |||||||||||
                        GTCC   CGGCCGGCGGG
                        C__  ____       A
GAM359 ALDH3A2       AGGAAGTGAGCAGTGCCATTA    5550      AA__  GATTI
                        GGAAGTGAG  GTCA
                        |||||||||  ||||
                        CCTTCACTC  CGGT
                          GTCA  AAIII
GAM359 ALDH3A2       AGGAAGTGAGCAGTGCCATTA    5550 TA     AA__  GATTACC
                        GGAAGTGAG  GTCA
                        |||||||||  ||||
                        CCTTCACTC  CGGT
                        __    GTCA  AATTIII
GAM359 AQP8       AAGTGAGAATTGTCAGCTT     5544     __  ATIII
                        AAGTGAGAA  GTCAG
                        |||||||||  |||||
                        TTCACTCTT  CAGTC
                          AA   GAAII
GAM359 CD1A       AGGAAGTGAGGAGCACAG-TTA    5549      A _ ATTI
                        GGAAGTGAG AGT CAG
                        ||||||||| ||| |||
                        CCTTCACTC TCG GTC
                          C  T  AAII
GAM359 CD1A       AGGAAGTGAGGAGCACAG-TTA    5549 TA     A _ A CC
                        GGAAGTGAG AGT CAG TTA
                        ||||||||| ||| ||| |||
                        CCTTCACTC TCG GTC AAT
                        __     C  T _  CI
GAM359 EYA1       AAGTAGAGATGTACAGATTACC    5543 AGT   A _    I
                        GAGA GT CAGATTAC
                        |||| || |||||||||
                        CTCT CA GTCTAATG
                        AT_   A T     I
GAM359 EYA1       AAGTAGAGATGTACAGATTACC    5543 TAGGAAGT   A _
                        GAGA GT CAGATTACC
                        |||| || ||||||||||
                        CTCT CA GTCTAATGG
                        T_____   A T
GAM359 FACL6       GAAGTGAGAGGACAAACTCTACC    5553 A   AGT   ACI
                        GTGAGA  CAGATT
                        ||||||  ||||||
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                        CACTCT  GTTTGA
                     _     CCT    GAT
GAM359  FACL6        GAAGTGAGAGGACAAACTCTACC  5553 TAGGAA    AGT    __  I
                            GTGAGA  CAGAT TACC
                            |||||| ||||| ||||
                            CACTCT  GTTTG ATGG
                     _____     CCT   AG   G
GAM359  GLP1R        GATGGGAGAAGTCAGAATTGCC  5552 TAGGAAGT       TTA__
                           GAGAAGTCAGA    CC
                           ||||||||||   ||
                           CTCTTCAGTCT    GG
                     CC_____        TAACG
GAM359  GLP1R        GATGGGAGAAGTCAGAATTGCC  5552 GAAGT       TTI
                           GAGAAGTCAGA
                           |||||||||||
                           CTCTTCAGTCT
                     C____        TAA
GAM359  HTN1         AGGAGAGTCAAGAAGTCAG       5545  _  _        III
                        AGGA AGT GAGAAGTCA
                        |||| ||| |||||||||
                        TCCT TCA TTCTTCAGT
                          C  G       CII
GAM359  HTN1         AGGAGAGTCAAGAAGTCAG       5545 TA  _  _        ATTAC
                           GGA AGT GAGAAGTCAG
                           ||| ||| ||||||||||
                           CCT TCA TTCTTCAGTC
                        __ C  G        AIIIC
GAM359  KRTHA4        TAGTAACTG-GAGCTCAGATTAC  5555  G G A AG      C
                         TAG AA TG GA  TCAGATTAC
                         ||| || || ||  |||||||||
                         ATC TT AC CT  AGTCTAATG
                          A  G  _  CG        I
GAM359  KRTHA4        TAGTAACTG-GAGCTCAGATTAC  5555_ G G A AG      I
                          AG AA TG GA  TCAGATTA
                          || || || ||  ||||||||
                          TC TT AC CT  AGTCTAAT
                          A A G _  CG        I
GAM359  MAD2L2       AGGAGGCTGAGAAGTCGAGGTT  5548 _ AAG      _ ATI
                          GG  TGAGAAGTC AG
                          ||  |||||||||| ||
                          CC  ACTCTTCAG TC
                          T G__       C CAI
GAM359  MAD2L2       AGGAGGCTGAGAAGTCGAGGTT  5548 TA  A _      _ ATTACC
                          GGA G TGAGAAGTC AG
                          ||| | |||||||||| ||
                          CCT C ACTCTTCAG TC
                          __  C G       C CAACII
GAM359  MET         AGGAACCAGTGGAGAAGTCAG    5546  ___  _       IIIC
                         AGGA  AGTG AGAAGTCA
                         ||||  |||| |||||||||
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                                    TCCT  TCAC TCTTCAGT
                                     TGG  C      CIII
GAM359 MET              AGGAACCAGTGGAGAAGTCAG    5546 TA  ___  _        ATTACC
                                GGA  AGTG AGAAGTCAG
                                III  IIII IIIIIIIII
                                CCT  TCAC TCTTCAGTC
                             __  TGG  C      GIIICC
GAM359 PCDHGA12         GGACAGTTGGGAAGTCAGA     5554 AG__ A       III
                                GGA  TG GAAGTCAG
                                III  II IIIIIIII
                                CCT  AC CTTCAGTC
                                GTCA C      TII
GAM359 PCDHGA12         GGACAGTTGGGAAGTCAGA     5554 TAGGA  GA_       TTAC
                                 AGT  GAAGTCAGA
                                 III  IIIIIIIII
                                 TCA  CTTCAGTCT
                             TG___  ACC      CGII
GAM359 PITPNB          AGGACTGTCAGCAAATCAGATTAC 5547 GGAA  G _        I
                                GT AG AAGTCAGATTA
                                II II IIIIIIIIIII
                                CA TC TTTAGTCTAAT
                             TGA_ G G        I
GAM359 PITPNB          AGGACTGTCAGCAAATCAGATTAC 5547 TA  A_ G _        CI
                                GGA  GT AG AAGTCAGATTAC
                                III  II II IIIIIIIIIII
                                CCT  CA TC TTTAGTCTAATG
                             __  GA  G G        AI
GAM359 ZNF80           AGTGAGAAGTAGCAAGATT      5551       C ATIII
                                AGTGAGAAGT AG
                                IIIIIIIIII II
                                TCACTCTTCA TC
                             _ GTTCT
GAM360 ABCD3           TGATAGCATTGCA-TACTC      5565 AATG      AAGG
                                ATAGCATTG ACTCG
                                IIIIIIIII IIIII
                                TATCGTAAC TGAGT
                             ____      GTA_
GAM360 ABCD3           TGATAGCATTGCA-TACTC      5565       AAGG I
                                TGATAGCATTG ACT
                                IIIIIIIIIII III
                                ACTATCGTAAC TGA
                                GTA_ G
GAM360 ABCD3           TGATAGCATTGCA-TACTC      5565 AATG      AAGG
                                ATAGCATTG ACTCG
                                IIIIIIIII IIIII
                                TATCGTAAC TGAGT
                             ____      GTA_
GAM360 ABCD3           TGATAGCATTGCA-TACTC      5565       AAGG I
                                TGATAGCATTG ACT
                                IIIIIIIIII III
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                        ACTATCGTAAC   TGA
                          GTA_  G
GAM360  ACPT          AAGGATAGCATTCAGCAGGA      5558 AAT       GA__   CTCGG
                        GATAGCATT   AGGA
                        |||||||||  ||||
                        CTATCGTAA   TCCT
                        TTC      GTCG   IIIGG
GAM360  ACPT          AAGGATAGCATTCAGCAGGA      5558 AAT       GA__   III
                        GATAGCATT   AGG
                        |||||||||  |||
                        CTATCGTAA   TCC
                        TTC      GTCG  TII
GAM360  ACPT          AAGGATAGCATTCAGCAGGA      5558 AAT         GA__   CTCGG
                        GATAGCATT   AGGA
                        |||||||||  ||||
                        CTATCGTAA   TCCT
                        TTC       GTCG   IIIGG
GAM360  ACPT          AAGGATAGCATTCAGCAGGA      5558 AAT       GA__   III
                        GATAGCATT   AGG
                        ||||||||| |||
                        CTATCGTAA   TCC
                        TTC       GTCG  TII
GAM360  AMY2B          GAAAGCACTTGAAGGACACGGG    5561 AATGAT     _      T
                          AGCATT GAAGGAC CGGG
                          |||||| ||||||| ||||
                          TCGTGA CTTCCTG GCCC
                          _____     A    T
GAM360  AMY2B          GAAAGCACTTGAAGGACACGGG   5561 AT      _     T  I
                          AGCATT GAAGGAC CGG
                          |||||| ||||||| |||
                          TCGTGA CTTCCTG GCC
                          T_     A    T  I
GAM360  AMY2B          GAAAGCACTTGAAGGACACGGG    5561 AATGAT     _      T
                          AGCATT GAAGGAC CGGG
                          |||||| ||||||| ||||
                          TCGTGA CTTCCTG GCCC
                          _____     A    T
GAM360  AMY2B          GAAAGCACTTGAAGGACACGGG   5561 AT      _     T  I
                          AGCATT GAAGGAC CGG
                          |||||| ||||||| |||
                          TCGTGA CTTCCTG GCC
                          T_      A    T  I
GAM360  APP         CTA-TTCATGCACTAGTTT       3499 ACTACTTC        CTC
                          GCACTAGTTT
                          ||||||||||
                          CGTGATCAAA
                        ATAAGTA_        CII
GAM360  APP         CTA-TTCATGCACTAGTTT       3499 CACTACTTC        CT
                          GCACTAGTTT
                          ||||||||||
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                          CGTGATCAAA
                     TAAGTA___        CT
GAM360  APP          CTA-TTCATGCACTAGTTT      3499 CTACTTC_        II
                          GCACTAGTT
                          ||||||||||
                          CGTGATCAA
                     GATAAGTA        AI
GAM360  APP          CTA-TTCATGCACTAGTTT      3499 TCACTACTTC        CT
                          GCACTAGTTT
                          |||||||||||
                          CGTGATCAAA
                     AAGTA_____        CT
GAM360  APP          CTA-TTCATGCACTAGTTT      3499 ACTACTTC        CTC
                          GCACTAGTTT
                          |||||||||||
                          CGTGATCAAA
                     ATAAGTA_        CII
GAM360  APP          CTA-TTCATGCACTAGTTT      3499 CACTACTTC        CT
                          GCACTAGTTT
                          |||||||||||
                          CGTGATCAAA
                     TAAGTA___        CT
GAM360  APP          CTA-TTCATGCACTAGTTT      3499 CTACTTC_        II
                          GCACTAGTT
                          ||||||||||
                          CGTGATCAA
                     GATAAGTA        AI
GAM360  APP          CTA-TTCATGCACTAGTTT      3499 TCACTACTTC        CT
                          GCACTAGTTT
                          |||||||||||
                          CGTGATCAAA
                     AAGTA_____        CT
GAM360  FPGS         TAGCATTGAAGAGCAAGACTCG    5564            _____  IIIC
                     TAGCATTGAAG    GACTC
                     |||||||||||    |||||
                     ATCGTAACTTC    CTGAG
                          TCGTT    CIII
GAM360  FPGS         TAGCATTGAAGAGCAAGACTCG    5564 AA  T_  TTGAA
                       TGA AGCA    GGACTCGGG
                       ||| ||||    |||||||||
                       ACT TCGT    TCTGAGCTT
                       A_  TC    _____
GAM360  FPGS         TAGCATTGAAGAGCAAGACTCG    5564            _____  IIIC
                     TAGCATTGAAG    GACTC
                     |||||||||||    |||||
                     ATCGTAACTTC    CTGAG
                          TCGTT    CIII
GAM360  FPGS         TAGCATTGAAGAGCAAGACTCG    5564 AA  T_  TTGAA
                       TGA AGCA    GGACTCGGG
                       ||| ||||    |||||||||
```

```
                              ACT TCGT   TCTGAGCTT
                              A_  TC     _____
GAM360 FUT6           GAT-GC-TAGAGGGACTCGGG   5563 AATGATA ATT A
                         GC  GA GGACTCGG
                         ||  || |||||||||
                         CG  CT CCTGAGCC
                         _____ AT_ C
GAM360 FUT6           GAT-GC-TAGAGGGACTCGGG   5563 ATA ATT A     I
                         GC  GA GGACTCGG
                         ||  || |||||||||
                         CG  CT CCTGAGCC
                         CTA AT_ C     I
GAM360 FUT6           GAT-GC-TAGAGGGACTCGGG   5563 AATGATA ATT A
                         GC  GA GGACTCGG
                         ||  || |||||||||
                         CG  CT CCTGAGCC
                         _____ AT_ C
GAM360 FUT6           GAT-GC-TAGAGGGACTCGGG   5563 ATA ATT A     I
                         GC  GA GGACTCGG
                         ||  || |||||||||
                         CG  CT CCTGAGCC
                         CTA AT_ C     I
GAM360 GPC3          GAGAGCAGTCCCAGGACTCGG   5562 AATGAT _ GA      G
                          AGCA TT AGGACTCGG
                          |||| || |||||||||
                          TCGT AG TCCTGAGCC
                          _____ C GG      G
GAM360 GPC3          GAGAGCAGTCCCAGGACTCGG   5562 AT _ GA     I
                          AGCA TT AGGACTCG
                          |||| || ||||||||
                          TCGT AG TCCTGAGC
                          C_  C GG     I
GAM360 GPC3          GAGAGCAGTCCCAGGACTCGG   5562 AATGAT _ GA      G
                          AGCA TT AGGACTCGG
                          |||| || |||||||||
                          TCGT AG TCCTGAGCC
                          _____ C GG      G
GAM360 GPC3          GAGAGCAGTCCCAGGACTCGG   5562 AT _ GA     I
                          AGCA TT AGGACTCG
                          |||| || ||||||||
                          TCGT AG TCCTGAGC
                          C_  C GG     I
GAM360 IL10RA       CACATACCCTGCACTAGTT    3498 _ TC    TCTC
                          CAC TACT GCACTAGTT
                          ||| |||| |||||||||
                          GTG ATGG CGTGATCAA
                          T  GA      |||C
GAM360 IL10RA       CACATACCCTGCACTAGTT    3498 _ TC    ||
                          CAC TACT GCACTAGT
                          ||| |||| ||||||||
```

```
                         GTG ATGG  CGTGATCA
                          T   GA      AI
GAM360  IL10RA    CACATACCCTGCACTAGTT    3498 TC _  TC     CT
                     AC TACT  GCACTAGTTT
                     || |||| |||||||||||
                     TG ATGG  CGTGATCAAG
                     __  T   GA      II
GAM360  IL10RA    CACATACCCTGCACTAGTT    3498  _  TC     TCTC
                     CAC TACT  GCACTAGTT
                     ||| |||| ||||||||||
                     GTG ATGG  CGTGATCAA
                      T   GA      IIIC
GAM360  IL10RA    CACATACCCTGCACTAGTT    3498  _  TC     II
                     CAC TACT  GCACTAGT
                     ||| |||| |||||||||
                     GTG ATGG  CGTGATCA
                      T   GA      AI
GAM360  IL10RA    CACATACCCTGCACTAGTT    3498 TC _  TC     CT
                     AC TACT  GCACTAGTTT
                     || |||| |||||||||||
                     TG ATGG  CGTGATCAAG
                     __  T   GA      II
GAM360  TBL1X     ATGTCAGCTCTGCAAGGACTCG   5559 AA A  A  _     GG
                       TG TAGC TTG AAGGACTCG
                       || |||| ||| ||||||||||
                       AC GTCG GAC TTCCTGAGC
                       __  A   A  G      GI
GAM360  TBL1X     ATGTCAGCTCTGCAAGGACTCG   5559 TGA  A  _     I
                        TAGC TTG AAGGACTC
                        |||| ||| |||||||||
                        GTCG GAC TTCCTGAG
                        CA_   A  G      I
GAM360  TBL1X     ATGTCAGCTCTGCAAGGACTCG   5559 TGA  A  _     I
                        TAGC TTG AAGGACTC
                        |||| ||| |||||||||
                        GTCG GAC TTCCTGAG
                        CA_   A  G      I
GAM360  TBL1X     ATGTCAGCTCTGCAAGGACTCG   5559 AA A  A  _     GG
                       TG TAGC TTG AAGGACTCG
                       || |||| ||| ||||||||||
                       AC GTCG GAC TTCCTGAGC
                       __  A   A  G      GI
GAM360  WBSCR5     CACTACTT--CTCTAGACTCTC   5560       GCA  T
                      CACTACTTC  CTAG TTCTC
                      |||||||||  |||| |||||
                      GTGATGAAG  GATC GAGAG
                         A__  T
GAM360  WBSCR5     CACTACTT--CTCTAGACTCTC   5560       GCA  T  I
                      CACTACTTC  CTAG TTC
                      |||||||||  |||| |||
```

```
                              GTGATGAAG  GATC GAG
                                   A__   T A
GAM360  WBSCR5          TCACTACTT--CTCTAGACTCTC  3505      GCA   T
                       TCACTACTTC  CTAG TTCTC
                       |||||||||  |||| |||||
                       AGTGATGAAG  GATC GAGAG
                            A__   T
GAM360  WBSCR5          TCACTACTT--CTCTAGACTCTC  3505 _      GCA   T  I
                        CACTACTTC  CTAG TTCT
                        ||||||||  |||| ||||
                        GTGATGAAG  GATC GAGA
                         A    A__   T  I
GAM360  WBSCR5          CACTACTT--CTCTAGACTCTC   5560      GCA   T
                       CACTACTTC  CTAG TTCTC
                       ||||||||  |||| |||||
                       GTGATGAAG  GATC GAGAG
                         A__   T
GAM360  WBSCR5          CACTACTT--CTCTAGACTCTC   5560      GCA   T  I
                       CACTACTTC  CTAG TTC
                       ||||||||  |||| |||
                       GTGATGAAG  GATC GAG
                         A__   T A
GAM360  WBSCR5          TCACTACTT--CTCTAGACTCTC  3505      GCA   T
                       TCACTACTTC  CTAG TTCTC
                       |||||||||  |||| |||||
                       AGTGATGAAG  GATC GAGAG
                            A__   T
GAM360  WBSCR5          TCACTACTT--CTCTAGACTCTC  3505 _      GCA   T  I
                        CACTACTTC  CTAG TTCT
                        ||||||||  |||| ||||
                        GTGATGAAG  GATC GAGA
                         A    A__   T  I
GAM360  ZNF146          CTACCTT-CACTAGTTTCTC      3500 _    CG        I
                       TACTT CACTAGTTTCT
                       ||||| |||||||||||
                       ATGGA GTGATCAAAGA
                         G    A_        I
GAM360  ZNF146          CTACCTT-CACTAGTTTCTC      3500 AC    CG
                        TACTT CACTAGTTTCTC
                        ||||| ||||||||||||
                        ATGGA GTGATCAAAGAG
                          __    A_
GAM360  ZNF146          CTACCTT-CACTAGTTTCTC      3500 CACT   CG
                         ACTT CACTAGTTTCTC
                         |||| ||||||||||||
                         TGGA GTGATCAAAGAG
                          ____    A_
GAM360  ZNF146          CTACCTT-CACTAGTTTCTC      3500 TCACTA  GC
                          CTTC ACTAGTTTCT
                          |||| |||||||||
```

```
                            GAAG  TGATCAAAGA
                         G_____    __
GAM360  ZNF146          CTACCTT-CACTAGTTTCTC      3500 _    CG         I
                           TACTT  CACTAGTTTCT
                           IIIII  IIIIIIIIIII
                           ATGGA  GTGATCAAAGA
                         G    A_          I
GAM360  ZNF146          CTACCTT-CACTAGTTTCTC      3500 AC    CG
                            TACTT  CACTAGTTTCTC
                            IIIII  IIIIIIIIIII
                            ATGGA  GTGATCAAAGAG
                          __     A_
GAM360  ZNF146          CTACCTT-CACTAGTTTCTC      3500 CACT   CG
                             ACTT  CACTAGTTTCTC
                             IIII  IIIIIIIIIII
                             TGGA  GTGATCAAAGAG
                           ____      A_
GAM360  ZNF146          CTACCTT-CACTAGTTTCTC      3500 TCACTA  GC
                             CTTC  ACTAGTTTCT
                             IIII  IIIIIIIIII
                             GAAG  TGATCAAAGA
                         G_____    __
GAM361  ARSA           CCTGAAGCTCCAGAGGGCCGGGG   5571 TCCCCT      __   CA  I
                            AAGCTCCA GGGCC GGG
                            IIIIIIIII IIIII III
                            TTCGAGGT CCCGG CCC
                         C_____     CT   C_  G
GAM361  ATP6V1C1        CCTAAGCTCC-GGCCTCACGG    5573 TCCCCT     AG   _  G
                            AAGCTCC GGCC CA G
                            IIIIIII IIII II I
                            TTCGAGG CCGG GT C
                           _____     __  A G
GAM361  AXL            TCCCCCCAGCTCCAGGCTCCCCGG  5576     A      G_  A GI
                            TCCCCT AGCTCCAGG  CCC GG
                            IIIIII IIIIIIIII  III II
                            AGGGGG TCGAGGTCC  GGG CC
                             G      GA  G  II
GAM361  EGLN1          CCTAAGCTCC--GGCGCAG       5572 TCCCCT     AG   C
                            AAGCTCC  GGC CAG
                            IIIIIII  III III
                            TTCGAGG  CCG GTC
                           _____      __   C
GAM361  FMNL           CCTTCAGCTCCAGGGCCGAGGG    5570 TCCCCTA        C
                            AGCTCCAGGGCC AGGG
                            IIIIIIIIIIII IIII
                            TCGAGGTCCCGG TCCC
                         AAG____         C
GAM361  MGAT4B         AACCTCCAGCTGGGCCCAGG      5568 TCCCCTA   CCA
                            AGCT  GGGCCCAGG
                            IIII  IIIIIIIIII
```

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                            TCGA   CCCGGGTCC
                     G_____      ___
GAM361 MYOG          CCCCCAAGCTCCAGCAGCCC    5569 TC         _    AGG
                          CCCTAAGCTCCAG GGCCC
                          |||||||||||| |||||
                          GGGGTTCGAGGTC TCGGG
                          __            G   GII
GAM361 PITX2         CTCAGCTCCAGGCACCCAGG    5574 TCCCCTAA      _
                            GCTCCAGG GCCCAGG
                            |||||||| |||||||
                            CGAGGTCC TGGGTCC
                         _____         G
GAM361 SART2         TCCTCCTCA-CTCCAGGGCGCCCGGG 5575   _ AA      _ A II
                          TCC CCT  GCTCCAGGGC CC GGG
                          ||| |||  |||||||||| || |||
                          AGG GGA  TGAGGTCCCG GG CCC
                          A   G_        C G II
GAM362 ARSF          TCACTTGAGGTCGGGAGTT      5604        CCCA  ATII
                          TCACTTGAG   GGA
                          |||||||||   |||
                          AGTGAACTC   CCT
                           CAGC   CAAI
GAM362 ARSF          TCACTTGAGGTCGGGAGTT      5604        CCCA  ATTGTGA
                          TCACTTGAG   GGA
                          |||||||||   |||
                          AGTGAACTC   CCT
                           CAGC   CAAIIIG
GAM362 ATP8A2        ACTGGGCATTAAATGAAGATC    5581 TCAACT    ATAG_    C
                          GGGCAT   GGAGATC
                          ||||||   |||||||
                          CCCGTA   CTTCTAG
                          _____  ATTTA    T
GAM362 CNGA1         TCACTTGAGATCAGGAGTT      5601        CC   ATII
                          TCACTTGAG CAGGA
                          ||||||||| |||||
                          AGTGAACTC GTCCT
                            TA   CAAI
GAM362 CNGA1         TCACTTGAGATCAGGAGTT      5601        CC   ATTGTGA
                          TCACTTGAG CAGGA
                          ||||||||| |||||
                          AGTGAACTC GTCCT
                            TA   CAAIIIG
GAM362 CORO2B        TCAACTGGGCAGTGT-GGCACATC 5596         TATAG AG_ CI
                          TCAACTGGGCA   GG ATC
                          |||||||||||   || |||
                          AGTTGACCCGT   CC TAG
                            CACA_ GTG II
GAM362 DIAPH2        CAACTGGGCCTAAAAGGGA      5583 TC    ATAT_  GATC
                          AACTGGGC   AGGGA
                          ||||||||   |||||
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                      TTGACCCG    TCCCT
                        __    GATTT   GIII
GAM362  DSCR3         CTGGGCAACATAGGGAGACCC    5589 TCAACTGG  _
                          GCA TATAGGGAGATCC
                          ||| |||||||||||||
                          CGT GTATCCCTCTGGG
                          _____   T
GAM362  DYRK1A        CTTAAGCCCAGGAATCTGAGA    5591 T           GTGI
                         TGAGCCCAGGAATT
                         ||||||||||||||
                         ATTCGGGTCCTTAG
                         _          ACTC
GAM362  DYRK1A        CTTAAGCCCAGGAATCTGAGA    5591 TCACTT          G
                         GAGCCCAGGAATT TGAG
                         ||||||||||| ||||
                         TTCGGGTCCTTAG ACTC

                         _____    _
GAM362  GLTSCR1        TCACTGGAGCCCAGGAGTT-TGAG 5606    T      ATTG  I
                         TCACT GAGCCCAGGA   TGAG
                         ||||| ||||||||||   ||||
                         AGTGA CTCGGGTCCT   ACTC
                           C      CAA_  I
GAM362  GLTSCR1        TCACTGGAGCCCAGGAGTT-TGAG 5606 _ T       ATTG  I
                          CACT GAGCCCAGGA   TGA
                          |||| ||||||||||   |||
                          GTGA CTCGGGTCCT   ACT
                          A   C      CAA_  I
GAM362  HDAC6         CAA-TGGGCAGG--GGGAGATCC   5584 TCAAC    TATA
                           TGGGCA   GGGAGATC
                           ||||||   ||||||||
                           ACCCGT   CCCTCTAG
                         TT___    CC__
GAM362  HNRPD         AACTGGGCATTTGGGAAAAT      5580 TCAA     ATA    TC
                          CTGGGCAT  GGGAGA
                          ||||||||  ||||||
                          GACCCGTA  CCCTTT
                          ____      AA_    TA
GAM362  LILRB4        CAGCTGGGCATAT-GACACATCC   5585 TCAA       A  GAG
                          CTGGGCATAT GG  ATCC
                          |||||||||| ||  ||||
                          GACCCGTATA CT  TAGG
                          TC__       _  GTG
GAM362  MAPK7         CTTCCGCCCAGGGAATTGTG      5590    GA   _    II
                          CTT GCCCAGG AATTGT
                          ||| ||||||| ||||||
                          GAA CGGGTCC TTAACA
                           GG    C   CI
GAM362  MAPK7         CTTCCGCCCAGGGAATTGTG      5590 TCACTTGA    _    A
                          GCCCAGG AATTGTG
                          ||||||| |||||||
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                          CGGGTCC TTAACAC
                        GG_____      C    A
GAM362 MTL5           TCAACTGGG-ATCATGCGGA     5597      CA  AG  GATC
                        TCAACTGGG TAT GGA
                        |||||||| ||| |||
                        AGTTGACCC GTA CCT
                          TA  CG  IIIC
GAM362 MUC3B          AACTGGGCA-ACAGGGTGA     5579 TCAA      T    A
                          CTGGGCA ATAGGG GAT
                          ||||||| |||||| |||
                          GACCCGT TGTCCC CTG
                          ____    _      A
GAM362 NAGA          CTGAGGAGTAT-GGGAGATCC     5588 TCAACTG CA  A
                            GG  TAT GGGAGATC
                            || ||| ||||||||
                            CC  ATA CCCTCTAG
                            _____ TC  _
GAM362 NCOA6         CTTGAGCCCAGGAGGT-TGAG     5593 _        ATTG  I
                          TTGAGCCCAGGA  TGA
                          ||||||||||||   |||
                          AACTCGGGTCCT   ACT
                          G      CCA_  I
GAM362 NCOA6         CTTGAGCCCAGGAGGT-TGAG     5593 TCACTT        ATTG
                            GAGCCCAGGA  TGA
                            ||||||||||   |||
                            CTCGGGTCCT   ACT
                          _____        CCA_
GAM362 NCOA6         TCACTTGAGGTCAGGAGTT-TGAG 5607        CC  ATTG  I
                          TCACTTGAG CAGGA  TGAG
                          ||||||||| |||||   ||||
                          AGTGAACTC GTCCT   ACTC
                            CA   CAA_  I
GAM362 NCOA6         TCACTTGAGGTCAGGAGTT-TGAG 5607 _     CC    ATTG I
                          CACTTGAG CAGGA   TGA
                          |||||||| |||||   |||
                          GTGAACTC GTCCT   ACT
                          A    CA   CAA_  I
GAM362 NEU3          CTTGAGCCCAGGAGTTG-GAG     5594 _       A  T  I
                          TTGAGCCCAGGA TTG GA
                          ||||||||||||| ||| ||
                          AACTCGGGTCCT AAC CT
                          G      C  _  I
GAM362 NEU3          CTTGAGCCCAGGAGTTG-GAG     5594 TCACTT      A  T
                            GAGCCCAGGA TTG GA
                            |||||||||| ||| ||
                            CTCGGGTCCT AAC CT
                          _____        C  _
GAM362 PPP2R2B         TCAACTGGGGA-AAAGGATGAACC 5600      CATAT   _ T  I
                          TCAACTGGG   AGGGA GA CC
                          ||||||||    ||||| || ||
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                        AGTTGACCC    TTCCT CT GG
                           CTT__    A T I
GAM362 PRIM2A           CTGGGCAACATAGGGAGACCC    5589 TCAACTGG  _
                           GCA TATAGGGAGATCC
                           III IIIIIIIIIII
                           CGT GTATCCCTCTGGG
                           _____  T
GAM362 PRKY             TCAACTGGGACTTTAATAGGTAG   5595     _AT__   G ATCCI
                        TCAACTGGG C   ATAGG AG
                        IIIIIIIII I   IIIII II
                        AGTTGACCC G   TATCC TC
                           T AAAT   A IIICC
GAM362 RAD1             CACTTGAGCCCAGGTGTTG-GAG    5586 _       AA T I
                         ACTTGAGCCCAGG TTG GA
                         IIIIIIIIIIII III II
                         TGAACTCGGGTCC AAC CT
                           G       AC _ I
GAM362 RAD1             CACTTGAGCCCAGGTGTTG-GAG    5586 TC       AA  T
                         ACTTGAGCCCAGG TTG GAG
                         IIIIIIIIIIII III III
                         TGAACTCGGGTCC AAC CTC
                           __        AC  _
GAM362 RERE             ACTGT-CATGCAGGGAGATCC     5582 TCAACTGGG  A
                           CAT TAGGGAGATC
                           III IIIIIIIIII
                           GTA GTCCCTCTAG
                        CA_____   C
GAM362 RGS9             TCGCTTGAGCCCAGGAGTT-TGAG   5608  A       ATTG  I
                         TC CTTGAGCCCAGGA   TGAG
                         II IIIIIIIIIIII   IIII
                         AG GAACTCGGGTCCT   ACTC
                          C       CAA_  I
GAM362 RGS9             TCGCTTGAGCCCAGGAGTT-TGAG   5608 _A       ATTG  I
                         C CTTGAGCCCAGGA   TGA
                         I IIIIIIIIIIII   III
                         G GAACTCGGGTCCT   ACT
                          A C       CAA_  I
GAM362 SGT              CTTGAGCCCAGAAGAGGTGA      5592       ATT  I
                         TTGAGCCCAGGA  GTG
                         IIIIIIIIIII  III
                         AACTCGGGTCTT  CAC
                           CTC  I
GAM362 SGT              CTTGAGCCCAGAAGAGGTGA      5592 TCACTT     ATT
                         GAGCCCAGGA  GTGA
                         IIIIIIIII  IIII
                         CTCGGGTCTT  CACT
                         _____       CTC
GAM362 SLC3A2           TCACTTGAGGCCAAGAGTTG      5605       C  A TGA
                         TCACTTGAG CCAGGA TTG
                         IIIIIIIII IIIII III
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                             AGTGAACTC GGTTCT AAC
                                 C    C   III
GAM362 SLC3A2       TCACTTGAGGCCAAGAGTTG    5605      C    ATTI
                        CACTTGAG CCAGGA
                        |||||||| ||||||
                        GTGAACTC GGTTCT
                             C    CAAI
GAM362 SMAC         TCACTTGAGCCCAGGAGTT    5602            ATII
                        TCACTTGAGCCCAGGA
                        ||||||||||||||||
                        AGTGAACTCGGGTCCT
                                CAAI
GAM362 SMAC         TCACTTGAGCCCAGGAGTT    5602          ATTGTGA
                        TCACTTGAGCCCAGGA
                        ||||||||||||||||
                        AGTGAACTCGGGTCCT
                               CAAIIIG
GAM362 SMAC         TCACTTGAGGTCAGGAATT    5603     CC     GTGA
                        TCACTTGAG CAGGAATT
                        ||||||||| ||||||||
                        AGTGAACTC GTCCTTAA
                             CA    IIIG
GAM362 SMAC         TCACTTGAGGTCAGGAATT    5603     CC     II
                        TCACTTGAG CAGGAAT
                        ||||||||| |||||||
                        AGTGAACTC GTCCTTA
                             CA    AI
GAM362 SMARCD1        TCAACTGGGCAGACAAGGGA    5598      T   A TC
                        TCAACTGGGCA ATAGGG GA
                        ||||||||||| |||||| ||
                        AGTTGACCCGT TGTTCC CT
                               C      _  II
GAM362 STMN1        TCAACTGGG-ATA-AGGAAAGTCC  5599     CAT      _
                        TCAACTGGG  ATAGGGAGA TCC
                        |||||||||  |||||||||| |||
                        AGTTGACCC  TATTCCTTT AGG
                            ___          C
GAM362 SUOX         CTGGGATCAAGATAGGGAGACCC  5587 TCAACTGGG T_      I
                          CA ATAGGGAGATCC
                          || ||||||||||||
                          GT TATCCCTCTGGG
                        CTA_____ TC       A
GAM363 ASTN         ATTACAGTGGTTCATGTACATTC  5613 AT__  AGG  G      CI
                          CAG  GGTT GTGTACATTC
                          |||  |||| ||||||||||
                          GTC  CCAA TACATGTAAG
                         TAAT  A__  G       II
GAM363 CLASP1       CAGAGGGGTCTGTGGAAAT    5614 ATCA      G  TACATTC
                          GAGGGGTT GTG
                          |||||||| |||
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                              CTCCCCAG CAC
                              ____      A  CTTTACT
GAM363  IL10RA        CAGAGGGGTGGGGGT-CAT      5615 ATCA     T  T  A  T
                              GAGGGGT GG GT CAT
                              ||||||| || || |||
                              CTCCCCA CC CA GTA
                              ____      C  C  _  C
GAM363  MN1           ATCAGAGGGGTCATGGAGT      5612        __  T ACATTC
                              ATCAGAGGGGT TGG GT
                              |||||||||| ||| ||
                              TAGTCTCCCCA ACC CA
                                   GT  T IIICCT
GAM363  MYO3A         AGAGGGGTTGGCG-AGATCCC     5611 ATCAGA       TAC
                              GGGGTTGGTG  ATTC
                              |||||||||| ||||
                              CCCCAACCGC  TAGG
                              _____       TC_
GAM363  NCOA6         TCAGAGGTCT--GTGTACATT     5616 ATCAG     G      C
                              AGGGGTT GTGTACATT
                              ||||||| |||||||||
                              TCTCCAG CACATGTAA
                              G____        A      A
GAM364  ATP11A        GGCAGGATGCAGTGCAGGA       5623        __  T III
                              GGCAGGATG GTGC GG
                              ||||||||| |||| ||
                              CCGTCCTAC CACG CC
                                   GT  T TII
GAM364  ATP11A        GGCAGGATGCAGTGCAGGA       5623 TG      __   T  GAGCG
                              GCAGGATG GTGC GGA
                              |||||||| |||| |||
                              CGTCCTAC CACG CCT
                              __       GT  T GIIIT
GAM364  CCND1         CATGTTGGTGCTGGGAAGCG      5620 AGGA      AG  I
                              TGGTGCTGG AGC
                              ||||||||| |||
                              ACCACGACC TCG
                              TACA        CT  I
GAM364  CCND1         CATGTTGGTGCTGGGAAGCG      5620 TGGCAGGA      AG
                              TGGTGCTGG AGCG
                              ||||||||| ||||
                              ACCACGACC TCGC
                              CA_____        CT
GAM364  CCND1         CAGGATGGTTGAGGTAAGCGT     5621       GCT A  I
                              AGGATGGT GG GAGCG
                              |||||||| || |||||
                              TCCTACCA CC TTCGC
                                 ACT A   I
GAM364  CCND1         CAGGATGGTTGAGGTAAGCGT     5621 TGGCAG      GCT A
                              GATGGT GG GAGCGT
                              |||||| || ||||||
```

```
                              CTACCA  CC TTCGCA
                              _____        ACT  A
GAM364 CDH6           TGGCAGGATGGT-CATGAAAGC  5630         GCTG   GT
                     TGGCAGGATGGT  GAGAGC
                     |||||||||||  |||||
                     ACCGTCCTACCA  CTTTCG
                              GTA_    ||
GAM364 CDH6          TGGCAGGATGGT-CATGAAAGC  5630 _      GC  AGI
                        GGCAGGATGGT  TGGAG
                        |||||||||| |||||
                        CCGTCCTACCA  ACTTT
                          A      GT  CII
GAM364 CSPG2         GCGGGACGGTGCTGGAAGATGCG  5622 CA          _ _ I
                        GGATGGTGCTGGA GA GC
                        ||||||||||||| || ||
                        CCTGCCACGACCT CT CG
                          __       T A I
GAM364 CSPG2         GCGGGACGGTGCTGGAAGATGCG  5622 TGGCA        _ _ TI
                         GGATGGTGCTGGA GA GCG
                         |||||||||||| || |||
                         CCTGCCACGACCT CT CGC
                          C____       T A CC
GAM364 DDX11        GGCAGGATGTTGTCTGGAG     5625      G _  ||
                        GGCAGGATG TG CTGGA
                        ||||||||| || |||||
                        CCGTCCTAC AC GACCT
                           A A   CI
GAM364 DDX11        GGCAGGATGTTGTCTGGAG     5625 TG    G _  AGCG
                         GCAGGATG TG CTGGAG
                         ||||||| || ||||||
                         CGTCCTAC AC GACCTC
                          __    A A   CIII
GAM364 G6PD         CAGGATGGT-CTCGAGTGC     5619      G G AGI
                        CAGGATGGT CT GAG
                        ||||||||| || |||
                        GTCCTACCA GA CTC
                          _ G ACG
GAM364 G6PD         CAGGATGGT-CTCGAGTGC     5619 TGGCAG   G G A
                         GATGGT CT GAG GC
                         |||||| || ||| ||
                         CTACCA GA CTC CG
                          _____   _ G A
GAM364 HCK         TGGC-GGATGGTGCTGGAG      5628  A        AGC
                        TGGC GGATGGTGCTGGAG
                        |||| |||||||||||||
                        ACCG CCTACCACGACCTC
                          _            |||
GAM364 HCK         TGGC-GGATGGTGCTGGAG      5628  A        I
                        TGGC GGATGGTGCTGGA
                        |||| ||||||||||||
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                        ACCG CCTACCACGACCT
                          _            C
GAM364  IDH3G           TGGCTGG--GGTGCTGGAG       5629    A  AT        AGC
                          TGGC GG  GGTGCTGGAG
                          |||| || ||||||||||
                          ACCG CC  CCACGACCTC
                            A __        |||
GAM364  IDH3G           TGGCTGG--GGTGCTGGAG       5629    A  AT      I
                          TGGC GG  GGTGCTGGA
                          |||| || |||||||||
                          ACCG CC  CCACGACCT
                            A __      C
GAM364  INHBB           TGGCAGGATGCGT-CTGGCTGTGCGT 5627       _  G    AGA_  II
                          TGGCAGGATG GT CTGG   GCGT
                          |||||||||| || ||||   ||||
                          ACCGTCCTAC CA GACC   CGCA
                               G _   GACA  II
GAM364  INHBB           TGGCAGGATGCGT-CTGGCTGTGCGT 5627 G       _  G    AGA_  I
                           GCAGGATG GT CTGG   GCG
                           |||||||| || ||||   |||
                           CGTCCTAC CA GACC   CGC
                            _   G _   GACA  I
GAM364  LLGL1           GGAAGGATGGTGTGTGGAG       5624  C        C_   II
                           GG AGGATGGTG TGGA
                           || ||||||||| ||||
                           CC TCCTACCAC ACCT
                            T     AC  CI
GAM364  LLGL1           GGAAGGATGGTGTGTGGAG       5624 TGGC      C_    AGCG
                            AGGATGGTG TGGAG
                            ||||||||| |||||
                            TCCTACCAC ACCTC
                           CT__      AC   CIII
GAM364  RASAL1            GGCAGGAT-GCGCTGAAGAG     5626 _      G      I
                            GCAGGATG TGCTGGAGA
                            |||||||| |||||||||
                            CGTCCTAC GCGACTTCT
                            C      _    I
GAM364  RASAL1            GGCAGGAT-GCGCTGAAGAG     5626 TG     G      CG
                            GCAGGATG TGCTGGAGAG
                            |||||||| ||||||||||
                            CGTCCTAC GCGACTTCTC
                                __     _     CI
GAM365  CD59            GCACTGCTCAGGATGTCTT        5637        T  _  ATII
                            GCACTGCTC GGA GT
                            ||||||||| ||| ||
                            CGTGACGAG CCT CA
                               T  A  GAAI
GAM365  DTNB            ACCCGAGCTCCGTCTGGAGTA      5634 CCC_  A  C      I
                            GC CTG TCTGGAGT
                            || ||| ||||||||
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                        CG GGC AGACCTCA
                       GGCT  A   _       I
GAM365  DTNB           ACCCGAGCTCCGTCTGGAGTA    5634 TA  __  A  C      TTG
                         CCC  GC CTG TCTGGAGTA
                         III II III IIIIIIIII
                         GGG  CG GGC AGACCTCAT
                        __  CT  A  _        CII
GAM365  GPR17          TACCTTGCGCTGCAAAGGAGTATTG 5638   C_  A  TCT       II
                         TACC GC CTGC  GGAGTATTG
                         IIII II IIII  IIIIIIIII
                         ATGG CG GACG  CCTCATAAC
                         AA  C  TTT        II
GAM365  GPR17          TACCTTGCGCTGCAAAGGAGTATTG 5638 ACCC A   TCT       I
                           GC CTGC  GGAGTATT
                           II IIII  IIIIIIII
                           CG GACG  CCTCATAA
                         GGAA  C  TTT        I
GAM365  HNRPA2B1         GCATCTGCTCTGGTGTCTT      5636  _       A ATII
                          GCA CTGCTCTGG GT
                          III IIIIIIIII II
                          CGT GACGAGACC CA
                          A       A  GAAI
GAM365  HNRPA2B1         GCATCTGCTCTGGTGTCTT      5636 TACCCGCAC    A ATT
                            TGCTCTGG GT
                            IIIIIIII II
                            ACGAGACC CA
                          _____    A GAA
GAM365  MECP2          ACCCGCACTGGCGCTCACGAGTA    5633 CCC   ___   TG  I
                          GCACT GCTC GAGT
                          IIIII IIII IIII
                          CGTGA CGAG CTCA
                          ___   CCG  TG  I
GAM365  MECP2          ACCCGCACTGGCGCTCACGAGTA    5633 TA     ___   TG   TTGI
                          CCCGCACT  GCTC GAGTA
                          IIIIIIII  IIII IIIII
                          GGGCGTGA  CGAG CTCAT
                          __      CCG  TG   CIII
GAM365  PVR            CTGCTCTGGTTGGCAGTATTG    5635        _____    IIIC
                          CTGCTCTGG   AGTATT
                          IIIIIIIII   IIIIII
                          GACGAGACC   TCATAA
                             AACCG    CIII
GAM366  ATOX1         ACACGCG--G-GTCACCGTGC    5642 _ G  TTGA
                          CA GCG  GTCACCGTG
                          II III  IIIIIIIII
                          GT CGC  CAGTGGCAC
                           T G  C___
GAM366  ATOX1         ACACGCG--G-GTCACCGTGC    5642 TTACAG   T A
                          GCGT G GTCACCGTG
                          IIII I IIIIIIIII
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                                   TGCG C CAGTGGCAC
                                   _____    _C
GAM366  BRCA1         TTACAGGCG-TGAGCCACCATGCC  5652      T        I
                      TTACAGGCGT GAGTCACCGTGCC
                      |||||||||| |||||||||||||
                      AATGTCCGCA CTCGGTGGTACGG
                                      I
GAM366  BRCA1         TTACAGGCG-TGAGCCACCATGCC  5652 _    T        I
                       TACAGGCGT GAGTCACCGTGC
                       ||||||||| |||||||||||
                       ATGTCCGCA CTCGGTGGTACG
                           A    _      I
GAM366  CHRNA5          TTACAGGTGT-GAGCCACCGTGCC  5657      C T        I
                       TTACAGG GT GAGTCACCGTGCC
                       ||||||| || |||||||||||||
                       AATGTCC CA CTCGGTGGCACGG
                           A _      I
GAM366  CHRNA5          TTACAGGTGT-GAGCCACCGTGCC  5657 _    C T        I
                        TACAGG GT GAGTCACCGTGC
                        |||||| || |||||||||||
                        ATGTCC CA CTCGGTGGCACG
                            A    A _        I
GAM366  COG7         TTACAGGCG-TGAGCCACCGTG    5648      T        CC
                     TTACAGGCGT GAGTCACCGTG
                     |||||||||| |||||||||||
                     AATGTCCGCA CTCGGTGGCAC
                          _              II
GAM366  COG7         TTACAGGCG-TGAGCCACCGTG    5648 _    T        I
                      TACAGGCGT GAGTCACCGT
                      ||||||||| ||||||||||
                      ATGTCCGCA CTCGGTGGCA
                          A    _      I
GAM366  CTSS         TTACAGGCGT-GAGCCACCGTGCC  5656      T        I
                     TTACAGGCGT GAGTCACCGTGCC
                     |||||||||| |||||||||||||
                     AATGTCCGCA CTCGGTGGCACGG
                          _              I
GAM366  CTSS         TTACAGGCGT-GAGCCACCGTGCC  5656 _    T        I
                      TACAGGCGT GAGTCACCGTGC
                      ||||||||| |||||||||||
                      ATGTCCGCA CTCGGTGGCACG
                          A    _      I
GAM366  CYP3A4       TTACAGGCG-TGAGCCACTGTGCC  5654      T    C I
                     TTACAGGCGT GAGTCAC GTGCC
                     |||||||||| ||||||| |||||
                     AATGTCCGCA CTCGGTG CACGG
                          _        A  I
GAM366  CYP3A4       TTACAGGCG-TGAGCCACTGTGCC  5654 _    T    C I
                      TACAGGCGT GAGTCAC GTGC
                      ||||||||| ||||||| ||||
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                        ATGTCCGCA CTCGGTG CACG
                        A       _   A   I
GAM366 CYP3A4       TTACAGGC---GAGTCCACCATGCC 5646      GTT    _
                        TTACAGGC  GAGTC ACCGTGCC
                        |||||||  ||||| ||||||||
                        AATGTCCG  CTCAG TGGTACGG
                             ___     G
GAM366 CYP3A4       TTACAGGC---GAGTCCACCATGCC 5646 _    GTT    _   I
                        TACAGGC  GAGTC ACCGTGC
                        |||||||  ||||| |||||||
                        ATGTCCG  CTCAG TGGTACG
                        A      ___    G   I
GAM366 CYP7B1       ACAGGAAT---GTCACCGTG     5641 _  C TGA
                        CAGG GT  GTCACCGT
                        |||| ||  |||||||||
                        GTCC TA  CAGTGGCA
                        T  T ___
GAM366 CYP7B1       ACAGGAAT---GTCACCGTG     5641 TTACAGGCGTTGA
                             GTCACCGTG
                             |||||||||
                             CAGTGGCAC
                        TCCTTA_____
GAM366 DCLRE1C      TTACAGGCAT-GAGCCACCGTGCC 5650      T       I
                        TTACAGGCGT GAGTCACCGTGCC
                        |||||||||| |||||||||||||
                        AATGTCCGTA CTCGGTGGCACGG
                             _            I
GAM366 DCLRE1C      TTACAGGCAT-GAGCCACCGTGCC 5650 _    T       I
                        TACAGGCGT GAGTCACCGTGC
                        ||||||||| ||||||||||||
                        ATGTCCGTA CTCGGTGGCACG
                        A      _      I
GAM366 DDOST        TTACAGGCAT-GAGCCACCGTGCC 5650      T    I
                        TTACAGGCGT GAGTCACCGTGCC
                        |||||||||| |||||||||||||
                        AATGTCCGTA CTCGGTGGCACGG
                             _         I
GAM366 DDOST        TTACAGGCAT-GAGCCACCGTGCC 5650 _    T    I
                        TACAGGCGT GAGTCACCGTGC
                        ||||||||| ||||||||||||
                        ATGTCCGTA CTCGGTGGCACG
                        A      _      I
GAM366 EFG2         TTACAGGCG-TGAGCCACCATGCC 5652     T     I
                        TTACAGGCGT GAGTCACCGTGCC
                        |||||||||| |||||||||||||
                        AATGTCCGCA CTCGGTGGTACGG
                             _         I
GAM366 EFG2         TTACAGGCG-TGAGCCACCATGCC 5652 _    T     I
                        TACAGGCGT GAGTCACCGTGC
                        ||||||||| ||||||||||||
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                              ATGTCCGCA CTCGGTGGTACG
                               A        _         I
GAM366 F2R          TTACAGGCG-TGAGCCACCGCGCC  5653        T        I
                        TTACAGGCGT GAGTCACCGTGCC
                        ||||||||| ||||||||||||
                        AATGTCCGCA CTCGGTGGCGCGG
                                 _         I
GAM366 F2R          TTACAGGCG-TGAGCCACCGCGCC  5653 _      T        I
                         TACAGGCGT GAGTCACCGTGC
                         |||||||| |||||||||||
                         ATGTCCGCA CTCGGTGGCGCG
                          A       _        I
GAM366 GAS7           TTACAGGCGT-GAGCCACCGTGCC  5656        T        I
                        TTACAGGCGT GAGTCACCGTGCC
                        ||||||||| ||||||||||||
                        AATGTCCGCA CTCGGTGGCACGG
                                 _         I
GAM366 GAS7           TTACAGGCGT-GAGCCACCGTGCC  5656 _      T        I
                         TACAGGCGT GAGTCACCGTGC
                         |||||||| |||||||||||
                         ATGTCCGCA CTCGGTGGCACG
                          A       _        I
GAM366 HFE           TTACAGGCGT-GAGCCACCGTGCC  5656        T        I
                        TTACAGGCGT GAGTCACCGTGCC
                        ||||||||| ||||||||||||
                        AATGTCCGCA CTCGGTGGCACGG
                                 _         I
GAM366 HFE           TTACAGGCGT-GAGCCACCGTGCC  5656 _      T        I
                         TACAGGCGT GAGTCACCGTGC
                         |||||||| |||||||||||
                         ATGTCCGCA CTCGGTGGCACG
                          A       _        I
GAM366 HIP1          TTACAGGCG-TGAGCCACTGTGCC  5654        T    C   I
                        TTACAGGCGT GAGTCAC GTGCC
                        ||||||||| ||||||| |||||
                        AATGTCCGCA CTCGGTG CACGG
                                 _      A  I
GAM366 HIP1          TTACAGGCG-TGAGCCACTGTGCC  5654 _      T    C   I
                         TACAGGCGT GAGTCAC GTGC
                         |||||||| ||||||| ||||
                         ATGTCCGCA CTCGGTG CACG
                          A       _      A  I
GAM366 IFNAR1         TTACAGGTGT-GAGCCACCGTGCC  5657        C T      I
                        TTACAGG GT GAGTCACCGTGCC
                        |||||| || |||||||||||
                        AATGTCC CA CTCGGTGGCACGG
                                A _        I
GAM366 IFNAR1         TTACAGGTGT-GAGCCACCGTGCC  5657 _      C T      I
                         TACAGG GT GAGTCACCGTGC
                         |||||| || ||||||||||
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                              ATGTCC CA CTCGGTGGCACG
                               A    A  _        I
GAM366 IL11          TTACAGGCG-TGAGCCACCATGCC  5652      T      I
                     TTACAGGCGT GAGTCACCGTGCC
                     IIIIIIIIII IIIIIIIIIIIII
                     AATGTCCGCA CTCGGTGGTACGG
                              _           I
GAM366 IL11          TTACAGGCG-TGAGCCACCATGCC  5652 _    T      I
                      TACAGGCGT GAGTCACCGTGC
                      IIIIIIIII IIIIIIIIIIII
                      ATGTCCGCA CTCGGTGGTACG
                               A    _      I
GAM366 IL17R         TTACAGGCGT-GAGCCACCGTGCC  5656      T      I
                     TTACAGGCGT GAGTCACCGTGCC
                     IIIIIIIIII IIIIIIIIIIIII
                     AATGTCCGCA CTCGGTGGCACGG
                              _           I
GAM366 IL17R         TTACAGGCGT-GAGCCACCGTGCC  5656 _    T      I
                      TACAGGCGT GAGTCACCGTGC
                      IIIIIIIII IIIIIIIIIIII
                      ATGTCCGCA CTCGGTGGCACG
                               A    _      I
GAM366 KERA          TACAC-CGTTGAGTC-CTGTG    5643   GG     ACCGI
                      TACA  CGTTGAGTC
                      IIII  IIIIIIIII
                      ATGT  GCAACTCAG
                       G_        GACAC
GAM366 KERA          TACAC-CGTTGAGTC-CTGTG    5643 TTACAGG    ACC  C
                            CGTTGAGTC  GTG
                            IIIIIIIII  III
                            GCAACTCAG  CAC
                      TGTG___      GA_ A
GAM366 LILRB1        TTACAGGCGT-GAGCCACCGTGCC  5656      T      I
                     TTACAGGCGT GAGTCACCGTGCC
                     IIIIIIIIII IIIIIIIIIIIII
                     AATGTCCGCA CTCGGTGGCACGG
                              _           I
GAM366 LILRB1        TTACAGGCGT-GAGCCACCGTGCC  5656 _    T      I
                      TACAGGCGT GAGTCACCGTGC
                      IIIIIIIII IIIIIIIIIIII
                      ATGTCCGCA CTCGGTGGCACG
                               A    _      I
GAM366 LRRC2         TTATAGGCGT-GAGTCACCGCGCC  5658 TAC_  T      I
                       AGGCGT GAGTCACCGTGC
                       IIIIII IIIIIIIIIIII
                       TCCGCA CTCAGTGGCGCG
                       AATA    _      I
GAM366 LRRC2         TTATAGGCGT-GAGTCACCGCGCC  5658 TTAC  T      I
                       AGGCGT GAGTCACCGTGCC
                       IIIIII IIIIIIIIIIIII
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                                TCCGCA CTCAGTGGCGCGG
                                AATA          _             I
GAM366  LRRC2        TTATAGGTGT-GAGCCACCGTGCC  5659 TAC_   C  T           I
                                AGG GT GAGTCACCGTGC
                                III II IIIIIIIIIIII
                                TCC CA CTCGGTGGCACG
                                AATA   A  _          I
GAM366  LRRC2        TTATAGGTGT-GAGCCACCGTGCC  5659 TTAC   C  T           I
                                AGG GT GAGTCACCGTGCC
                                III II IIIIIIIIIIIII
                                TCC CA CTCGGTGGCACGG
                                AATA   A  _          I
GAM366  MUC3B        TTACAGGTGTGGGAGTCACCG      5645       C  T_      TGCC
                                TTACAGG GT  GAGTCACCG
                                IIIIIII II  IIIIIIIIII
                                AATGTCC CA  CTCAGTGGC
                                     A  CC       IIIC
GAM366  MUC3B        TTACAGGTGTGGGAGTCACCG      5645 T    C  T_     I
                                 ACAGG GT  GAGTCACC
                                 IIIII II  IIIIIIIII
                                 TGTCC CA  CTCAGTGG
                                 _     A  CC      I
GAM366  MYO1C        TTACAGGCG-TGAGCCACCATGCC  5652         T       I
                                TTACAGGCGT GAGTCACCGTGCC
                                IIIIIIIIII IIIIIIIIIIII
                                AATGTCCGCA CTCGGTGGTACGG
                                      _                I
GAM366  MYO1C        TTACAGGCG-TGAGCCACCATGCC  5652 _       T       I
                                TACAGGCGT GAGTCACCGTGC
                                IIIIIIIII IIIIIIIIIIII
                                ATGTCCGCA CTCGGTGGTACG
                                A     _           I
GAM366  NFKBIL2      TTACAGGCG-TGAGCCACCGCGCC  5653         T       I
                                TTACAGGCGT GAGTCACCGTGCC
                                IIIIIIIIII IIIIIIIIIIII
                                AATGTCCGCA CTCGGTGGCGCGG
                                      _                I
GAM366  NFKBIL2      TTACAGGCG-TGAGCCACCGCGCC  5653 _       T       I
                                TACAGGCGT GAGTCACCGTGC
                                IIIIIIIII IIIIIIIIIIII
                                ATGTCCGCA CTCGGTGGCGCG
                                A     _           I
GAM366  NT5C2        TTACAGGCG-TGAGCCGCCGTGCC  5655         T  A    I
                                TTACAGGCGT GAGTC CCGTGCC
                                IIIIIIIIII IIIII IIIIIII
                                AATGTCCGCA CTCGG GGCACGG
                                      _    C         I
GAM366  NT5C2        TTACAGGCG-TGAGCCGCCGTGCC  5655 _       T  A    I
                                TACAGGCGT GAGTC CCGTGC
                                IIIIIIIII IIIII IIIIII
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                      ATGTCCGCA CTCGG GGCACG
                      A       _   C   I
GAM366  PA2G4         TTACAGGCG-TGAGCCACCGCGCC  5653       T       I
                      TTACAGGCGT GAGTCACCGTGCC
                      |||||||||| |||||||||||||
                      AATGTCCGCA CTCGGTGGCGCGG
                                      I
GAM366  PA2G4         TTACAGGCG-TGAGCCACCGCGCC  5653 _     T       I
                       TACAGGCGT GAGTCACCGTGC
                      ||||||||| |||||||||||||
                      ATGTCCGCA CTCGGTGGCGCG
                      A       _       I
GAM366  PCDH11Y       TTACAGGCG-TGAGCCACCGCGCC  5653       T        I
                      TTACAGGCGT GAGTCACCGTGCC
                      |||||||||| |||||||||||||
                      AATGTCCGCA CTCGGTGGCGCGG
                                      I
GAM366  PCDH11Y       TTACAGGCG-TGAGCCACCGCGCC  5653 _     T        I
                       TACAGGCGT GAGTCACCGTGC
                      ||||||||| |||||||||||||
                      ATGTCCGCA CTCGGTGGCGCG
                      A       _       I
GAM366  PIK3R2        TTACAGGCAT-GAGCCACCGTGCC  5650       T       I
                      TTACAGGCGT GAGTCACCGTGCC
                      |||||||||| |||||||||||||
                      AATGTCCGTA CTCGGTGGCACGG
                                      I
GAM366  PIK3R2        TTACAGGCAT-GAGCCACCGTGCC  5650 _     T       I
                       TACAGGCGT GAGTCACCGTGC
                      ||||||||| |||||||||||||
                      ATGTCCGTA CTCGGTGGCACG
                      A       _       I
GAM366  PSMB9         TTACAGGCGT-GAGCCACCGTGCC  5656       T       I
                      TTACAGGCGT GAGTCACCGTGCC
                      |||||||||| |||||||||||||
                      AATGTCCGCA CTCGGTGGCACGG
                                      I
GAM366  PSMB9         TTACAGGCGT-GAGCCACCGTGCC  5656 _     T       I
                       TACAGGCGT GAGTCACCGTGC
                      ||||||||| |||||||||||||
                      ATGTCCGCA CTCGGTGGCACG
                      A       _       I
GAM366  RAB3B         TTACAGGCG-TGAGCCACCGCGCC  5653       T       I
                      TTACAGGCGT GAGTCACCGTGCC
                      |||||||||| |||||||||||||
                      AATGTCCGCA CTCGGTGGCGCGG
                                      I
GAM366  RAB3B         TTACAGGCG-TGAGCCACCGCGCC  5653 _     T       I
                       TACAGGCGT GAGTCACCGTGC
                      ||||||||| |||||||||||||
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                        ATGTCCGCA CTCGGTGGCGCG
                         A    _      I
GAM366 RAD51L1     TTACAGGCG-TGATCCACCG   5647      T GT   TGC
                     TTACAGGCGT GA  CACCG
                     |||||||||| || |||||
                     AATGTCCGCA CT  GTGGC
                        _ AG    |||
GAM366 RAD51L1     TTACAGGCG-TGATCCACCG   5647 _     T GT  I
                      TACAGGCGT GA  CACC
                      |||||||| || ||||
                      ATGTCCGCA CT  GTGG
                       A    _ AG   I
GAM366 SFRS2IP    TACAGGCG-TGAGCTACTGTGCC   5644 _    T TC C  I
                    ACAGGCGT GAG  AC GTGC
                    |||||||| ||| || ||||
                    TGTCCGCA CTC  TG CACG
                      A    _ GA A   I
GAM366 SFRS2IP    TACAGGCG-TGAGCTACTGTGCC   5644 TT    T TC C
                    ACAGGCGT GAG  AC GTGCC
                    |||||||| ||| || |||||
                    TGTCCGCA CTC  TG CACGG
                      __    _ GA A
GAM366 SLC14A2     TTACAGGCGT-GAGCCACCGTGCC   5656      T        I
                     TTACAGGCGT GAGTCACCGTGCC
                     |||||||||| ||||||||||||
                     AATGTCCGCA CTCGGTGGCACGG
                        _               I
GAM366 SLC14A2     TTACAGGCGT-GAGCCACCGTGCC   5656 _      T        I
                      TACAGGCGT GAGTCACCGTGC
                      ||||||||| |||||||||||
                      ATGTCCGCA CTCGGTGGCACG
                       A    _         I
GAM366 SMG1        TTACAGGCG-TGAGCCACTGTGCC   5654      T    C   I
                     TTACAGGCGT GAGTCAC GTGCC
                     |||||||||| ||||||| |||||
                     AATGTCCGCA CTCGGTG CACGG
                        _      A   I
GAM366 SMG1        TTACAGGCG-TGAGCCACTGTGCC   5654 _    T    C   I
                      TACAGGCGT GAGTCAC GTGC
                      ||||||||| ||||||| ||||
                      ATGTCCGCA CTCGGTG CACG
                       A    _   A   I
GAM366 SRGAP1      TTACAGGCG-TGAGTCACTGTG   5649      T   C CC
                     TTACAGGCGT GAGTCAC GTG
                     |||||||||| ||||||| |||
                     AATGTCCGCA CTCAGTG CAC
                        _      A II
GAM366 SRGAP1      TTACAGGCG-TGAGTCACTGTG   5649 _     T   C I
                      TACAGGCGT GAGTCAC GT
                      ||||||||| ||||||| ||
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                          ATGTCCGCA CTCAGTG CA
                          A         _     A  |
GAM366 TCTA        TTACAGGCG-TGAGCCACCATGCC  5652        T          |
                   TTACAGGCGT GAGTCACCGTGCC
                   |||||||||| |||||||||||||
                   AATGTCCGCA CTCGGTGGTACGG
                          _              |
GAM366 TCTA        TTACAGGCG-TGAGCCACCATGCC  5652 _      T          |
                    TACAGGCGT GAGTCACCGTGC
                    ||||||||| ||||||||||||
                    ATGTCCGCA CTCGGTGGTACG
                         A        _      |
GAM366 TRIM14       TTACAGGCG-TGAGCCACCGCGCC  5653        T          |
                    TTACAGGCGT GAGTCACCGTGCC
                    |||||||||| |||||||||||||
                    AATGTCCGCA CTCGGTGGCGCGG
                           _             |
GAM366 TRIM14       TTACAGGCG-TGAGCCACCGCGCC  5653 _      T          |
                     TACAGGCGT GAGTCACCGTGC
                     ||||||||| ||||||||||||
                     ATGTCCGCA CTCGGTGGCGCG
                          A       _       |
GAM366 TRIM9       TTACAGGCATGG-GCCACCGTGCC  5651        T A        |
                   TTACAGGCGT G GTCACCGTGCC
                   |||||||||| | ||||||||||||
                   AATGTCCGTA C CGGTGGCACGG
                            _ C        |
GAM366 TRIM9       TTACAGGCATGG-GCCACCGTGCC  5651 _      T A        |
                    TACAGGCGT G GTCACCGTGC
                    ||||||||| | |||||||||||
                    ATGTCCGTA C CGGTGGCACG
                         A      _ C      |
GAM366 UC28        TTACAGGCGT-GAGCCACCGTGCC  5656        T          |
                   TTACAGGCGT GAGTCACCGTGCC
                   |||||||||| |||||||||||||
                   AATGTCCGCA CTCGGTGGCACGG
                          _             |
GAM366 UC28        TTACAGGCGT-GAGCCACCGTGCC  5656 _      T          |
                    TACAGGCGT GAGTCACCGTGC
                    ||||||||| ||||||||||||
                    ATGTCCGCA CTCGGTGGCACG
                         A        _      |
GAM366 USP14       TTACAGGCGT-GAGCCACCGTGCC  5656        T          |
                   TTACAGGCGT GAGTCACCGTGCC
                   |||||||||| |||||||||||||
                   AATGTCCGCA CTCGGTGGCACGG
                           _            |
GAM366 USP14       TTACAGGCGT-GAGCCACCGTGCC  5656 _      T          |
                    TACAGGCGT GAGTCACCGTGC
                    ||||||||| ||||||||||||
```

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                    ATGTCCGCA CTCGGTGGCACG
                    A       _       I
GAM366 VDR          TTACAGGCG-TGAGCCACCGCGCC  5653        T       I
                    TTACAGGCGT GAGTCACCGTGCC
                    |||||||||| |||||||||||||
                    AATGTCCGCA CTCGGTGGCGCGG
                            _       I
GAM366 VDR          TTACAGGCG-TGAGCCACCGCGCC  5653 _      T       I
                    TACAGGCGT GAGTCACCGTGC
                    ||||||||| |||||||||||
                    ATGTCCGCA CTCGGTGGCGCG
                    A       _       I
GAM366 WIG1         TTACAGGCG-TGAGCCACCGCGCC  5653        T       I
                    TTACAGGCGT GAGTCACCGTGCC
                    |||||||||| |||||||||||||
                    AATGTCCGCA CTCGGTGGCGCGG
                            _       I
GAM366 WIG1         TTACAGGCG-TGAGCCACCGCGCC  5653 _      T       I
                    TACAGGCGT GAGTCACCGTGC
                    ||||||||| |||||||||||
                    ATGTCCGCA CTCGGTGGCGCG
                    A       _       I
GAM366 XT3          TTACAGGCGT-GAGCCACCGTGCC  5656        T       I
                    TTACAGGCGT GAGTCACCGTGCC
                    |||||||||| |||||||||||||
                    AATGTCCGCA CTCGGTGGCACGG
                            _       I
GAM366 XT3          TTACAGGCGT-GAGCCACCGTGCC  5656 _      T       I
                    TACAGGCGT GAGTCACCGTGC
                    ||||||||| |||||||||||
                    ATGTCCGCA CTCGGTGGCACG
                    A       _       I
GAM367 APBA2        CAGCCATCATCACCCGGAGGC     5663 TGGCAG    __   TG  CT
                    CCATCA ACCCG GGC
                    |||||| ||||| |||
                    GGTAGT TGGGC CCG
                    _____     AG    CT  TC
GAM367 CHRNE        TGGCAGCCACCAGAGTCCCGTGGGGCT5671          A___       C III
                    TGGCAGCCATCA   CCCGTGGG CT
                    ||||||||||||   |||||||| ||
                    ACCGTCGGTGGT   GGGCACCC GA
                            CTCA       C III
GAM367 DPYSL3       TGGGTGCCCTCACCACGTGGGCCT  5675   CA  A  A _      I
                    TGG  GCC TCA CC CGTGGGCCT
                    |||  ||| ||| || |||||||||
                    ACC  CGG AGT GG GCACCCGGA
                         CA  G  _  T      I
GAM367 ECEL1        TGGCCGCCGGCCTCCTCGTGGGCCT 5673   A ATCAA _      II
                    TGGC GCC   CC CGTGGGCCT
                    |||| |||    || |||||||||
```

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                          ACCG CGG    GG GCACCCGGA
                          G  CCGGA  A        II
GAM367 FZD1         TGCCAGCGCCCACACCCGTGGGCC  5672  G   CA  _         TI
                          TG CAGC  TCA ACCCGTGGGCC
                          || |||| ||| |||||||||||
                          AC GTCG  GGT TGGGCACCCGG
                          G   CG  G       II
GAM367 HRASLS       CAGCCATC-ACTCG-GGCC    5664 TGGCAG    A C  T
                            CCATCA C CG GGGC
                            |||||| | || ||||
                            GGTAGT G GC CCCG
                          _____     _A _
GAM367 JTB         GCAGCCATCTAGCCCCGTGG    5666 TGGC    AA__     CC
                          AGCCATC   CCCGTGGG
                          |||||||   ||||||||
                          TCGGTAG   GGGCACCT
                          ____      ATCG     CI
GAM367 LGR6         GCAGCCATCATTCACCGAGGG   5665 TGGC     AC__ T CCT
                          AGCCATCA   CCG GGG
                          ||||||||   ||| |||
                          TCGGTAGT   GGC CCC
                          ____      AAGT  T  CCI
GAM367 LYL1        GGCCGCGCCTC--CTCGTGGGCCT  5667 TG_ A A AACC
                          GC GCC TC   CGTGGGCCT
                          || ||| ||   |||||||||
                          CG CGG AG   GCACCCGGA
                          CGG _ _ GA__
GAM367 PRKY        TGTCATGCCATCAACACCCAGGG   5670  G _     _ GT  CCTI
                          TG CA GCCATCAAC CC  GGG
                          || || |||||||||| || |||
                          AC GT CGGTAGTTG GG  CCC
                          A A      T GT  IIIT
GAM367 RFX5        TGGCAGCCATTAA---GTGGCCC   5674       C CCC  G
                          TGGCAGCCAT AA  GTGG CC
                          |||||||||| || |||| ||
                          ACCGTCGGTA TT  CACC GG
                          A ___  G
GAM367 SUV39H1      GGCAGCCATCAGAACC-TTCGCCT  5668 TG    AC_ GTGG  I
                          GCAGCCATCA  CC  GCCT
                          ||||||||||  ||  ||||
                          CGTCGGTAGT  GG  CGGA
                          __      CTT AAG_  A
GAM367 TEM5        GGCGCCCATCAACCCATCGCCC    5669 TG AG      GG
                          GC CCATCAACCCGT GCCT
                          || |||||||||| ||||
                          CG GGTAGTTGGGTA CGGG
                          CG __      G_
GAM367 VIPR2       AGCCCCGAACC-GTGGGCCT      5662 TGGCAGCCATCAAC
                            CCGTGGGCC
                            |||||||||
```

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                              GGCACCCGG
                         GGCTT_____
GAM368  ABCB9         GCTGGGTGCCGGGCTGGGC    5692      C_ CA  CC
                      GCTGGGTGCT GC GGGC
                      ||||||||| || ||||
                      CGACCCACGG CG CCCG
                         CC A_   II
GAM368  ABCB9         GCTGGGTGCCGGGCTGGGC    5692      C_ CA  II
                      GCTGGGTGCT GC GGG
                      ||||||||| || |||
                      CGACCCACGG CG CCC
                         CC A_  GI
GAM368  CAPN2         GCTGGG-GCGCGGCCAGGGCCC   5689    _  TC     I
                      GCTGGG TGC GCCAGGGCCC
                      |||||| ||| ||||||||||
                      CGACCC GCG CGGTCCCGGG
                         C  C_    I
GAM368  CAPN2         GCTGGG-GCGCGGCCAGGGCCC   5689 CT_   TC     I
                       GGGTGC GCCAGGGCC
                       |||||| |||||||||
                       CCCGCG CGGTCCCGG
                        GAC   C_    I
GAM368  CLCN7         GCAGGGTGCTCGCCATTGCC    5694 T        GG  CI
                      GC GGGTGCTCGCCA GCC
                      || |||||||||||| |||
                      CG CCCACGAGCGGT CGG
                       T      AA  II
GAM368  CLCN7         GCAGGGTGCTCGCCATTGCC    5694 CT       GG  I
                       GGGTGCTCGCCA GC
                       |||||||||||| ||
                       CCCACGAGCGGT CG
                        GT       AA  I
GAM368  COL9A3       GGGTGCTCGCTGGCAAGGCCC    5699        ___    III
                     GGGTGCTCGC CAGGGCC
                     |||||||||| |||||||
                     CCCACGAGCG GTTCCGG
                        ACC      GII
GAM368  COL9A3       GGGTGCTCGCTGGCAAGGCCC    5699 GCTGGG    ___    I
                      TGCTCGC CAGGGCCC
                      ||||||| |||||||||
                      ACGAGCG GTTCCGGG
                       _____    ACC     C
GAM368  COX15        GCTGGGGCACCTGCTCGCCAG    5685    _____       GGCCCI
                     GCTGGG  TGCTCGCCAG
                     ||||||  ||||||||||
                     CGACCC  ACGAGCGGTC
                       CGTGG     IIICCC
GAM368  COX15        GCTGGGGCACCTGCTCGCCAG    5685    _____       IIIC
                     GCTGGG  TGCTCGCCA
                     ||||||  |||||||||
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                        CGACCC    ACGAGCGGT
                          CGTGG        CIII
GAM368 FBLN5            CTTGGGGCGTCTGCCAGGGCCC   5678 GC   T _ _       II
                        TGGG GC TC GCCAGGGCCC
                        |||| || || ||||||||||
                        ACCC CG AG CGGTCCCGGG
                        A_  _ C  A      TI
GAM368 FBLN5            CTTGGGGCGTCTGCCAGGGCCC   5678 T   _ C       I
                          GGGTG CT GCCAGGGCC
                          ||||| || |||||||||
                          CCCGC GA CGGTCCCGG
                          C   A _        I
GAM368 FBXL7           CTGGGTGCTCTATGCCAAGG        5679         ___      III
                        CTGGGTGCTC GCCAGG
                        |||||||||| ||||||
                        GACCCACGAG CGGTTC
                               ATA    CII
GAM368 FBXL7           CTGGGTGCTCTATGCCAAGG        5679 GC        ___     CCCI
                         TGGGTGCTC GCCAGGG
                         ||||||||| |||||||
                         ACCCACGAG CGGTTCC
                          __       ATA    AIII
GAM368 FLOT2           GCTGAGCTCTGGCCAGGGCC        5695       G  C      CI
                        GCTGGGT CT GCCAGGGCC
                        ||||||| || |||||||||
                        CGACTCG GA CGGTCCCGG
                             A  C       II
GAM368 FLOT2           GCTGAGCTCTGGCCAGGGCC        5695       G  C      I
                        CTGGGT CT GCCAGGGC
                        |||||| || |||||||||
                        GACTCG GA CGGTCCCG
                             A  C     I
GAM368 LLGL1          GCTGG-TGCTGCTCCAGGGCCC       5686      G   CG_      I
                        GCTGG TGCT  CCAGGGCCC
                        ||||| ||||  |||||||||
                        CGACC ACGA  GGTCCCGGG
                         _    CGA        I
GAM368 LLGL1          GCTGG-TGCTGCTCCAGGGCCC       5686 CTG     CG_      I
                          GGTGCT  CCAGGGCC
                          |||||| |||||||||
                          CCACGA  GGTCCCGG
                        GA_    CGA       I
GAM368 MDFI          GGGTGCTCGCCTGGCGCCC       5700          A _  II
                        GGGTGCTCGCC GG GCC
                        ||||||||||| || |||
                        CCCACGAGCGG CC CGG
                          A  G  GI
GAM368 MDFI          GGGTGCTCGCCTGGCGCCC       5700 GCTGGG      A _
                          TGCTCGCC GG GCCC
                          |||||||| || ||||
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                              ACGAGCGG CC CGGG
                              _____      A G
GAM368 MECP2          CTGGGTGCT-GCCTGGAGCC    5681      C  A _ II
                              CTGGGTGCT GCC GG GC
                              ||||||||| ||| || ||
                              GACCCACGA CGG CC CG
                                 _  A T GI
GAM368 MECP2          CTGGGTGCT-GCCTGGAGCC    5681 GC    C  A _  C
                               TGGGTGCT GCC GG GCC
                               |||||||| ||| || |||
                               ACCCACGA CGG CC CGG
                                __      _ A T  A
GAM368 NDST1          CTGGGTGCTCCCCCAGCCCC     5684      G  AG  I
                               TGGGTGCTC CC GGCC
                               ||||||||| || ||||
                               ACCCACGAG GG TCGG
                                G G_  G
GAM368 NDST1          CTGGGTGCTCCCCCAGCCCC     5684 GC     G  AG   I
                               TGGGTGCTC CC GGCCC
                               ||||||||| || |||||
                               ACCCACGAG GG TCGGG
                                __      G G_  G
GAM368 NDUFA9         GCTGGGTGCTCAAACCACATGGGCC 5687         __  ___  CIII
                              GCTGGGTGCTC GCCA  GGGCC
                              |||||||||| |||| |||||
                              CGACCCACGAG TGGT  CCCGG
                                 TT  GTA   IIIC
GAM368 OLFM1          CTGGGTGCTGGCC--GGCC     5682      C  AG  I
                              CTGGGTGCT GCC  GGC
                              ||||||||| ||| |||
                              GACCCACGA CGG  CCG
                                  C __  G
GAM368 OLFM1          CTGGGTGCTGGCC--GGCC     5682 GC    C  AG
                               TGGGTGCT GCC  GGCC
                               |||||||| ||| ||||
                               ACCCACGA CGG  CCGG
                                __        C __
GAM368 PSCD4         GCTGGGTGCCCAGGCCAGGG     5688         __     CCCI
                              GCTGGGTGCTC GCCAGGG
                              |||||||||| |||||||
                              CGACCCACGGG CGGTCCC
                                 TC     IIIC
GAM368 PSCD4         GCTGGGTGCCCAGGCCAGGG     5688         __     III
                              GCTGGGTGCTC GCCAGG
                              |||||||||| ||||||
                              CGACCCACGGG CGGTCC
                                 TC    CII
GAM368 RAP1GA1        GCTGGGTGCTGGCTGAGGAGCC   5690        C  C_ _ CII
                              GCTGGGTGCT GC AGG GCC
                              |||||||||| || ||| |||
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                              CGACCCACGA CG TCC CGG
                                   C  AC  T  III
GAM368 RAP1GA1        GCTGGGTGCTGGCTGAGGAGCC    5690 CT      C C_  _ I
                         GGGTGCT GC AGG GC
                         ||||||| || ||| ||
                         CCCACGA CG TCC CG
                          __      C  AC  T  I
GAM368 RGS3          CTGGCT--TGGCCAGGGCCC     5683 GCTG  GCTC
                          GGT  GCCAGGGCCC
                          |||  ||||||||||
                          CCG  CGGTCCCGGG
                          A___  AAC_
GAM368 RGS3          CTGGCT--TGGCCAGGGCCC     5683 TG  GCTC      I
                          GGT  GCCAGGGCC
                          |||  |||||||||
                          CCG  CGGTCCCGG
                          GA  AAC_       I
GAM368 RGS3          TGGCTCATCCCCAGGGCCC     5702 TG  GC_ G      II
                          GGT  TC CCAGGGCC
                          |||  || ||||||||
                          CCG  AG GGTCCCGG
                          A_  AGT G      GI
GAM368 ROR2          TGGGTGCTCCTAGGCAGGGC    5701        GC___   III
                          TGGGTGCTC   CAGGG
                          |||||||||   |||||
                          ACCCACGAG   GTCCC
                           GATCC    GII
GAM368 ROR2          TGGGTGCTCCTAGGCAGGGC    5701 GCTG    GC___   CCI
                          GGTGCTC   CAGGGC
                          |||||||   ||||||
                          CCACGAG   GTCCCG
                          ____      GATCC    TCI
GAM368 SET7        CTGGGTGCTC-CCGGCGGC      5680        G A GII
                          CTGGGTGCTC CC GG
                          |||||||||| || ||
                          GACCCACGAG GG CC
                             _ _ GCC
GAM368 SET7        CTGGGTGCTC-CCGGCGGC      5680 GC      G AG_  CC
                          TGGGTGCTC CC GGC
                          ||||||||| || |||
                          ACCCACGAG GG  CCG
                          __      _ CCG  AI
GAM368 SFRP1        GCTGGGTGCGCCCCGGCTCCC     5698        TC AG  _ I
                          GCTGGGTGC GCC GGC CC
                          ||||||||| ||| ||| ||
                          CGACCCACG CGG CCG GG
                          __  GG  A G
GAM368 SFRP1        GCTGGGTGCGCCCCGGCTCCC     5698        TC AG CI
                          CTGGGTGC GCC GGC
                          |||||||| ||| |||
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                        GACCCACG CGG CCG
                          ___ GG  AG
GAM368 SFRP2            GCTGGGTGCGACTCGGGGCCC   5697       ___ CCA    I
                        GCTGGGTGC TCG GGGCCC
                        ||||||||| ||| ||||||
                        CGACCCACG AGC CCCGGG
                          CTG ___  I
GAM368 SFRP2            GCTGGGTGCGACTCGGGGCCC   5697       ___ CCA    I
                         CTGGGTGC TCG GGGCC
                         |||||||| ||| |||||
                         GACCCACG AGC CCCGG
                          CTG ___  I
GAM368 TESK1         GCAGGGTCC---CCAGGGCCC    5696  T TGC G
                        GC GGG  TC CCAGGGCCC
                        || ||| || |||||||||
                        CG CCC  AG GGTCCCGGG
                         T ___ G
GAM368 TESK1         GCAGGGTCC---CCAGGGCCC    5696 CT_ TGC G
                         GGG  TC CCAGGGCC
                         |||  || ||||||||
                         CCC  AG GGTCCCGG
                        CGT ___ G
GAM368 TM7SF3          GCTGGGCCCACGCCAGGGC    5691       GCT     CC
                        GCTGGGT CGCCAGGGC
                        ||||||| |||||||||
                        CGACCCG GCGGTCCCG
                          GGT       II
GAM368 TM7SF3          GCTGGGCCCACGCCAGGGC    5691       GCT     II
                        GCTGGGT CGCCAGGG
                        ||||||| ||||||||
                        CGACCCG GCGGTCCC
                          GGT     GI
GAM368 TNC          GCTGGGTGCT-GCTGGGGC     5693       C CA   CC
                        GCTGGGTGCT GC GGGC
                        |||||||||| || ||||
                        CGACCCACGA CG CCCG
                         _ AC  II
GAM368 TNC          GCTGGGTGCT-GCTGGGGC     5693       C CA   I
                        GCTGGGTGCT GC GGG
                        |||||||||| || |||
                        CGACCCACGA CG CCC
                         _ AC  G
GAM369 ACVR1B        GAGATGGGGTCTCCCCACA    5707          GA TCII
                        GAGATGGGGTCT CC
                        |||||||||||| ||
                        CTCTACCCCAGA GG
                          GG TGTI
GAM369 ACVR1B        GAGATGGGGTCTCCCCACA    5707 TG       GA T GTT
                        AGATGGGGTCT CC CA
                        ||||||||||| || ||
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                    TCTACCCCAGA  GG GT
                    __        GG  T  AII
GAM369  CRY2        GAGATGGG-TCTGACCCCAG      5709 _      G        I
                    AGATGGG TCTGACCTCA
                    ||||||| ||||||||||
                    TCTACCC AGACTGGGGT
                    C       _        I
GAM369  CRY2        GAGATGGG-TCTGACCCCAG      5709 TG     G        TT
                    AGATGGG TCTGACCTCAG
                    ||||||| |||||||||||
                    TCTACCC AGACTGGGGTC
                    __      _         CI
GAM369  DNMT3L      TGGGGTTTGGGGACCTCAGT      5717     CT___       III
                    TGGGGT   GACCTCAG
                    ||||||   ||||||||
                    ACCCCA   CTGGAGTC
                    AACCC        AII
GAM369  DNMT3L      TGGGGTTTGGGGACCTCAGT      5717 TGAGA    TCTG       T
                    TGGGG   ACCTCAGT
                    |||||   ||||||||
                    ACCCC   TGGAGTCA
                    AA___   ____      C
GAM369  ELF3        AGATGCT-TCTGACCTCAGT      5706 _    GGG          I
                    GATG  TCTGACCTCAG
                    ||||  |||||||||||
                    CTAC  AGACTGGAGTC
                    T  GA_        I
GAM369  ELF3        AGATGCT-TCTGACCTCAGT      5706 TGAG  GGG          T
                    ATG  TCTGACCTCAGT
                    |||  ||||||||||||
                    TAC  AGACTGGAGTCA
                    ____  GA_          C
GAM369  HOXB5       GAGATGGG-TCTGACC-CAG      5708        G     CI
                    GAGATGGG TCTGACCT
                    |||||||| ||||||||
                    CTCTACCC AGACTGGG
                    _      TC
GAM369  HOXB5       GAGATGGG-TCTGACC-CAG      5708 TG     G     T  T
                    AGATGGG TCTGACC CAG
                    ||||||| ||||||| |||
                    TCTACCC AGACTGG GTC
                    __      _     _ T
GAM369  IFNA1       TGAGATGGGTGACTCTGAACCT     5714        G___    _ CAGTTC
                    TGAGATGGG   TCTGA CCT
                    |||||||||   ||||| |||
                    ACTCTACCC   AGACT GGA
                    ACTG   T  IIICTT
GAM369  IFNA1       TGAGATGGGTGACTCTGAACCT     5714        G___    _ IIIA
                    TGAGATGGG   TCTGA CC
                    |||||||||   ||||| ||
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                          ACTCTACCC   AGACT GG
                          ACTG    T  AIII
GAM369  IFNA13          TGAGATGGGTGACTCTGAACCT   5714      G___  _  CAGTTC
                          TGAGATGGG   TCTGA CCT
                          |||||||||   ||||| |||
                          ACTCTACCC   AGACT GGA
                          ACTG    T  IIICTT
GAM369  IFNA13          TGAGATGGGTGACTCTGAACCT   5714      G___  _  IIIA
                          TGAGATGGG   TCTGA CC
                          |||||||||   ||||| ||
                          ACTCTACCC   AGACT GG
                          ACTG    T  AIII
GAM369  IFNAR1          GAGATGGGGTTTCACCAC-GTT   5711 _     CTG TCA I
                          AGATGGGGT ACC  GT
                          ||||||||| |||  ||
                          TCTACCCCA TGG  CA
                          C     AAG TG_ I
GAM369  IFNAR1          GAGATGGGGTTTCACCAC-GTT   5711 TG    CTG TCA C
                          AGATGGGGT ACC  GTT
                          ||||||||| |||  |||
                          TCTACCCCA TGG  CAA
                          __     AAG TG_ C
GAM369  MAT1A           TGAGATGTG--CTGACCTCA   5715     GG T    GT
                          TGAGATG G CTGACCTCA
                          ||||||| | |||||||||
                          ACTCTAC C GACTGGAGT
                              A_ _      II
GAM369  MAT1A           TGAGATGTG--CTGACCTCA   5715 _    GG T    I
                          GAGATG G CTGACCTC
                          |||||| | |||||||||
                          CTCTAC C GACTGGAG
                          A  A_ _      I
GAM369  NHLH1           TGGGGTCTGCCACTGAGCTC   5718      A TC__  II
                          TGGGGTCTG CC   AGTT
                          ||||||||| ||   ||||
                          ACCCCAGAC GG   TCGA
                           _ TGAC   GI
GAM369  NHLH1           TGGGGTCTGCCACTGAGCTC   5718 __ AGA_  G  ACCTCAGTT
                          TG   TGGG TCTG
                          ||   |||| ||||
                          AC   ACTC AGAT
                          AG GGTG   G  CTTIIICTT
GAM369  POLL            GAGATGGGGCACGGCCGCAG   5710      C A T I
                          AGATGGGGT TG CC CA
                          ||||||||| || || ||
                          TCTACCCCG GC GG GT
                             T  C C I
GAM369  POLL            GAGATGGGGCACGGCCGCAG   5710 TG    C A T T
                          AGATGGGGT TG CC CAGT
                          ||||||||| || || ||||
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                              TCTACCCCG GC GG GTCG
                              __      T C C   I
GAM369 SCN4A          TGAGG-GGGGTCTGAGCCCACTTC  5716    AT       C  G  I
                          TGAG  GGGGTCTGA CTCA TTC
                          IIII IIIIIIIII IIII III
                          ACTC  CCCCAGACT GGGT AAG
                              C_       C  G  I
GAM369 SCN4A          TGAGG-GGGGTCTGAGCCCACTTC  5716 _  AT       C  G  I
                           GAG  GGGGTCTGA CTCA TT
                           III IIIIIIIII IIII II
                           CTC  CCCCAGACT GGGT AA
                             A C_      C  G  I
GAM369 SMURF1          AGGTGGGGCCTCTGACCTCA      5705 A     __         III
                           AG TGGGGT CTGACCTC
                           II IIIIII IIIIIIIII
                           TC ACCCCG GACTGGAG
                             C   GA     TII
GAM369 SMURF1          AGGTGGGGCCTCTGACCTCA      5705 TGAGA    __        GTT
                            TGGGGT CTGACCTCA
                            IIIIII IIIIIIIIII
                            ACCCCG GACTGGAGT
                             C____   GA      AGI
GAM369 TNFSF15        TGAGACTGAGTGGTCTGACCT     5712        __ _        CAGTTC
                          TGAGAT GG GGTCTGACCT
                          IIIIII II IIIIIIIIII
                          ACTCTG TC CCAGACTGGA
                            AC A        IIICTT
GAM369 TNFSF15        TGAGACTGAGTGGTCTGACCT     5712        __ _        III
                          TGAGAT GG GGTCTGACC
                          IIIIII II IIIIIIIII
                          ACTCTG TC CCAGACTGG
                            AC A      AII
GAM369 VDR           TGAGAGTGGGGGTCTGAGCTCA     5713      T__      C  GTTC
                          TGAGA  GGGGTCTGA CTCA
                          IIIII IIIIIIIII IIII
                          ACTCT  CCCCAGACT GAGT
                            CAC       C   IIIC
GAM369 VDR           TGAGAGTGGGGGTCTGAGCTCA     5713  AT       C  I
                          GAG  GGGGTCTGA CTC
                          III IIIIIIIII III
                          CTC  CCCCAGACT GAG
                            AC       C  I
GAM370 ARVCF          CGG-GCCTTCTGTCACTCGC       5723  T AG _       GTCT
                          CGG GC TC GTCACTCGC
                          III II II IIIIIIIII
                          GCC CG  AG CAGTGAGCG
                            _ GA A       IIIG
GAM370 COL5A3         CGGTGCA---GTCACTCGC        5725        GTC    GT
                          CGGTGCAGTC ACTCGC
                          IIIIIIIIII IIIIII
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                        GCCACGTCAG  TGAGCG
                           ___        II
GAM370 COLQ             CGGATGCAGTCGTCACCCACATC  5722  _              TGI
                        CGG TGCAGTCGTCACTCGCGTC
                        ||| ||||||||||||||||||
                        GCC ACGTCAGCAGTGGGTGTAG
                         T         III
GAM370 GRB10            GCAGTCGTCAGGCAGGCGTTTG  5726 ____  T  T  CACTCGCGTCTG
                        CGG GCAG CGT
                        ||| |||| |||
                        GTC CGTC GCA
                        AGCA  _   C  AACCTCTIIIGT
GAM370 HSF4            GGTGCAGTC-TCGGCCCGGCTCTG  5727 CG     G A_  CG  I
                        GTGCAGTC TC CTCG TCTG
                        |||||||| || |||| ||||
                        CACGTCAG AG GGGC AGAC
                          __      _ CC  CG  G
GAM370 IFNAR2          AGTCGTCACTGTCCTCGTC     5721 CGGTGCAGTC  A  _  T
                        GTC CTCG CGTC
                        ||| |||| ||||
                        CAG GAGC GTAG
                        GTGA_____ _  A  T
GAM370 KCNK4           GGAGCTGTCGTCACT-GCG      5728 CGGT A      C  TC
                        GC GTCGTCACT GCG
                        || ||||||||| |||
                        CG CAGCAGTGA CGC
                        CT__ A     _  CI
GAM370 PCDH7          CGGTGCAGGGGAGACTACTCGCGTC 5724      TC___ TC     TGII
                        CGGTGCAG   G ACTCGCGTC
                        ||||||||   | |||||||||
                        GCCACGTC   T TGAGCGCAG
                          CCCTC GA      IIIG
GAM371 ATRN          ACACACACACCGCACGGCCGGCTC  5735       ____   __  IIIG
                        ACACACACA  ACGGC GCT  A
                        ||||||||| ||||| ||| |
                        TGTGTGTGT  TGCCG CGA  T
                          GGCG   GC  GIII
GAM371 ATRN          ACACACACACCGCACGGCCGGCTC  5735 TA      A__  __    GGI
                        ACACACAC  ACGGC GCTCTG
                        ||||||||  ||||| ||||||
                        TGTGTGTG  TGCCG CGAGGC
                          __     GCG   GC    III
GAM371 BAZ2A         ACACACACACACGGCGCTCT     5737          _      II
                        ACACACACA ACGGCGCTC
                        ||||||||| |||||||||
                        TGTGTGTGT TGCCGCGAG
                            G    AI
GAM371 BAZ2A         ACACACACACACGGCGCTCT     5737 TA     A      GG
                        ACACACACA CGGCGCTCT
                        ||||||||| |||||||||
```

```
                         TGTGTGTGT GCCGCGAGA
                          __      _     GA
GAM371 BAZ2A        ACACACACAGC-GCGTTGTG    5742 C     A    TCTI
                         ACACACA CGGCGC

                         |||||||| ||||||
                         TGTGTGT GTCGCG
                          _     _    CAAC
GAM371 BAZ2A        ACACACACAGC-GCGTTGTG    5742 TAACAC   A    TC G
                          ACACA CGGCGC  TG

                          ||||| |||||| ||
                          TGTGT GTCGCG  AC
                         _____    _     CA A
GAM371 BAZ2A        ACACACACACTGCGCGCTG     5739 _      ACG  T I
                         CACACACA  GCGC CT

                         |||||||| |||| ||
                         GTGTGTGT  CGCG GA
                          T    GA_    C I
GAM371 BAZ2A        ACACACACACTGCGCGCTG     5739 TA      ACG   T GG
                          ACACACACA  GCGC CTG

                          ||||||||| |||| |||
                          TGTGTGTGT  CGCG GAC
                           __      GA_  C  AC
GAM371 CLCN7       ACACACACAGCTGATCCCTGG    5744 CA    A  G___   I
                           CACACA CGGC   CTCTG

                           |||||| ||||   |||||
                           GTGTGT GTCG   GGGAC
                            __    _   ACTA   I
GAM371 CLCN7       ACACACACAGCTGATCCCTGG    5744 TAAC     ACGGCG
                           ACACACA   CTCTGGG

                           ||||||| ||||||||
                           TGTGTGT   GGGACCT
                           ____    CGACTA
GAM371 CRY2       ACACACACATGCTCGCTCT       5741       ACGG  II
                           ACACACACA   CGCTC

                           ||||||||| |||||
                           TGTGTGTGT   GCGAG
                            ACGA    AI
GAM371 CRY2       ACACACACATGCTCGCTCT       5741 TAAC    ACGG   G
                           ACACACA  CGCTCTG

                           ||||||| ||||||||
                           TGTGTGT  GCGAGAT
                            ____    ACGA    A
GAM371 GRB10      AACAAACCCATCT-CGCTCTGGG   5734 _  C A ACGG     I
                           ACA AC CA   CGCTCTGG

                           ||| || ||   |||||||||
                           TGT TG GT   GCGAGACC
                            T   T  G AGA_    I
GAM371 GRB10      AACAAACCCATCT-CGCTCTGGG   5734 TA  C A ACGG
                           ACA AC CA   CGCTCTGGG

                           ||| || ||   |||||||||
```

```
                          TGT TG GT   GCGAGACCC
                          __  T G  AGA_
GAM371 HLCS               ACACACACATCCTCCCTCTG    5743 TAAC      ACGGCG
                             ACACACA    CTCTGG
                             |||||||    ||||||
                             TGTGTGT    GAGACT
                                  ____      AGGAGG
GAM371 HLCS               ACACACATCCTCCCTCTG    5743        ACGGCG   I
                             CACACACA    CTCT
                             ||||||||    ||||
                             GTGTGTGT    GAGA
                                  AGGAGG   I
GAM371 IL18RAP            AACACACACACAGAGCTGTG    5732 _      A  C  CTI
                             ACACACACA CGG GCT
                             ||||||||| ||| |||
                             TGTGTGTGT GTC CGA
                             G    _  T  CAI
GAM371 IL18RAP            AACACACACACAGAGCTGTG    5732 TA      _  C  C  G
                             ACACACACA ACGG GCT TGG
                             ||||||||| |||| ||| |||
                             TGTGTGTGT TGTC CGA ACT
                                  __      G  T  C  I
GAM371 KCNK10            ACACACACACAACGCTC      5736        _      II
                             ACACACACA ACGGCGCT
                             ||||||||| |||||||||
                             TGTGTGTGT TGTTGCGA
                                  G    GI
GAM371 KCNK10            ACACACACACAACGCTC      5736 TA     A      TGG
                             ACACACACA CGGCGCTC
                             ||||||||| ||||||||
                             TGTGTGTGT GTTGCGAG
                                  __     _    TCI
GAM371 KCNN4             CACACACAATGG---TCTG      5746        C CGCTCT
                             CACACACAA GG
                             ||||||||| ||
                             GTGTGTGTT CC
                                  A  AGACII
GAM371 KCNN4             CACACACAATGG---TCTG      5746 TAACAC    C CGC
                             ACACAA GG   TCT
                             |||||| ||   |||
                             TGTGTT CC   AGA
                                  _____    A  ___
GAM371 RDX              ACACACACAGTCTCTCT      5740        A  CG_  II
                             ACACACACA CGG   CTC
                             ||||||||| |||   |||
                             TGTGTGTGT GTC   GAG
                                  _  AGA  AI
GAM371 RDX              ACACACACAGTCTCTCT      5740 TA      ACGGCG   GG
                             ACACACACA    CTCT
                             |||||||||    ||||
```

```
                       TGTGTGTGT     GAGA
                 __         CAGA__    GA
GAM371 SLC25A13        AACACACACGAAACACTGCTCTG   5731      AC   GC   I
                       ACACAC AACG GCTCT
                       |||||| |||| |||||
                       TGTGTG TTGT CGAGA
                          CT   GA   I
GAM371 SLC25A13        AACACACACGAAACACTGCTCTG   5731 TA      __    GC     GI
                       ACACACAC AACG GCTCTGG
                       |||||||| |||| |||||||
                       TGTGTGTG TTGT CGAGACT
                         __       CT  GA    II
GAM371 SLC26A4         ACACACACAGGCTGCGGTCT       5738        AC  _  TCII
                       ACACACACA GGC GC
                       ||||||||| ||| ||
                       TGTGTGTGT CCG CG
                          __   A CCAG
GAM371 SLC26A4         ACACACACAGGCTGCGGTCT       5738 TAAC     ACG_  C  GG
                       ACACACA   GCG TCT
                       |||||||   ||| |||
                       TGTGTGT   CGC AGA
                       ____       CCGA  C  AA
GAM371 VPS26          AAAACACACAACGGTACTACTGG    5733 AC        CG  _  I
                       ACACACAACGG CT CTG
                       |||||||||||| || |||
                       TGTGTGTTGCC GA GAC
                       T_       AT T  I
GAM371 VPS26          AAAACACACAACGGTACTACTGG    5733 TAAC       CG  _  I
                       ACACACAACGG CT CTGGG
                       |||||||||||| || |||||
                       TGTGTGTTGCC GA GACCT
                       TT__       AT T  I
GAM371 ZNF277         CACAC-CTACGCCGCGCTCTGG     5745 A ACA   __      I
                       CAC  ACG GCGCTCTG
                       |||  ||| ||||||||
                       GTG  TGC CGCGAGAC
                       _  GA_  GG      I
GAM371 ZNF277         CACAC-CTACGCCGCGCTCTGG     5745 TAACACACACA  __
                          ACG  GCGCTCTGG
                          |||  |||||||||
                          TGC  CGCGAGACC
                       TGGA_____  GG
GAM372 AF3P21         GGGTAGGAGTGAAGGGCAGCGA     5756 TCCGGG    ACA    AG
                       TAGGAG  AAGGGCG
                       ||||||  |||||||
                       ATCCTC  TTCCCGT
                       _____     AC_    CG
GAM372 CAPZA1         GGGAAGGAGACAATGAGAGA       5757 TCCGGGT      A  C
                       AGGAGACAA GGG GA
                       ||||||||| ||| ||
```

```
                         TCCTCTGTT CTC CT
                      T_____        A  T
GAM372 CHGA          TCAGGAGTAGGAGACAAGGCGCG   5761  C  _        A  _  AGI
                       TC GG GTAGGAGACAA GG GCG
                       || || |||||||||| || |||
                       AG CC CATCCTCTGTT CC CGC
                        T T        _ G  |||
GAM372 CSPG4          TCTGGGGCAGAGACAAAGGG    5763 TCC  TA       CGA
                         GGG  GGAGACAAAGGG
                         ||| ||||||||||||
                         CCC  TCTCTGTTTCCC
                        AGA  CG         |||
GAM372 DDEF2          TCCGGCCCGCGGACAAAGGG-GAG  5764      GTAGGA     C  I
                        TCCGG    GACAAAGGG GAG
                        |||||    ||||||||| |||
                        AGGCC    CTGTTTCCC CTC
                         GGGCGC        _   I
GAM372 HNF3A          GGGTAGAGAGGACAAAGGG    5753 TCCG  T GA      CGA
                        GG AG  GACAAAGGG
                        || || |||||||||
                        TC TC  CTGTTTCCC
                        A___ _ TC      CAA
GAM372 HR            CCGGGAACTGGAG-CAAAGGGCG   5749 TC  TA__  A      AG
                        CGGG   GGAG CAAAGGGCG
                        ||||   |||| |||||||||
                        GCCC   CCTC GTTTCCCGC
                         __   TTGA  _      CI
GAM372 IRS1          GGGGAGGGGACAA-GGGCGAG    5758 TCCGGGT  A    A
                         AGG GACAA GGGCGA
                         ||| ||||| |||||
                         TCC CTGTT CCCGCT
                        C_____      C   _
GAM372 MDFI          GGGTAGGAGAGGACCAGGGAGAG   5755 TCC  T GA AA  C  I
                        GGG AG GAC AGGG GAG
                        ||| || ||| |||| |||
                        TCC TC CTG TCCC CTC
                        A__  _ TC G_  T  C
GAM372 OFD1          CGGTTCTGAGGCA-AGGGCGAG    5752 TCCGGGTAG  ACA
                         GAG  AAGGGCGAG
                         |||  |||||||||
                         CTC  TTCCCGCTC
                        CAAGA____    CG_
GAM372 PON1          TCGGGGGAT-AGACAAAGGG     5762 TC  TAGG      CGA
                         CGGG  AGACAAAGGG
                         ||||  ||||||||||
                         GCCC  TCTGTTTCCC
                        A_  CCTA       |||
GAM372 SLC2A3        GGGT-GGAGCCTGAAAGGGCGA    5754 TCCGGGTA  AC__       G
                         GGAG   AAAGGGCGA
                         ||||   |||||||||
```

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                             CCTC    TTTCCCGCT
                           A_____   GGAC       G
GAM372 SNCB          CGGGTAGGACAGACAGATGG    5751 TCCG    __   AA_   GA
                          GGTAGGA  GACA   GGGC
                          |||||||  ||||   ||||
                          CCATCCT  CTGT   CCTG
                          ____        GT   CTA    ||
GAM372 SPHK2         CCGGGTAGGAG-CAGGTGGCAAG   5750 TC      A  AAG
                          CGGGTAGGAG CA  GGCGAG
                          |||||||||| ||  ||||||
                          GCCCATCCTC GT  CCGTTC
                          __        _ CCA
GAM372 TAZ           GGGTAGGAGCC--AGGCCGAG    5760 TCCGGG    ACAA  G
                          TAGGAG   AGG CGA
                          ||||||   ||| |||
                          ATCCTC   TCC GCT
                          _____        GG__  G
GAM372 VGF           GGGTAGGAG-CGACGGTCGAG    5759 TCCGGG    ACAAA  G
                          TAGGAG    GG CGA
                          ||||||    || |||
                          ATCCTC    CC GCT
                          _____       GCTG_  A
GAM373 ADRA2A       GGCGTCCGCCTGG--TGGCGC    5784 TG      GGTGG
                          GCGTCTG  GGTGGGCGC
                          |||||||  |||||||||
                          CGCAGGC  CCACCCGCG
                          __       GGA__
GAM373 ATSV         TGG-GTGTGGGTGGGGAGGGC     5794  C C      T  GC
                          TGG GT TGGGTGGGG GGGC
                          ||| || ||||||||| ||||
                          ACC CA ACCCACCCC CCCG
                          _  C    T  ||
GAM373 CAPS         TGGCGT--GGGTGGGGAGAGCG    5798    CT    T  C
                          TGGCGT GGGTGGGG GGGCG
                          |||||| |||||||| |||||
                          ACCGCA CCCACCCC CTCGC
                          __      T   |
GAM373 CBFA2T3      TGGAG-CTGGGTGGGGTTGGCACG  5799   C T      G   |
                          TGG G CTGGGTGGGGT GGCGCG
                          ||| | ||||||||||| ||||||
                          ACC C GACCCACCCCA CCGTGC
                          T _      A   |
GAM373 CDH5         TGGCGTCTGACTGGCCTGGGC    5795      G GG   GCG
                          TGGCGTCTGG TGG TGGGC
                          |||||||||| ||| |||||
                          ACCGCAGACT ACC ACCCG
                          G GG   |||
GAM373 CLDN3        TGGCTTCTGG---GGGTGGGC    5796  G    TGG    G
                          TGGC TCTGGG  GGTGGGC
                          |||| ||||||  ||||||
```

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                        ACCG AGACCC  CCACCCG
                          A      ___        I
GAM373 DIA1            GGCGT--GGCTGGGGTGGGC     5781 TG   CT G      G
                          GCGT  GG TGGGGTGGGC
                          |||| || |||||||||||
                          CGCA  CC ACCCCACCCG
                          __   __ G      G
GAM373 FASN           TGGCGG--GGGTGGGGTGGG     5791     TCT        CG
                          TGGCG  GGGTGGGGTGGG
                          ||||| |||||||||||
                          ACCGC  CCCACCCCACCC
                             C__       II
GAM373 FASN           TGGGGTG-GGGTGGGGTGGG     5793  C CT       CGC
                          TGG GT GGGTGGGGTGGG
                          ||| || |||||||||||
                          ACC CA CCCACCCCACCC
                           C C_        III
GAM373 FSTL3          GGCCCAGGGTGGGGTGGGC     5780 TG G T       GC
                          GC TC GGGTGGGGTGGGC
                          || || |||||||||||||
                          CG GG CCCACCCCACCCG
                          __ G T       AI
GAM373 FXYD1          GGCGGCGGAGGGGGCGGTGGGCGCG 5771 T_   TCT  T _      II
                          GGCG  GGG GG GGTGGGCGCG
                          ||||   ||| || ||||||||||
                          CCGC  CCC CC CCACCCGCGC
                          CG   CT_  _ G      GI
GAM373 GNAO1          TGGCGTCTGTGGT-GTCTGGGCG   5789       _ GGG    CG
                          TGGCGTCTG GGTG  TGGGCG
                          ||||||||| |||| ||||||
                          ACCGCAGAC CCAC  ACCCGC
                              A  AG_    II
GAM373 GRP58          GGCGGCGAGGTGGGGTGGG     5779 T_  TCT      CGC
                          GGCG  GGGTGGGGTGGG
                          ||||  ||||||||||||
                          CCGC  TCCACCCCACCC
                          CG   ___       CII
GAM373 HCRT          TGGCGCTCAGGGTGGGGTAGCCG    5788     _ T     G CGI
                          TGGCG TC GGGTGGGGTGG CG
                          ||||| || ||||||||||| ||
                          ACCGC AG CCCACCCCATC GC
                          G T       G III
GAM373 HNRPM         GCGTCTGGGCTTTGTGTGAGCG    5770 TGGC     GGG__    CG
                          GTCTGGGT  GTGGGCG
                          ||||||||  ||||||
                          CAGACCCG  CACTCGC
                          ____       AAACA    TT
GAM373 HPD           TGGCCTCCG--TGGGGTGGGCG    5797  G GG        C
                          TGGC TCT GTGGGGTGGGCG
                          |||| ||| |||||||||||||
```

```
                          ACCG AGG  CACCCCACCCGC
                             G  __          I
GAM373   HSF4             TGGAGTG-GGGTGGGGTGGG    5790  C CT        CGC
                             TGG GT GGGTGGGGTGGG
                             ||| || ||||||||||||
                             ACC CA CCCACCCCACCC
                               T C_           |||
GAM373   IGLL1            GGCCTTTGGGTGGGGTCGGGGC   5783 TGGC   __     _ C G
                             GTCT GGGTGGGGT GGG GC
                             |||| ||||||||| ||| ||
                             CGGA CCCACCCCA CCC CG
                             ____     AA     G _ A
GAM373   ITGA4            GGCCGCTGGGTGGGGTCCCGGGCG  5777 T G  T       ___   CGI
                             G CG CTGGGTGGGGT  GGGCG
                             | || ||||||||||   |||||
                             C GC GACCCACCCCA  CCCGC
                             _ G _        GGG   A||
GAM373   MAP3K1           CGACTCGGTAAGGTGGGCGC      5767 TGGCGT  G
                             CT GGTGGGGTGGGCGC
                             || ||||||||||||||
                             GA CCATTCCACCCGCG
                             _____      G
GAM373   NTSR1            GTCCGGGCAGGAGTGGGCGCG     5786 TGGCGTCT  TG  _
                             GGG  GG GTGGGCGCG
                             |||  || |||||||||
                             CCC  CC CACCCGCGC
                             _____      GT  T
GAM373   PRX2             GGCGTCTGGGTCCTGGTGGG      5774 TG      GG_   CGC
                             GCGTCTGGGT  GGTGGG
                             ||||||||||  ||||||
                             CGCAGACCCA  CCACCC
                             __        GGA    T||
GAM373   RANBP3           TGGACG-CTGCCGGTGGGGTGGGGGCG5787  _ T __      C ||
                             TGG CG CTG  GGTGGGGTGGG GCG
                             ||| || |||  |||||||||| |||
                             ACC GC GAC  CCACCCCACCC CGC
                               T _ GG        C ||
GAM373   RNF26            GGCATCTGGGTGGGCCCTGGGC    5776 TG        G__   CG
                             GCGTCTGGGTGGG  TGGGCG
                             ||||||||||||  ||||||
                             CGTAGACCCACCC  ACCCGT
                             __             GGG   ||
GAM373   RRAS2            GGCGTCTGGAGGGCCGGTCAGCGCG  5775 TG      T G ___   ||
                             GCGTCTGGG GGG TGG  GCGCG
                             ||||||||| ||| |||  |||||
                             CGCAGACCT CCC GCC  CGCGC
                             __      _ G  AGT   C|
GAM373   S100A1           GGGGTGGGGGTGGGGTGGGC      5782 T C CT        C
                             GG GT GGGTGGGGTGGGCG
                             || || ||||||||||||||
```

```
                    CC CA  CCCACCCCACCCGT
                    _ _  CC              I
GAM373  SCN8A       GGCGGGCGGGACTGCGGTGGGCGC  5772 TG  TC  __ G     GI
                    GCG  TGGG  TG GGTGGGCGC
                    III IIII II IIIIIIIII
                    CGC GCCC  AC CCACCCGCG
                    __  CC  TG  G     GI
GAM373  SLC12A7     TGGGGTG-GGGTGGGGTGGG     5793  C CT       CGC
                    TGG GT GGGTGGGGTGGG
                    III II IIIIIIIIIII
                    ACC CA  CCCACCCCACCC
                       C C_     III
GAM373  SSPN        CTGGGTGGGTGGGTGGGTGCG    5768 TGGCGTCT   G  C
                    GGGTGGG TGGG GCG
                    IIIIIIII IIII III
                    CCCACCC ACCC CGC
                    _____     _  A
GAM373  TACSTD2     GGCGTCTGGGATGGTCTGCAGGCG  5773 TG     _ G__TG  CGI
                    GCGTCTGGG TGG  G GGCG
                    IIIIIIIII III  I IIII
                    CGCAGACCC ACC  C CCGC
                    __      T AGA GT  AII
GAM373  TCF3        TGGGGACATGGTGGGGTGGG     5792 T___   CTG      CGC
                    GGCGT  GGTGGGGTGGG
                    IIIII  IIIIIIIIIII
                    CTGTA  CCACCCCACCC
                    ACCC  ____        III
GAM373  WDR1        GCCTCTTGTGGTGGGGTGGGGGC   5769 TGGCG _ _       C  I
                    TCT G GGTGGGGTGGG GCG
                    III I IIIIIIIIIII III
                    AGA C CCACCCCACCC CGT
                    G____  A A      C A
GAM373  WSX1        GGCGTCTG---GGGGTGGGGGC    5785 TG    T _ T  GC
                    GCGTCTGGG GG GG GGGC
                    IIIIIIIII II II IIII
                    CGCAGACCC CC CC CCCG
                    __      _ A _  GI
GAM373  WT1         GGC-TCTGGGT-GGGTGGG      5778 TG G      G  CG
                    GC TCTGGGTGGG TGGG
                    II IIIIIIIIIII IIII
                    CG AGACCCACCC ACCC
                    __ _      _  AI
GAM374  ABCD1       GGCA---GGGGCCGGGGACG     5808    TCC      TI
                    GGCA GGGGCCGGGG
                    IIII IIIIIIIIII
                    CCGT CCCCGGCCCC
                    ___      TG
GAM374  ABCD1       GGCA---GGGGCCGGGGACG     5808 TG TCC      TC
                    GCA GGGGCCGGGG GC
                    III IIIIIIIIII II
```

```
                        CGT   CCCCGGCCCC TG
                        __   ___        __
GAM374 AES          GCATACCTGGGACCCGGGGTCGGGG 5804 _____   C      C    TCGCGGII
                        TGG ATCCGGGG CGGGG
                        ||| |||||||| |||||
                        ACC TGGCCCC GCCCC
                        TATGG  C     A   CTIIIGGC
GAM374 AES          GCATACCTGGGACCCGGGGTCGGGG 5804 AT _    _     CGI
                        CC GGGGCC GGGGTCG
                        || |||||| |||||||
                        GG CCCTGG CCCCAGC
                        T_  A    G    CII
GAM374 FLNA         GGCGGCCTGGGCCGGGGTTGAGG   5811 _ ATCCG       CGCI
                        GGC   GGGCCGGGGT
                        |||   ||||||||||
                        CCG   CCCGGCCCCA
                        G  GA___        ACTC
GAM374 FLNA         GGCGGCCTGGGCCGGGGTTGAGG   5811 T_ ATCCG      CGC I
                        GGC   GGGCCGGGGT GG
                        |||   |||||||||| ||
                        CCG   CCCGGCCCCA CC
                        CG  GA___       ACT C
GAM374 GALNT2       GGGATGCCGGGGCCGAGGCCG     5805 GCAT              I
                        CCGGGGCCGGGGTC
                        ||||||||||||||
                        GGCCCCGGCTCCGG
                        CTAC           I
GAM374 GALNT2       GGGATGCCGGGGCCGAGGCCG     5805 T C _         CGG
                        GG AT CCGGGGCCGGGGTCG
                        || || |||||||||||||||
                        CC TA GGCCCCGGCTCCGGC
                        _ _ C       CII
GAM374 INSM1       TCGGGGGCCGGGGTGGAGG        5812 C        CGCGII
                        TC GGGGCCGGGGT
                        || |||||||||||
                        AG CCCCGGCCCCA
                        C        CCTCCI
GAM374 INSM1       TCGGGGGCCGGGGTGGAGG        5812 TGGCAT    CC_  T
                        CCGGGG GGGG CGCG
                        |||||| |||| ||||
                        GGCCCC TCCC GCGC
                        CC____    ACC    _
GAM374 NGB         GGCTGCCGGG--CGGGGTCGC      5810  AT  GC    I
                        GGC CCGGG CGGGGTC
                        ||| ||||| ||||||||
                        CCG GGCCC GCCCCAG
                        AC  __    C
GAM374 NGB         GGCTGCCGGG--CGGGGTCGC      5810 TG AT  GC      G
                        GC CCGGG CGGGGTCGC
                        || ||||| |||||||||
```

```
                                    CG  GGCCC  GCCCCAGCG
                                    __  AC     __      G
GAM374 PTPRS          GGCATCCGGGGGCCAGTGGTGTCGG  5806 G         _  CG  I
                         CATCCGGGGCCGG GGT  CG
                         |||||||||||| ||| ||
                         GTAGGCCCCGGTC CCA  GC
                            _              A  CA  I
GAM374 PTPRS          GGCATCCGGGGGCCAGTGGTGTCGG  5806 TG        _  CG  I
                         GCATCCGGGGCCGG GGT  CGG
                         ||||||||||||| ||| |||
                         CGTAGGCCCCGGTC CCA  GCC
                            __             A  CA  C
GAM374 RPS6KA2         GGC-TCCGAGGCCGGGGTC      5807  A          I
                         GGC TCCGGGGCCGGGGT
                         ||| ||||||||||||
                         CCG AGGCTCCGGCCCCA
                            _              G
GAM374 RPS6KA2         GGC-TCCGAGGCCGGGGTC      5807 TG  A         GC
                         GC TCCGGGGCCGGGGTC
                         || |||||||||||||
                         CG AGGCTCCGGCCCCAG
                            __  _          AI
GAM374 RUNX3          ATCCCGGGCCGGGGTGGGGG      5802  G       CGCGI
                         TCC GGGCCGGGGT
                         ||| ||||||||||
                         AGG CCCGGCCCCA
                         G       CCCCI
GAM374 RUNX3          ATCCCGGGCCGGGGTGGGGG      5802 TGGCATCCG       CGC
                         GGGCCGGGGT  G
                         |||||||||| |
                         CCCGGCCCCA  C
                         G_____       CCC
GAM374 SGT           GGCA--CAGGGCCGGGGTGGC     5809   TC       CI
                         GGCA CGGGGCCGGGGT
                         |||| |||||||||||
                         CCGT GTCCCGGCCCCA
                            __          CC
GAM374 SGT           GGCA--CAGGGCCGGGGTGGC     5809 TG  TC       C  G
                         GCA CGGGGCCGGGGT GC
                         ||| ||||||||||| ||
                         CGT GTCCCGGCCCCA CG
                            __  __        C  G
GAM374 TRAF1          CATTCGGGGCCGGAGTGGC      5803  C       CGII
                         CAT CGGGGCCGGGGT
                         ||| ||||||||||||
                         GTA GCCCCGGCCTCA
                         A           CCGI
GAM374 TRAF1          CATTCGGGGCCGGAGTGGC      5803 TGGCATC       C  G
                         CGGGGCCGGGGT GC
                         |||||||||||| ||
```

```
                                GCCCCGGCCTCA CG
                            A_____          C A
GAM375 ABCD1          GGCA---GGGGCCGGGGACG    5808   TTC      TI
                      GGCA GGGGCCGGGG
                      |||| ||||||||||
                      CCGT CCCCGGCCCC
                           ___          TG
GAM375 AES            GCATACCTGGGACCCGGGGTCGGGG 5804 ATTC    _    CI
                           GGGGCC GGGGTCG
                           |||||| |||||||
                           CCCTGG CCCCAGC
                           GGA_    G    CI
GAM375 ALOX12B          TGCCCTTGGTGGCCGGGGT      5832 TG ATTC _     II
                          GC  GG GGCCGGGG
                          ||  || |||||||||
                          CG  CC CCGGCCCC
                          A_ GGAA A     AI
GAM375 BMPR2           GGGATTCGAT-CCGGGGTCGGGG  5827  C   GG    CI
                      GG ATTCGG CCGGGGTCG
                      || |||||| |||||||||
                      CC TAAGCT GGCCCCAGC
                         _   A_     CC
GAM375 CHGA           TGG-ACTGGCGGCCGGGGTCG   5833 _ C  C _     I
                      GG ATT GG GGCCGGGGTC
                      || ||| || ||||||||||
                      CC TGA CC CCGGCCCCAG
                      A _ _ G     I
GAM375 FLOT1          TCGGGAAGGGCGGGGTCGCG    5828   C___      III
                      TCGGGG  CGGGGTCGC
                      ||||||  |||||||||
                      AGCCCT  GCCCCAGCG
                        TCCC      CII
GAM375 GTF2I          GGCAGCTCCGGGGCCGGGG    5820   __       III
                      GGCA TTCGGGGCCGGG
                      |||| |||||||||||
                      CCGT AGGCCCCGGCCC
                        CG        CII
GAM375 GTF2I          GGCAGCTCCGGGGCCGGGGCCTCG 5822 _ A        GCI
                      GC TTCGGGGCCGGGGTC
                      || |||||||||||||||
                      CG AGGCCCCGGCCCCGG
                      T _        AGI
GAM375 HIF1A          GGCAATCG---CCGGGGTC-CGG  5826  T GGG    GI
                      GGCA TC  GCCGGGGTC
                      |||| ||  |||||||||
                      CCGT AG  CGGCCCAG
                        T ___      GC
GAM375 HIPK2          CGGGGCCGGGGTGTCCGCGG    5816         ___ III
                      CGGGGCCGGGGT CGCG
                      |||||||||||| ||||
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                         GCCCCGGCCCCA  GCGC
                           CAG    CII
GAM375  INSM1       GGCACAGTTCGGGGGCCGGGGTGGAGG5819 A      _      CGCI
                         TTCGGGG CCGGGGT

                         |||||||  |||||||
                         AAGCCCC GGCCCCA
                           C    C    CCII
GAM375  KCNH3       GCAGACCGGGATCCGGGGTCGCG  5817 CAT    _        I
                         TCGGGG CCGGGGTCGC

                         ||||||  |||||||||||
                         GGCCCT GGCCCCAGCG
                           CT_    A       I
GAM375  LMO2        TGGCACCTTTCCGGCCCCGGGTCGCGG5830 GGCA  G  G  G      I
                         TTC GG CC GGGTCGCG

                         ||| || || |||||||||
                         AAG CC GG CCCAGCGC
                         TGGA  G  G       I
GAM375  MAN2A1      GGCAGCTCCCGGGCCGGGGCCGCG 5821_  A  G          I
                         GC TTC GGGCCGGGGTCGC

                         || ||| ||||||||||||||
                         CG AGG CCCGGCCCCGGCG
                           T _  G       I
GAM375  NCOR2       GCATTCGGGGGAGGCAGTGGCG   5818       CC   CGCI
                         ATTCGGGG GGGGT

                         |||||||| |||||
                         TAAGCCCC CTCCG
                            __     TCAC
GAM375  NFATC2      GGC-TGCGGGGCCGGGGGCGAGG  5825 _ ATT       TC  I
                         GC CGGGGCCGGGG GCG

                         || |||||||||| |||
                         CG GCCCCGGCCCC CGC
                         C AC_         __  T
GAM375  NGB         GGC-TGCCGGGC-GGGGTCGC     5823  AT   GC    I
                         GGC TCGGG CGGGGTC

                         ||| ||||| |||||||
                         CCG GGCCC GCCCCAG
                           AC   __    C
GAM375  NR2F6       GGCAG-CGGGGCCGGGG-CGC     5824   TT        CI
                         GGCA CGGGGCCGGGGT

                         |||| |||||||||||
                         CCGT GCCCCGGCCCCG
                           C_        CG
GAM375  RABL2A      ATT-GGGGCCGGG--CGCGG      5815 TTC      GT
                         GGGGCCGGG CGCG

                         ||||||||| ||||
                         CCCCGGCCC GCGC
                           TAA        __
GAM375  RABL2B      ATT-GGGGCCGGG--CGCGG      5815 TTC      GT
                         GGGGCCGGG CGCG

                         ||||||||| ||||
```

```
                        CCCCGGCCC GCGC
                        TAA          __
GAM375 RAD23B         TGGCCTGGCGGGGCCCCGGGGTCGC 5831 __ ATTC    __      I
                        GGC   GGGGCC GGGGTCG
                        |||   |||||| |||||||
                        CCG   CCCCGG CCCCAGC
                        GA    ____   GG      I
GAM375 ROR2           TTCG-GGCCGGGG-CGCGG     5836    G    T   I
                        TTCGGG CCGGGG CGCG
                        |||||| |||||| ||||
                        AAGCCC GGCCCC GCGC
                           _    _    C
GAM375 RPS6KA2          GGC-TCCGAGGCCGGGGTC      5807  A            I
                        GGC TTCGGGGCCGGGGT
                        ||| |||||||||||||
                        CCG AGGCTCCGGCCCCA
                         _          G
GAM375 RUNX3           ATCCCGGGCCGGGGTGGGGG      5802  G        CGCGI
                        TTC GGGCCGGGGT
                        ||| ||||||||||
                        AGG CCCGGCCCCA
                         G        CCCCI
GAM375 SGT             GGCA--CAGGGCCGGGGTGGC     5809   TT       CI
                        GGCA CGGGGCCGGGGT
                        |||| |||||||||||
                        CCGT GTCCCGGCCCCA
                          __        CC
GAM375 SIL             TCTGGGACGTTGGGGTCGCGG     5829 TC_   C__      III
                        GGGGC GGGGTCGCG
                        ||||| |||||||||
                        CCCTG CCCCAGCGC
                        AGA   CAA      CII
GAM375 TIMM23         TGACACTCCCAGACGGGGTCGCGG 5834     GG  C      I
                        GGCATTC GG CGGGGTCGCG
                        ||||||| || |||||||||
                        CTGTGAG TC GCCCCAGCGC
                         GG  T       I
GAM375 TRAF1          CATTCGGGGCCGGAGTGGC       5803           CGII
                        CATTCGGGGCCGGGGT
                        ||||||||||||||||
                        GTAAGCCCCGGCCTCA
                          CCGI
GAM375 ZNF137         TTAGGGGCCGGG--CGCGG       5835 TTC     GT  I
                        GGGGCCGGG CGCG
                        ||||||||| ||||
                        CCCCGGCCC GCGC
                        AAT    __   C
GAM376 CAMLG          TGTAAAC-CAATTTGCCTCC      5848   T       CT
                        TGTAAAC CAATTTGCCTCC
                        ||||||| ||||||||||||
```

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                    ACATTTG GTTAAACGGAGG
                       _              II
GAM376 GNA14        GTAAACTCAAATATCTTCC      5842 TG       TTTGCC  CT
                       TAAACTCAA    TCC
                       IIIIIIIII    III
                       ATTTGAGTT    AGG
                          __      TATAGA  TI
GAM376 MAN1A2       AAACTCAATTTTGCTCTCT      5839 TGTAAA      _ _  C
                       CTCAATTT GC CTC CT
                       IIIIIIIII II III II
                       GAGTTAAA CG GAG GA
                       _____       A A A
GAM376 MOX2         TGTATGCTCATATTTGCCTCC    5846   AA  _      CTI
                       TGTA CTCA ATTTGCCTCC
                       IIII IIII IIIIIIIIII
                       ACAT GAGT TAAACGGAGG
                         AC  A        III
GAM376 PCDHGA7      GTAAACTCATTTTTACCTC      5841 TG    A_    CCT
                       TAAACTCA TTTGCCTC
                       IIIIIIII IIIIIIII
                       ATTTGAGT AAATGGAG
                          __      AA   AII
GAM376 RNMT         TAAACAAAATGATTTGCCTC     5843 TGTAAACTCA      CCT
                       ATTTGCCTC
                       IIIIIIIII
                       TAAACGGAG
                     TTGTTTTAC_      ACI
GAM376 SLC12A6      TGTTAATTCTAATTTGCCT      5845 A C _      CCCT
                       TGT AA TC AATTTGCCT
                       III II II IIIIIIIII
                       ACA TT AG TTAAACGGA
                         A  A  A       IIIT
GAM376 SLC7A8       TGCAACCTCAAAAGCTGCCTCCCT 5847  A  T__       II
                       TGTAA CTCAA  TTGCCTCCCT
                       IIIII IIIII  IIIIIIIIII
                       ACGTT GAGTT  GACGGAGGGA
                         G    TTC       II
GAM376 TPM4         GTAAATCCTCAATTTGCTGTTCCCT 5840 TGTAAA      C__  III
                       CTCAATTTGC TCCCT
                       IIIIIIIIII IIIII
                       GAGTTAAACG AGGGA
                     ATTTAG        ACA  CII
GAM376 ZNF151       TGTAAACTCCAGCTTGGCTCCC   5844      AA_ C  TI
                       TGTAAACTC TTTG CTCCC
                       IIIIIIIII IIII IIIII
                       ACATTTGAG GAAC GAGGG
                         GTC   C   II
GAM377 GUCY1A2      AGGCGGTGGCG---GCGAGGACG  5851 AA  A  CCCT
                       GGCG TGGC  GCGAGGAC
                       IIII IIII  IIIIIIII
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                             CCGC ACCG   CGCTCCTG
                             __    C   C___
GAM377 TRC8          GCGATGGCC---GAGAGGGCG   5852 AAGGCG    CCT C    A
                          ATGGCC  G GAGG
                          ||||||  | ||||
                          TACCGG  C CTCC
                          _____     ___T  C
GAM378 ACHE          GGCGCCCAGCGAGGCGGGAGGG   5861 TG  ATTC _       CA
                          GCGC   CG GGCGGGAGGG
                          ||||   || |||||||||
                          CGCG   GC CCGCCCTCCC
                          __  GGTC  T      CI
GAM378 BSN           GCATCTCGGA-GGGAGGGCA    5856 TGGCGCATTC   C
                          CGGG GGGAGGGC
                          |||| |||||||||
                          GCCT CCCTCCCG
                        GA_____   _
GAM378 COL5A1         TGGCGCGCTCGCCCACGGGCGGGAGGGC5871    A  _____        AIII
                          TGGCGC TTC   CGGGCGGGAGGGC
                          |||||| |||   ||||||||||||
                          ACCGCG GAG    GCCCGCCCTCCCG
                            C  CGGGT      IIIA
GAM378 CRLF1         CGCAGGCCGGGCGCGGGAGGGC   5855 TGGCGCATT    __     A
                          CCGGGC GGGAGGGC
                          |||||| |||||||||
                          GGCCCG CCCTCCCG
                        TCC_____    CG      C
GAM378 CYBA          GGTGCA--CCTGGCGGGAGGGCA   5868 TGGC  TT G
                          GCA CC GCGGGAGGGCA
                          ||| || |||||||||||
                          CGT GG CCGCCCTCCCGT
                          CA__  __ A
GAM378 FUT3          TGGCAGGTTTCCTGGGGCGGGAGG  5870   CA_  __      GCAI
                          TGGCG TTCC GGGCGGGAGG
                          ||||| |||| |||||||||
                          ACCGT AAGG CCCGCCCTCC
                            CCA  AC      IIIA
GAM378 FXYD7         GGCTCATTCCG---GGGAGCGC    5866 TG G     CGG  G
                          GC CATTCCGGG  GAG GC
                          || |||||||||  ||| ||
                          CG GTAAGGCCC  CTC CG
                          __  A      ___  G
GAM378 HRMT1L2       GGCTCGTGCAGGGCGGGAGAGC   5867 TGGC__  TTCC        A
                          GCA  GGGCGGGAGGGC
                          |||  |||||||||||
                          CGT  CCCGCCCTCTCG
                        CGAGCA  ____        G
GAM378 HS3ST3A1      TGGCTCGGTCCC--CGGGAGGGCA  5874   GCAT GGG
                          TGGC  TCC CGGGAGGGCA
                          ||||  ||| ||||||||||
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                        ACCG  AGG  GCCCTCCCGT
                        AGCC  G__
GAM378  ILF1        GGAGCACGCGCGGGCGGGAGG    5860 T  ATTC        CA
                        GGCGC  CGGGCGGGAGGG
                        |||||  |||||||||||
                        TCGTG  GCCCGCCCTCCT
                        C   CGC_            II
GAM378  MAF        GGCGTCTGTCCGGGCGGCGCGGGC 5859 TG  CAT_        GA_  AI
                        GCG  TCCGGGCGG GGGC
                        |||  ||||||||| ||||
                        CGC  AGGCCCGCC CCCG
                        __  AGAC       GCG  GI
GAM378  MAN1A1      GGCGCAGCGTGGGCGGGAG      5862 TG  TTCC        GC
                        GCGCA  GGGCGGGAGG
                        |||||  ||||||||||
                        CGCGT  CCCGCCCTCT
                        __  CGCA          II
GAM378  MAPK8IP1    TGGC-CAT-CCGGGC-GGAGCGC  5873  G  T      G  G
                        TGGC CAT CCGGGCGG AG GC
                        |||| ||| ||||||||| || ||
                        ACCG GTA GGCCCGCC TC CG
                        _  _       _ G
GAM378  MN1         GCGCACCGTTGCAGGCGCGGGAGGGCA5857 TG  ATTCC__  _         III
                        GCGC    GG GCGGGAGGGCA
                        ||||    || ||||||||||
                        CGTG    CC CGCCCTCCCGT
                        __  GCAACGT  G        CGI
GAM378  NFKBIA      GGCGC-TGGCGGGCGGGACGGC   5865 TG  ATTC       G  A
                        GCGC   CGGGCGGGA GGC
                        ||||   |||||||| |||
                        CGCG   GCCCGCCCT CCG
                        __  ACC_        G  C
GAM378  NRXN2       GGCGCATG--GGGCGGGAGGG    5864 TG  TCC         C
                        GCGCAT GGGCGGGAGGG
                        ||||||  |||||||||||
                        CGCGTA CCCGCCCTCCC
                        __  C__         C
GAM378  PODXL       GCGCGT-CCGGGCGGTAGG      5858 TG  CAT         G
                        GCG  TCCGGGCGG AGGG
                        |||  ||||||||| ||||
                        CGC  AGGCCCGCC TCCT
                        __  ___         A
GAM378  PYGM        TGGCCAGCATT---GGCGGGAGG  5869  __  CCG         GC
                        TGGC GCATT GGCGGGAGG
                        |||| ||||| |||||||||
                        ACCG CGTAA CCGCCCTCC
                        GT  ___         II
GAM378  SH3GL2      TGGCGGCTGCTGTGCGGGAGGG   5872     CATTCCGG       CA
                        TGGCG    GCGGGAGGG
                        |||||    |||||||||
```

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                            ACCGC       CGCCCTCCC
                            CGACGACA          II
GAM378 SMURF1          GGCG---TCCGGGCGGCAGG      5863 TG  CAT       GA
                            GCG  TCCGGGCGG GGG
                            |||  ||||||||| |||
                            CGC  AGGCCCGCC TCC
                             __   ___    G_
GAM379 DYT1           GGGATGCCCTCCTGTTCAGGAA    2529        A  _    GCA
                            GGGATGCCCTC TGTT GGGAA
                            ||||||||||| |||| |||||
                            CCCTACGGGAG ACAA TCCTT
                                G   G   |||
GAM379 IL1RAP          GATGCCTT--TCTTGGGAAGC     2528 GGGA   CTCATG
                            TGCC    TTGGGAAGC
                            ||||    |||||||||
                            ACGG    AACCCTTCG
                             ____    AAAG__
GAM379 SLC21A3          GGCATTGCCTCAC-TTGGGAAGC  2530 G GC   G     A
                            GG AT  CCTCAT TTGGGAAGC
                            || ||  |||||| |||||||||
                            CC TA  GGAGTG AACCCTTCG
                             G  AC    _       I
GAM379 SOST          GGGAAGCC---AGGCTGGGAAGCA   2531    T CTCAT
                            GGGA GCC    GTTGGGAAGCA
                            |||| |||    |||||||||||
                            CCCT CGG    CGACCCTTCGT
                             T  TC___
GAM380 APG5L          TCC-CCGCACTGGTG--GGGACGC  5891  G C  T TC  A
                            TCC CC CACT GTG  GGGA GC
                            ||| || |||| ||| |||| ||
                            AGG GG GTGA CAC  CCCT CG
                             _  C  C  __   G
GAM380 APG5L          TCC-CCGCACTGGTG--GGGACGC  5891  G C  T TC  AI
                            TCC CC CACT GTG  GGGA
                            ||| || |||| ||| ||||
                            AGG GG GTGA CAC  CCCT
                             _  C  C  __   GC
GAM380 CD1A          CCCACTTGTAAGTCAGGGAAG      5881        __    AAIII
                            CCCACTTGT GTCGGG
                            ||||||||| ||||||
                            GGGTGAACA CAGTCC
                               TT    CTTCI
GAM380 CDKN3           CCGCCCCAC----GTCGAGA     5884 _     TTGT
                            CGCCCCAC  GTCGGG
                            ||||||||  ||||||
                            GCGGGGTG  CAGCTC
                              G       ____
GAM380 CDKN3           CCGCCCCAC----GTCGAGA     5884 TC     TTGT
                            CGCCCCAC  GTCGGGA
                            ||||||||  |||||||
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                                GCGGGGTG    CAGCTCT
                                 __        ____
GAM380  CSNK2A2        CCCCATGCTTTCTGGGTCGGGAAG  5882    __  GT___        IIIC
                        CCCCA CTT    GTCGGGAA
                        IIIII III   IIIIIIIII
                        GGGGT GAA    CAGCCCTT
                          AC AGACC       CIII
GAM380  CSNK2A2        CCCCATGCTTTCTGGGTCGGGAAG  5882 TCC CCCAC  T      CI
                        GC    TTG GTCGGGAAG
                        II    III IIIIIIIII
                        CG    GAC CAGCCCTTC
                        TA_ AAA__  C      TT
GAM380  CYP4A11       TCCCGCCCACTTGTG--GGGA      5890 _     C    TC   AG
                        TCCGCCC ACTTGTG  GGGA
                        IIIIIIII IIIIIIII  IIII
                        GGGCGGG TGAACAC  CCCT
                          A     _    __      II
GAM380  CYP4A11       TCCCGCCCACTTGTG--GGGA      5890 __     C    TC  I
                        CCGCCC ACTTGTG  GGG
                        IIIIIII IIIIIIII III
                        GGCGGG TGAACAC  CCC
                        AG     _    __    I
GAM380  H1F0        TCCTCCCCGGCTCGGGTGTCGGGAGAGC 5889  G   A_ __       _  III
                        TCC CCCC  CTT  GTGTCGGGA AGC
                        III IIII  III  IIIIIIIIII III
                        AGG GGGG  GAG  CACAGCCCT TCG
                          A  CC  CC        C  III
GAM380  H1F0        TCCTCCCCGGCTCGGGTGTCGGGAGAGC 5889 G   CA  __       AGI
                        CCC  CTT GTGTCGGGA
                        III  III IIIIIIIII
                        GGG  GAG CACAGCCCT
                        _  CC  CC        CII
GAM380  HR           CGCCCCACTGGCCTGTGTC         5886         ____     IIIG
                        CGCCCCACT  TGTGT
                        IIIIIIIII  IIIII
                        GCGGGGTGA  ACACA
                          CCGG    GIII
GAM380  HR           CGCCCCACTGGCCTGTGTC         5886 TCCG    ____       GGGAAG
                        CCCCACT  TGTGTC
                        IIIIIII  IIIIII
                        GGGGTGA  ACACAG
                        ____       CCGG    ACIIIC
GAM380  LIF          GCCCTGGCGCTTGTGTCGGGA       5887    CA___        III
                        GCCC  CTTGTGTCGGG
                        IIII  IIIIIIIIIII
                        CGGG  GAACACAGCCC
                          ACCGC        TII
GAM380  LIF          GCCCTGGCGCTTGTGTCGGGA       5887 TCC CCCA          A
                        GC   CTTGTGTCGGGA GC
                        II   IIIIIIIIIIII II
```

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                          CG   GAACACAGCCCT CG
                        GAC  C___              _
GAM380 MLLT4            GCACCGCT-G-GTCGGGAAG    5888  C A T T      I
                        GC CC CT G GTCGGGA
                        || || || | ||||||
                        CG GG GA C CAGCCCT
                         T  C  _ _       T
GAM380 MLLT4            GCACCGCT-G-GTCGGGAAG    5888 T   CCCACT T
                         CCGC   TG GTCGGGAA
                         ||||    || |||||||||
                         GGCG    AC CAGCCCTT
                           _   _____
GAM380 SLC19A1          CCGCCCCACGCGTGGCTGGCAG    5885      T  TCG AAI
                         CGCCCCAC TGTG  GG
                         |||||||| ||||   ||
                         GCGGGGTG GCAC  CC
                            C  CGA GTI
GAM380 SLC19A1          CCGCCCCACGCGTGGCTGGCAG    5885 TC     T  TCG A C
                         CGCCCCAC TGTG  GG AG
                         |||||||| ||||  || ||
                         GCGGGGTG GCAC  CC TC
                          __       C  CGA G C
GAM380 XRCC3            CCGAGCCCCGTGTGTCGGG    5883 CC__    ACT      II
                          GCCCC  TGTGTCGG
                          |||||  |||||||||
                          CGGGG  ACACAGCC
                         GGCT   C__      CI
GAM380 XRCC3            CCGAGCCCCGTGTGTCGGG    5883 TCC   ACT      AAG
                          GCCCC  TGTGTCGGG
                          |||||  |||||||||
                          CGGGG  ACACAGCCC
                         GCT   C__      CII
GAM381 ALPPL2          CAGGGGAACTCCGGGATGGGGA    5900 TGACAA    __       T
                         GGGAAT TGGGATGGGGA
                         ||||||  |||||||||||
                         CCCTTG GCCCTACCCCT
                         _____    AG       T
GAM381 C3              GACAGAGGGAGA--GGATGGGGA    5903 TG  _   ATT      T
                          ACA AGGGA  GGGATGGGGA
                          ||| |||||   |||||||||
                          TGT TCCCT  TCCTACCCCT
                          __  C   C__      C
GAM381 DLEC1           TGACAAGGGA--GGGCCAGATGGG    5909       ATTG_    GAT
                         TGACAAGGGA   GGATGGG
                         ||||||||||   |||||||
                         ACTGTTCCCT   TCTACCC
                              CCCGG       III
GAM381 GRIK3           TGCCCAGGCATATGGGATGGGTAT    5912 ACA  GAAT      GATI
                         TG AGG  TGGGATGGG
                         || |||  |||||||||
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                        AC  TCC    ACCCTACCC
                        GGG  GTAT      ATAI
GAM381  IRS1         DACAAGGGCGAGAGGGGATGGGG  5904 TG     AATT__      ATI
                        ACAAGGG    GGGATGGGG
                        ||||||     |||||||||
                        TGTTCCC    CCCTACCCC
                          __    GCTCTC      CII
GAM381  LIF          DACATGGGTGGGAGTGGGATGGGG  5905 TGACAA__  AT       ATI
                         GGGA TGGGATGGGG
                         |||| |||||||||
                         CCCT ACCCTACCCC
                        TGTACCCA  C_       CII
GAM381  MFAP2          AAGGAACATGGGGATGGGGA    5894 TGACAAGGGAATT
                           GGGATGGGGA
                           ||||||||||
                           CCCTACCCCT
                        TTGTAC_____
GAM381  MSN          ACAAGG-AATTGGGGTAGG     5898 TGACA       A
                          AGGGAATTGGG TGGGG
                          |||||||||| |||||
                          TTCCTTACCC ATCCT
                           _____          C
GAM381  MYO1C          TGCCAAGGGAATCAGGA-GGAGA  5911 TGA    TG  T   T
                          CAAGGGAAT GGA GGGGA
                          ||||||||| ||| |||||
                          GTTCCCTTA CCT CCTCT
                        ACG       GT  _   I
GAM381  NF1          CACGGGGGTGGGGATGGGG    5901 TGACAA  AATT    A
                          GGG   GGGATGGGG
                          |||   |||||||||
                          CCC   CCCTACCCC
                        C_____ CAC_      C
GAM381  NOS1          TGAGCAGGGGAAATTGGGAT   5908 _ A  _    GGGGA
                          TGA CA GGGAA TTGGGAT
                          ||| || ||||| |||||||
                          ACT GT CCCTT AACCCTA
                          C  C  T    IIITA
GAM381  PAX5          ACAAGGGAAGTTGGGCTAGG   5897 TGAC   _  A  GA
                          AAGGGAA TTGGG TGGG
                          ||||||| ||||| ||||
                          TTCCCTT AACCC ATCC
                           ____     C  G  AG
GAM381  PPP2R4          ACAGAGGGAG--GGATGGGGA  5896 TGACA  ATT
                           AGGGA GGGATGGGGA
                           ||||| |||||||||
                           TCCCT CCCTACCCCT
                        TC___  C__
GAM381  PTGIR          DACAATGAGAT--GGATGGGGA  5907 TG  _  ATTG
                          ACAA GGGA   GGATGGGGA
                          |||| ||||   |||||||||
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                                    TGTT CTCT   CCTACCCCT
                                 __     A   A___
GAM381 RUNX3          TGTCAGGGGATGGGGGATGGGG   5910 TGA  A   ATT      AT
                            CA GGGA  GGGATGGGG
                            || |||| |||||||||
                            GT CCCT  CCCTACCCC
                        ACA  C  ACC       ||
GAM381 TRPV4         CAAGGGAAT--GAAAGGGGA    5902 TGACAA    T GG T
                           GGGAAT G  A GGGG
                           |||||| |  | ||||
                           CCCTTA C  T CCCC
                        _____      _ TT _
GAM381 UNRIP          AGGAAAGTAGGGGATGGGGA    5899 TGACAAGGGAATT
                              GGGATGGGGA
                              ||||||||||
                              CCCTACCCCT
                       TCATC_____
GAM381 WBSCR1         ACACAGGCAACAGGGATGGGG   5895 TG  A  G  T      AT
                          ACA GG AAT GGGATGGGG
                          ||| || ||| |||||||||
                          TGT CC TTG CCCTACCCC
                       __  _ G  T      CC
GAM381 XPNPEP2        GACAAGGGAGAGAGGGAGGG   5906 TG      ATT_  T GA
                          ACAAGGGA   GGGA GGG
                          |||||||| |||| |||
                          TGTTCCCT   CCCT CCC
                       __        CTCT  _  GI
GAM382 AKAP13        AGCCAAGCCCCGGGTAGATCTC   5916 G    ___      CII
                          AG CGAGCC  GGTAGATCTC
                          || ||||||  ||||||||||
                          TC GTTCGG  CCATCTAGAG
                           G   GGC       III
GAM382 AKAP13        AGCCAAGCCCCGGGTAGATCTC   5916 G    ___      III
                          AG CGAGCC  GGTAGATCT
                          || ||||||  |||||||||
                          TC GTTCGG  CCATCTAGA
                           G   GGC      GII
GAM382 BARX2         AGG-GAGACGGGTAGATCTC   5917 C _ C      CI
                          AGG GAG C GGTAGATCTC
                          ||| ||| | ||||||||||
                          TCC CTC G CCATCTAGAG
                           _  T C         II
GAM382 BARX2         AGG-GAGACGGGTAGATCTC   5917 C _ C      II
                          AGG GAG C GGTAGATCT
                          ||| ||| | |||||||||
                          TCC CTC G CCATCTAGA
                           _  T C       GI
GAM382 CALB2         GGCGAGCCGCTCGGAGACCTC   5921         ____ T  III
                          GGCGAGCC  GG AGATCT
                          ||||||||  || ||||||
```

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                        CCGCTCGG  CC TCTGGA
                          CGAG _    GII
GAM382 CALB2            GGCGAGCCGCTCGGAGACCTC    5921 AG      ____  T    CII
                        GCGAGCC  GG AGATCTC
                        ||||||| || |||||||
                        CGCTCGG  CC TCTGGAG
                        __    CGAG _    TII
GAM382 HK1             GGCGAGCC-GTGGTCCTCC     5923      GTAGA   I
                        GGCGAGCCG   TCTC
                        ||||||||| ||||
                        CCGCTCGGC  GGAG
                          ACCA_  G
GAM382 HK1             GGCGAGCC-GTGGTCCTCC      5923 AG    GTAGA
                        GCGAGCCG   TCTCC
                        |||||||| |||||
                        CGCTCGGC  GGAGG
                        __    ACCA_
GAM382 IHPK3          AGGTGAGATGGGTAGATCTC     5918   C  CC_     CI
                        AGG GAG  GGTAGATCTC
                        ||| ||| ||||||||||
                        TCC CTC  CCATCTAGAG
                          A  TAC       II
GAM382 IHPK3          AGGTGAGATGGGTAGATCTC     5918   C  CC_     II
                        AGG GAG  GGTAGATCT
                        ||| ||| |||||||||
                        TCC CTC  CCATCTAGA
                          A  TAC       GI
GAM382 KCNK5        AGGGCAGACACTAGATCTCC       5919 _  G  C  G      I
                        GGC AG CG TAGATCTC
                        ||| || || |||||||||
                        CCG TC GT ATCTAGAG
                        C  _  T  G      I
GAM382 KCNK5        AGGGCAGACACTAGATCTCC       5919 A_  G  C  G      I
                        GGC AG CG TAGATCTCC
                        ||| || || |||||||||
                        CCG TC GT ATCTAGAGG
                        TC  _  T  G      I
GAM382 SBF1          GGCGAGCCGCTGGTAGCTCC      5922        ___   A  CII
                        GGCGAGCC  GGTAG TCT
                        |||||||| ||||| |||
                        CCGCTCGG  CCATC AGG
                          CGA   G  III
GAM382 SBF1          GGCGAGCCGCTGGTAGCTCC      5922 AG      ___    AT  I
                        GCGAGCC  GGTAG CTCC
                        ||||||| ||||| ||||
                        CGCTCGG  CCATC GAGG
                        __    CGA __   C
GAM382 SF1          AGGCGAGCCCGAGGGAGCTC       5915       _ TA  T  CI
                        AGGCGAGCC GG GA CTC
                        ||||||||| || || |||
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                    TCCGCTCGG CT  CT GAG
                       G  CC  C   II
GAM382 SF1          AGGCGAGCCCGAGGGAGCTC   5915      GGTAGATIII
                       AGGCGAGCC
                       IIIIIIIII
                       TCCGCTCGG
                          G_____
GAM382 TCTE1L          GCGACACGCCGGTAGAGCACC   5920  ___      TCTCIII
                       GCGA  GCCGGTAGA
                       IIII  IIIIIIIII
                       CGCT  CGGCCATCT
                          GTG      CGTGGII
GAM382 TCTE1L          GCGACACGCCGGTAGAGCACC   5920 A  A      TCT II
                        GGCG GCCGGTAGA  CC
                        IIII IIIIIIIII  II
                        CTGT CGGCCATCT  GG
                        _  G      CGT CG
GAM383 ACHE          TGGCAA--GA-GGATCAGGAGAAT 5944    CT T  A
                     TGGCAA GA GGA CAGGAGAAT
                     IIIIII II III IIIIIIIII
                     ACCGTT CT CCT GTCCTCTTA
                           __ _   A
GAM383 ACTN1         CAGCAGATGGAACAGATAGAA    5928 TGGCAACT      _  T
                        GATGGAACAGG AGAA
                        IIIIIIIIIII IIII
                        CTACCTTGTCT TCTT
                     GT_____        A  C
GAM383 ATF5          TGGGCACTGATGGCAACAGGAGA  5938 T_  A   _      ATI
                        GGCA CTGATGG AACAGGAGA
                        IIII IIIIIII IIIIIIIII
                        CCGT GACTACC TTGTCCTCT
                        AC  _   G     III
GAM383 CANX          TGACAACA-ATGGAACAGG      5941     T        AGA
                     TGGCAAC GATGGAACAGG
                     IIIIIII IIIIIIIIIII
                     ACTGTTG TTACCTTGTCC
                        _          III
GAM383 CDH11         TGGTTACGTGGTAGGCACAGGAGAAT 5936   CA _ A A_      II
                     TGG AC TG TGG  ACAGGAGAAT
                     III II II III  IIIIIIIIII
                     ACC TG AC ATC  TGTCCTCTTA
                        AA C  C  CG        II
GAM383 ECT2          AACTGATGGCAACTTCAGAAT    5927 __     GAT  CAGGAGAAT
                        TGGCAACT GGAA
                        IIIIIIII IIII
                        ACCGTTGA TCTT
                     CT    AG_  AATAAIIIT
GAM383 EGR3          GGCAACTTACTGACCACAGGAGAA 5930 TG    GA_ A_     TI
                        GCAACT TGG ACAGGAGAA
                        IIIIII III IIIIIIIII
```

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                        CGTTGA  ACT  TGTCCTCTT
                           __   ATG  GG      CI
GAM383 EZH1          GGAAACTGGAGGAACAGGAGTAT  5932 TGGC   AT       AATI
                            AACTG  GGAACAGGAG
                            |||||  ||||||||||
                            TTGAC  CCTTGTCCTC
                        CT__   CT        ATAA
GAM383 FGF1          GGGACCTGATGGAACTGCAGAA   5931 T CAA       AGG   T
                         GG  CTGATGGAAC  AGAA
                         ||  ||||||||||  ||||
                         CC  GACTACCTTG  TCTT
                        _  TG_      ACG   T
GAM383 HFL1          CAACTGATGAAGCTGGAGCAT    5929 TGGCAA     ACA   AAT
                            CTGATGGA  GGAG
                            ||||||||  ||||
                            GACTACTT  CCTC
                        _____      CGA   GTA
GAM383 MPP2          GGGAAAAGA-GGAGCAGGAGAAT  5933 T  C  CT  T  A
                         GG AA  GA GGA CAGGAGAAT
                         || ||  || ||| |||||||||
                         CC TT  CT CCT GTCCTCTTA
                        _  _  TT  _  C
GAM383 MYLK          TGGCAACTGGGCCAGTGGGACAGGA 5937      A_____ A    GAATII
                            TGGCAACTG    TGG ACAGGA
                            |||||||||    ||| ||||||
                            ACCGTTGAC    ACC TGTCCT
                             CCGGTC  C    IIITAA
GAM383 NOLA2         TGGCA-CTGATGG-ACAGAAGA   5943    A    A    A
                            TGGCA CTGATGGA CAGGAGA
                            ||||| |||||||| |||||||
                            ACCGT GACTACCT GTCTTCT
                              _    _    I
GAM383 PPID         TGGGAAGCTGA-GG--CAGGAGAAT 5935   C  _  T AA
                           TGG AA CTGA GG  CAGGAGAAT
                           ||| || |||| ||  |||||||||
                           ACC TT GACT CC  GTCCTCTTA
                           C  C     _  __
GAM383 RAB13        TGACAAGTGACAGAACAGGAG    5942    C         AAT
                           TGGCAA TGATGGAACAGGAG
                           |||||| ||||||||||||||
                           ACTGTT ACTGTCTTGTCCTC
                             C          III
GAM383 RET          TGGTCACTGATGGACACAG      5939  CA     _ GAGAA
                           TGG ACTGATGGA ACAG
                           ||| |||||||| ||||
                           ACC TGACTACCT TGTC
                             AG    G  IIITA
GAM383 SLC24A1      TGACCACTGATGGAGACAACACGAAT 5940  A      _ GA_ II
                           TGGC ACTGATGGA ACAG  GAAT
                           |||| |||||||| |||| ||||
```

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                          ACTG TGACTACCT TGTT  CTTA
                          G        C  GTG  II
GAM383  SMOH              AACTGAAATGGAACAGGAGAA      5926 TGGCAA T         T
                          C GATGGAACAGGAGAA
                          I IIIIIIIIIIIIII
                          C TTACCTTGTCCTCTT
                          _____ T          C
GAM383  ZNF157            TGGGAGACTGA-GG--CAGGAGAAT 5934 T_ CA    T AA
                          GG  ACTGA GG  CAGGAGAAT
                          II  IIIII II  IIIIIIIII
                          CC  TGACT CC  GTCCTCTTA
                          AC  TC    _  __
GAM384  ABCD4             GAGAAGACAGAAAGCTGTAA      5963 TG    C  C  CAAAG
                          AGAAGACA AAA CTG
                          IIIIIIII III III
                          TCTTCTGT TTT GAC
                          __       C  C  ATTAI
GAM384  ALDH3A2           GAAGACCTACTAACCTGCAA      5957 TGAGAA __ A      AG
                          GAC  AC AACCTGCAA
                          III  II IIIIIIIII
                          CTG  TG TTGGACGTT
                          _____ GA  A      GA
GAM384  BSND              GAGAAGACACTGAAATCGCTGCAA  5960 TG     AAAC____    AGAI
                          AGAAGACAC      CTGCAA
                          IIIIIIIII      IIIIII
                          TCTTCTGTG      GACGTT
                          __          ACTTTAGC   GIII
GAM384  CARD10            GAGAAGACACAGACACACATAAGA  5962 TG      A C  _  I
                          AGAAGACACA AC TGCA AAGA
                          IIIIIIIIII II IIII IIII
                          TCTTCTGTGT TG GTGT TTCT
                          __         C  T   A  G
GAM384  CCR9              AAGACACAAAGATGCAAAG       5947 TGAGAAGA    CC_
                          CACAAA  TGCAAAG
                          IIIIII  IIIIIII
                          GTGTTT  ACGTTTC
                          _____   TCT
GAM384  CPNE3             AGGCACAGCAACCTGCAAA       5954 TGAGAAGACACA      G
                          AACCTGCAAA
                          IIIIIIIIII
                          TTGGACGTTT
                          GTCG_____        G
GAM384  DHCR24            AGATGACAACAACCTGCAA       5952 TGAGAA CA      AG
                          GACA AACCTGCAA
                          IIII IIIIIIIII
                          CTGT TTGGACGTT
                          TA____  TG    CA
GAM384  EHF               AAGAATTAATACCTGCAAAGA     5948 TGAGAAGACACAA
                          ACCTGCAAAGA
                          IIIIIIIIIII
```

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                       TGGACGTTTCT
                  TAATTA_____
GAM384  FLOT2         GAGATGAGACACAAACCTG      5959 T  GA         CAAAG
                      GA  AGACACAAACCTG
                      ||  ||||||||||||
                      CT  TCTGTGTTTGGAC
                       T  AC          TIIIA
GAM384  KPNA1         AAGACACAAAGACCAAAGA      5949 TG_     A    CCTGCAAAG
                         AGAAGAC CAAA
                         ||||||| ||||
                         TTTTCTG GTTT
                      GTG     _   CTCTTCIII
GAM384  KRT19         AGAAGACAC---CCTCCAAAG     5953 TGAG    AAA  G
                        AAGACAC  CCT CAAA
                        |||||||  ||| ||||
                        TTCTGTG  GGA GTTT
                      ____     ___  G
GAM384  MTAP         TGTGAAGACACAGAAAGATTCAAAGA 5966 TGA         AACCTG__    II
                         GAAGACACA     CAAAGA
                         |||||||||     ||||||
                         CTTCTGTGT     GTTTCT
                      ACA        CTTTCTAA    II
GAM384  OTP          GAGAAGACAGAAA-CAGAAAAG    5965 TG     C  CTGC  A
                        AGAAGACA AAAC   AAAG
                        |||||||| ||||   ||||
                        TCTTCTGT TTTG   TTTC
                      __      C   TCT_  C
GAM384  PCDH11Y       AGAGAGACACAAACAAGCA      5950 TG  A     CT  AAG
                        AGA GACACAAAC  GCA
                        ||| |||||||||  |||
                        TCT CTGTGTTTG  CGT
                      __  _     TT  CAI
GAM384  PCSK2         GAGAAGACAGAAATCCATGCCAA   5961 TG    C  _ _  AAAGAI
                        AGAAGACA AAA CC TGC
                        |||||||| ||| || |||
                        TCTTCTGT TTT GG ACG
                      __      C  A  T  GTTAII
GAM384  PIK3CG        TGAGAAAAAACCAAACCTGCAAA   5967 T__    A      GAI
                        GAGAAGAC CAAACCTGCAAA
                        |||||||| ||||||||||||
                        CTTTTTTG GTTTGGACGTTT
                      ACT      _         III
GAM384  PLN          GAAGACA---ACCTGCAAA      5958 TGAGAA  CAA
                         GACA  ACCTGCAA
                         ||||  ||||||||
                         CTGT  TGGACGTT
                      _____   ___
GAM384  PNN          GACAAGACACAAA-CT-CAAA     5964 TGAG      CTG
                        AAGACACAAAC  CAAAG
                        ||||||||||| |||||
```

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                        TTCTGTGTTTG  GTTTT
                  TG__          A__
GAM384 RAD23B         AGAAGAAATAAAGACCTGCAAA  5951 T    ACACAA      A
                  GAGAAG    ACCTGCAAAG
                  ||||||    ||||||||||
                  TTCTTT    TGGACGTTTT
                  _     ATTTC_       C
GAM384 SHMT2          TGTGAAGAGTCCAACCTGCAAGGA  5968 TGA    CACA      A  I
                  GAAGA    AACCTGCAA GA
                  |||||    ||||||||| ||
                  CTTCT    TTGGACGTT CT
                  ACA    CAGG      C  I
GAM384 TNFRSF11A        GAACGACACAAACTTAAAAAGA   5956 TGAGAA      C  C
                  GACACAAAC TG AAAGA
                  ||||||||| || |||||
                  CTGTGTTTG AT TTTCT
                  G_____      A  T
GAM384 TRIM14         AGACACAAATCCCTGGAAAGA    5955 TGAGAAGACACAAA   C
                  CCTG AAAGA
                  |||| |||||
                  GGAC TTTCT
                  GTTTAG_____      C
GAM385 EPB41L2        TATCATTTAATACAACTTGA    5974       TTCC    ACC
                  TATCATTTAAT   CTTGA
                  |||||||||||   |||||
                  ATAGTAAATTA   GAACT
                        TGTT     III
GAM385 OGG1          ATTATTTAATTTCTTCCCTT    5971 TATC    ___     GAACC
                  ATTTAATT  TCCCTT
                  ||||||||  ||||||
                  TAAATTAA  AGGGAA
                  AA__    AGA    GIIIT
GAM385 PPP1R2        TATCATTTAATT---CTTG    5973       TCC   AA
                  TATCATTTAATT  CTTG
                  ||||||||||||  ||||
                  ATAGTAAATTAA  GAAC
                        ___    II
GAM385 ZNF175        TATCATTGATATAATTTCCC    5972     ____      TTGAACC
                  TATCATT  TAATTTCCC
                  |||||||  |||||||||
                  ATAGTAA  ATTAAAGGG
                  CTAT      IIITCCA
GAM386 BLK          GCGGCACAGAGAGGCCGCGTAACT  5979 CG   CC      _  I
                  GCAG  GAGGCCGCG AAC
                  ||||  ||||||||| |||
                  TGTC  CTCCGGCGC TTG
                  CG  T_    A  I
GAM386 BLK          GCGGCACAGAGAGGCCGCGTAACT  5979 T   G  CC      _  I
                  GGCG CAG  GAGGCCGCG AACT
                  |||| |||  ||||||||| ||||
```

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                              CCGT GTC  CTCCGGCGC TTGA
                              _  _ T_      A  G
GAM386 DLX2          TGGCGGCAG-CG-GGCCGGGA    5983      C A    C AC
                              TGGCGGCAGC G GGCCG GA
                              ||||||||| | ||||| ||
                              ACCGCCGTCG C CCGGC CT
                                        C II
GAM386 DLX2          TGGCGGCAG-CG-GGCCGGGA    5983      C A    CI
                              TGGCGGCAGC G GGCCG
                              ||||||||| | |||||
                              ACCGCCGTCG C CCGGC
                                       __      CC
GAM386 MMP25           TGGCGGCAGCCG-GG-AGGGAAC   5984       A CCGC   T
                              TGGCGGCAGCCG GG   GAAC
                              ||||||||||| ||   ||||
                              ACCGCCGTCGGC CC   CTTG
                                       _ TCC_   I
GAM386 MMP25           TGGCGGCAGCCG-GG-AGGGAAC   5984       __ CC GAI
                              TGGCGGCAGCC GAGG GC
                              |||||||||| |||| ||
                              ACCGCCGTCGG CTCC TG
                                       CC   CT III
GAM386 MUC4            GCCGAGGCCCCAGCGACCT    5978       ___  ACIII
                              GCCGAGGCC  GCGA
                              |||||||| ||||
                              CGGCTCCGG  CGCT
                                        GGT   GGAII
GAM386 NDRG1          GGCGGCAGCTGGGCAGGCCGC    5980      CG___    III
                              GGCGGCAGC   AGGCCG
                              |||||||| ||||||
                              CCGCCGTCG   TCCGGC
                                        ACCCG    GII
GAM386 NDRG1          GGCGGCAGCTGGGCAGGCCGC    5980 TG    CG___     GAAC
                              GCGGCAGC   AGGCCGC
                              |||||||| |||||||
                              CGCCGTCG   TCCGGCG
                              __       ACCCG      IIIT
GAM386 P23          GGCGGCAGCGGCGGGCTCGACCT   5981     __ A  CG ACI
                              GCGGCAGC CG GGC CGA
                              |||||||| || ||| |||
                              CGCCGTCG GC CCG GCT
                                        CC _ A_ GGI
GAM386 P23          GGCGGCAGCGGCGGGCTCGACCT   5981 TG    __ A CG A I
                              GCGGCAGC CG GGC CGA CT
                              |||||||| || ||| ||| ||
                              CGCCGTCG GC CCG GCT GA
                              __       CC _ A_  G G
GAM386 POLS          TGCCGGTGGCCGAGGCCGCG    5982  G CA        AAC
                              TG CGG  GCCGAGGCCGCG
                              || ||| ||||||||||
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                        AC GCC  CGGCTCCGGCGC
                         G  AC           III
GAM386 POLS            TGCCGGTGGCCGAGGCCGCG    5982 G  CA        I
                        G CGG  GCCGAGGCCGC
                        I III  IIIIIIIIIII
                        C GCC  CGGCTCCGGCG
                         G  AC           I
GAM386 STIP1          GCAGCCGAGACAGC-AACT     5977        C   ACI
                      GCAGCCGAGGC GCGA
                      IIIIIIIIIII IIII
                      CGTCGGCTCTG CGTT
                          T  GAI
GAM386 STIP1          GCAGCCGAGACAGC-AACT      5977 T__     CG  CCGCGAA
                        GGCGGCAGC AGG
                        IIIIIIIIII III
                        CTGTCGTTG TCC
                        GCT      A_  CCIIITC
GAM387 AGXT           GAGGCTGCCTGGTTCTGCCTCCCG 5997 TGAGAGG   GG       I
                        CTGGT TTGCCTCCCG
                        IIIII IIIIIIIIII
                        GACCA GACGGAGGGC
                        CGACG__   A_      C
GAM387 ASPH          TGAG-GGCTGGTGG--ACCTCC   6004  A      TT   C
                      TGAG GGCTGGTGG GCCTCC
                      IIII IIIIIIIII IIIIII
                      ACTC CCGACCACC TGGAGG
                       _     __         I
GAM387 ATF7          GAGCGGCTGGTAGCTCCGTTGCCTCCCG5994 TG  A        _____        III
                      AG GGCTGGTGGT   TGCCTCCCG
                      II IIIIIIIIII   IIIIIIIII
                      TC CCGACCATCG   ACGGAGGGC
                      __ G     AGGCA       GII
GAM387 ATP6V0A4       AGCCTGGCCTTTGCCTCCC     5991 TGAGAGGC   GG
                        TGGT TTGCCTCCC
                        IIII IIIIIIIII
                        ACCG AACGGAGGG
                        _____    GA
GAM387 CASP3          GAGGCCTGGAGCCTGCCTCCCG   5996 TGAGA G   T  _
                        G CTGG GGT TGCCTCCCG
                        I IIII III IIIIIIIII
                        C GACC TCG ACGGAGGGC
                        _____ G  _ G
GAM387 CLK2          AGAG-CTGGTGGTGTTCCTC     5988 TGAGA     TG_  CC
                        GGCTGGTGGT  CCTC
                        IIIIIIIIII  IIII
                        TCGACCACCA  GGAG
                        _____     CAA  AC
GAM387 COL1A1         TGAGGGGCTGGTGGCT-CC-CCCG 6006   A       G T
                        TGAG GGCTGGTGGTT CC CCCG
                        IIII IIIIIIIIIII II IIII
```

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                          ACTC CCGACCACCGA GG GGGC
                              C          _  _
GAM387 FHL2          GGCTGGTGGCTGCGGCTCC     6001 TGAGA    G    G TCCC
                          GGCTG TGGTT CC
                          ||||| ||||| ||
                          CCGAC GCCGA GG
                          CA___     _    _ CGAC
GAM387 KCNJ6        GAGAGGCTGTTAGGAGACTCC    5995 TG     GT_ TTGC   CG
                          AGAGGCTG GG   CTCC
                          |||||||| ||   ||||
                          TCTCCGAC CC  GAGG
                          __      AAT  TCT_   TI
GAM387 LFG          AGACTCGTGTGTGCCTCCCG     5992 TGAGAGGCTG  GT
                              GTG TGCCTCCC
                              ||| ||||||||
                              CAC ACGGAGGG
                          AG_____   AC
GAM387 MEN1        AGAGGCTGGCAGTGGCTTCC     5989 TGAG    TG T C  C
                          AGGCTGG GT GC TCC
                          ||||||| || || |||
                          TCCGACC CA CG AGG
                          ____      GT  C  A  T
GAM387 MYO1C        GAGGCCCTTGGTTGCCTTCCG    5998 TGAGAG  GG      C
                              GCT TGGTTGCCT CCG
                              ||| ||||||||| |||
                              CGG  ACCAACGGA GGC
                          _____    GA       A
GAM387 PROK1       AGGTTGGTGTGTAGTTGCCTCCC  5990 TGAGA C _        GI
                          GG TG GTGGTTGCCTCCC
                          || || |||||||||||||
                          CC AC CATCAACGGAGGG
                          A____  _ A         AC
GAM387 RNH         TGAGAGGCTCCTGGTGCCCT      6003       GG  T  CCC
                          TGAGAGGCT TGGT GCCT
                          ||||||||| |||| ||||
                          ACTCTCCGA ACCA CGGG
                              GG _  All
GAM387 SET7        GGCTGCGCGGCTGCCTCCCG     6000 TGAGAGGCTG
                              GTGGTTGCCTCCC
                              |||||||||||||
                              CGCCGACGGAGGG
                          G_____
GAM387 SLC13A4      AGAGGCTGGGCTCCTGGCCTCC    5987 TGAG     _ GG _   CG
                          AGGCTGG T TTG CCTCC
                          ||||||| | ||| |||||
                          TCCGACC G DAC GGAGG
                          ____      C AG  C   AC
GAM387 SLC7A1       GAGGGTGG-GGT-GCCTCCCG     5999 TGAGA C  T  T
                          GG TGG GGT GCCTCCC
                          || ||| ||| |||||||
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                          CC ACC CCA CGGAGGG
                          ____  _   _   _
GAM387 SNL            TGAAAGGCAAGGGGGCTTGCCTCCCG 6002      T_ T  _      II
                          TGAGAGGC  GG GGTT GCCTCCCG
                          IIIIIIII  II IIII IIIIIIII
                          ACTTTCCG  CC CCGA CGGAGGGC
                              TT C    A     II
GAM387 SUFU          GAGAGGCTGGTCATGGTGGC      5993 TG       ___  T CTCCC
                          AGAGGCTGGT  GGT GC
                          IIIIIIIIII  III II
                          TCTCCGACCA  CCA CG
                          __        GTA  C TIIIG
GAM387 XK          TGGGAGGCTGGTGGCT-ACTCCC  6005 A          C  G
                          TG GAGGCTGGTGGTTGC TCCC
                          II IIIIIIIIIIIIII IIII
                          AC CTCCGACCACCGATG AGGG
                          C          _  I
GAM388 BBS4         GGGACTAATAAACCTCACAACCTG  6014      __  ___     IIIC
                          GGGACT TAAAC ACAACCT
                          IIIIII IIIII IIIIIII
                          CCCTGA ATTTG TGTTGGA
                          TT   GAG     CIII
GAM388 BBS4         GGGACTAATAAACCTCACAACCTG  6014 TGCG__   AAA      AI
                          GGACTT CACAACCTGG
                          IIIIII IIIIIIIIII
                          TTTGGA GTGTTGGACT
                          TGATTA  ___       CC
GAM388 CDH5         TGCAGCAGTTAAACACAGTCTG   6018    GAC     AC GA
                          TGCGG TTAAACACA CTG
                          IIIII IIIIIIIIII III
                          ACGTC AATTGTGT GAC
                          GTC       CA II
GAM388 CDH5         TGCAGCAGTTAAACACAGTCTG    6018_  GAC     ACI
                          GCGG TTAAACACA
                          IIII IIIIIIIII
                          CGTC AATTGTGT
                          T  ___     CAG
GAM388 EXTL2        GCTGGA-TTAA---CAACCTGGA   6012 CG_ C  AAC
                          GGA TTA ACAACCTGG
                          III III IIIIIIIII
                          CCT AAT TGTTGGACC
                          CGA  _  ___
GAM388 EXTL2        GCTGGA-TTAA---CAACCTGGA   6012 TGCG C  AAC
                          GGA TTA ACAACCTGG
                          III III IIIIIIIII
                          CCT AAT TGTTGGACC
                          GA__  _  ___
GAM388 GJA1        GGGACTTAAGGACAATCCT       6016      AC  _ II
                          GGGACTTAA ACAA CC
                          IIIIIIIII IIII II
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                         CCCTGAATT TGTT GG
                           CC   A  AI
GAM388 GJA1            GGGACTTAAGGACAATCCT      6016 TGCGGG    AC   _  GG
                         ACTTAA  ACAA CCT
                         |||||| |||| |||
                         TGAATT  TGTT GGA
                         _____     CC   A  GA
GAM388 HYAL1           CGGGACTGGTCGAGGACAACCTGG  6009 ___   GACTTAAAC    I
                          GG        ACAACCTG
                          ||        ||||||||
                          CC        TGTTGGAC
                         TGA  AGCTCC___      I
GAM388 HYAL1           CGGGACTGGTCGAGGACAACCTGG  6009 TGCG   TAAAC___      AI
                          GGACT      ACAACCTGG
                          |||||      |||||||||
                          CCTGA      TGTTGGACC
                         ____    CCAGCTCC     GG
GAM388 MAP3K12          GGGACTTAAACAGCACCCCGG   6015 G       _  A  I
                         GACTTAAACA CA CCTG
                         |||||||||| || ||||
                         CTGAATTTGT GT GGGC
                         _     C  G  I
GAM388 MAP3K12          GGGACTTAAACAGCACCCCGG   6015 TGCGGG    _  A  A
                          ACTTAAACA CA CCTGG
                          ||||||||| || |||||
                          TGAATTTGT GT GGGCC
                         _____     C  G  A
GAM388 NONO            GGAGTTCAAGATCAACCTGGA    6013 GACTTAAACA      I
                            CAACCTGG
                            ||||||||
                            GTTGGACC
                         TCAAGTTCTA      I
GAM388 NONO            GGAGTTCAAGATCAACCTGGA    6013 TG   CTTAAACA
                          CGGGA    CAACCTGGA
                          |||||    |||||||||
                          GTTCT    GTTGGACCT
                         AA   A_____
GAM388 PTHLH           CGGGACTTATTTAGCAACC      6010       AACA_  II
                         CGGGACTTA   CAAC
                         |||||||||   ||||
                         GCCCTGAAT   GTTG
                         AAATC  GI
GAM388 PTHLH           CGGGACTTATTTAGCAACC      6010 TGCG    AACA_  T
                          GGACTTA   CAACC GG
                          |||||||   ||||| ||
                          CCTGAAT   GTTGG CC
                         ____     AAATC   _
GAM388 RRM2            GAATTAACTCACACAACCT      6011 _____   AA     III
                         GACTT ACACAACC
                         ||||| |||||||||
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                              TTGAG TGTGTTGG
                       CTTAA        AII
GAM388 RRM2            GAATTAACTCACACAACCT      6011 TGCGG   AA      G
                          GACTT ACACAACCTG
                          ||||| |||||||||||
                          TTGAG TGTGTTGGAT
                          _____   __        G
GAM388 SCA2           TGCGGGACTCTGAAACAGCATATGGA 6017        __  _ ACC  II
                         TGCGGGACTT AAACA CA  TGGA
                         |||||||||| ||||| || ||||
                         ACGCCCTGAG TTTGT GT ACCT
                              AC   C AT_  II
GAM388 SCA2           TGCGGGACTCTGAAACAGCATATGGA 6017 GC     __  _ ACC  I
                          GGGACTT AAACA CA  TGG
                          ||||||| ||||| || |||
                          CCCTGAG TTTGT GT  ACC
                          __     AC   C AT_  I
GAM389 ANXA8          TGGTCAGCCACCAGGGGAGCCCACGCCT6029 _ _      ___  A GIII
                          TGG CAGC ACCAGGGGA  CAC CCT
                          ||| |||| ||||||||| ||| |||
                          ACC GTCG TGGTCCCCT  GTG GGA
                           A  G       CGG  C  IIIG
GAM389 ARF3          GGCAGCACCAAGGCAACCTCCT   6027 TG       _ ACA
                          GCAGCACCAGGG GAC  CCTG
                          |||||||||||| ||| ||||
                          CGTCGTGGTTCC TTG  GGAT
                          __        G  GA_
GAM389 BCAT2         GGCAGCACCAGGGGTCTGGCCTG  6028 TG       ACACA  I
                          GCAGCACCAGGGG   CCTG
                          |||||||||||||   ||||
                          CGTCGTGGTCCCC   GGAC
                          __          AGACC  T
GAM389 COL16A1       GCAGCACCAGAGGAACCCAC     6022 TGGC      CA_  CT
                         AGCACCAGGGGA  CAC
                         ||||||||||||  |||
                         TCGTGGTCTCCT  GTG
                         ____         TGG  AC
GAM389 DOCK1         GCAG-ACTCAGGGGACACA     6021 TGGC C _      CC
                         AG AC CAGGGGACACA
                         || || |||||||||||
                         TC TG GTCCCCTGTGT
                         ____  _ A      CT
GAM389 JAG1          GGCTGCA--AGGGGACACAC    6026 TG A CC      C
                         GC GCA AGGGGACACAC
                         || ||| ||||||||||
                         CG CGT TCCCCTGTGTG
                         __  A __        T
GAM389 LIF           GGCAGCAT--GGGGACACA     6025 TG   CCA    CC
                         GCAGCA GGGGACACA
                         |||||| ||||||||||
```

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                              CGTCGT   CCCCTGTGT
                              __       A__       CI
GAM389 PRKCM         TGACAACACCAATGGGACACACC  6031           _       TGI
                         TGGCAGCACCAG GGGACACACC
                         IIIIIIIIIII IIIIIIIII
                         ACTGTTGTGGTT CCCTGTGTGG
                              A       III
GAM389 SCD           TGACAGCATCTG-GGACACAC  6032       CCAG      CT
                         TGGCAGCA  GGGACACAC
                         IIIIIIII  IIIIIIIII
                         ACTGTCGT  CCCTGTGTG
                              AGA_      II
GAM389 TNFRSF8          GGCAGCACCAGGAGGGTCCCAC  6023 TG        ACA__ CTG
                         GCAGCACCAGGGG   CAC
                         IIIIIIIIIII    III
                         CGTCGTGGTCCTC   GTG
                         __            CCAGG  TII
GAM389 TRPV4           GGCAGAGCCAGGGGACCACA     6024 TG  CA      A CT
                         GCAG  CCAGGGGAC CAC
                         IIII  IIIIIIIII III
                         CGTC  GGTCCCCTG GTG
                         __    TC     _  TC
GAM389 WHSC1          TGGCAGAACTCGCCCGCGGGACACACCTG6030     CA_____ AG          III
                         TGGCAG    CC GGGACACACCTG  C
                         IIIIII    II IIIIIIIIIII  I
                         ACCGTC    GG CCCTGTGTGGAC  G
                         TTGAGCG  CG          III
GAM390 APOBEC2          GAGGGGCTGTGGCTCAGGAGTC  6040 TGAGAG   __  A  C  C
                         GGGCT GGTT AGG GTC
                         IIIII IIII III III
                         CCCGA CCGA TCC CAG
                         _____    CA  G  T  T
GAM390 HR            AGGGGCTGG-AGAGGCGCCC      6037 TGAGAGGG    TTA
                         GCTGG  AGGCGTC
                         IIIII  IIIIIII
                         CGACC  TCCGCGG
                         _____     TC_
GAM390 KCNK7         TGGGAGGGGCTGGGCAGGGCG  6043 A       T  A  TCC
                         TG GAGGGGCTGG TA GGCG
                         II IIIIIIIIII II IIII
                         AC CTCCCCGACC GT CCGC
                         C       C  C  III
GAM390 MYLK         AGTGGGACAGGA-AAGGCGTCC   6036 TGAGA    T  TT
                         GGGGC GG AAGGCGTCC
                         IIIII II IIIIIIIII
                         CCCTG CC TTCCGCAGG
                         A____     T T_
GAM390 PLA2G10        GGGGCGGCGCAAAGGCGTCC    6041 TGAGAGG  TG T
                         GGC  GT AAGGCGTC
                         III  II IIIIIIII
```

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                          CCG  CG TTCCGCAG
                          _____  __ T
GAM390 PTPRN         AGAGGGGCTG----AGGCG      6035 TGAG       GTTA
                          AGGGGCTG   AGGCG
                          ||||||||   |||||
                          TCCCCGAC   TCCGC


                          ____      ____
GAM390 REV3L         TGACAGGGGCCTGGGTGAGG      6042  G    _  TTA  CGTC
                          TGA AGGGGC TGG  AGG
                          ||| |||||| |||  |||
                          ACT TCCCCG ACC  TCC
                           G    G  CAC  |||C
GAM390 SLC9A1        GAGAGGGGCAGGGGTCCAGGCG     6038 TG      T__  A    CC
                          AGAGGGGC  GGTT AGGCGT
                          ||||||||  |||| ||||||
                          TCTCCCCG  CCAG TCCGCG
                           __      TCC  G   ||
GAM390 TAF6         GAGGCGGCAGG--AAGGCGTCC      6039 TGAGA G  T  TT
                          G GGC GG  AAGGCGTC
                          | ||| ||  |||||||||
                          C CCG CC  TTCCGCAG
                          _____ G  T __
GAM391 CEP2         GGTGCACAGCGAGTGCAAAAA       6050 TGGG     TC___     GTG
                          TGCACAGT    CAAAAAT
                          ||||||||    |||||||
                          ACGTGTCG    GTTTTTG
                          ____      CTCAC    G||
GAM391 CEP2         GGTGCACAGCGAGTGCAAAAA       6050         TCCAAAA|||
                          GGTGCACAGT
                          ||||||||||
                          CCACGTGTCG
                             CTCACGTTTT
GAM391 CHC1L        TGGGATTGGAAAGTTCCAAA        6061     TGCAC__      AATGT
                          TGGG    AGTTCCAAA
                          ||||    |||||||||
                          ACCC    TCAAGGTTT
                           TAACCTT     |||GT
GAM391 CHC1L        TGGGATTGGAAAGTTCCAAA        6061     TGCAC__      |||
                          TGGG    AGTTCCAA
                          ||||    ||||||||
                          ACCC    TCAAGGTT
                           TAACCTT     T||
GAM391 CYP1B1       GGTACAAAGATTCCAAAAA         6051     C  _      ||
                          GGTGCA AG TTCCAAAA
                          |||||| || |||||||||
                          CCATGT TC AAGGTTTT
                            T  T     T|
GAM391 CYP1B1       GGTACAAAGATTCCAAAAA         6051 TGGG  C  _      T
                          TGCA AG TTCCAAAAA GT
                          |||| || ||||||||| ||
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                              ATGT TC AAGGTTTTT CG
                              ___     T T          _
GAM391  ETV5          TGCACACTTC-AAAAATGT      6058     G   C      I
                          TGCACA TTC AAAAATG
                          IIIIII III IIIIIII
                          ACGTGT AAG TTTTTAC
                               G  _     A
GAM391  FGFR2         GTGCACTCTGACAAAAATGT      6054    AGTTC        I
                          TGCAC    CAAAAATG
                          IIIII    IIIIIIIII
                          ACGTG    GTTTTTAC
                           AGACT      I
GAM391  FUT9          TGGACAACTACAAAAATGTG      6060 GC  GT C        I
                           ACA  T CAAAAATGT
                           III  I IIIIIIIII
                           TGT  A GTTTTTACA
                           CC  TG T       I
GAM391  GABRP          TGGGTGCACACTTGGCCTAAAAT  6063       G __  A   GTGI
                          TGGGTGCACA TT CC AAAAT
                          IIIIIIIIII II II IIIII
                          ACCCACGTGT AA GG TTTTA
                               G CC A    IIIG
GAM391  GABRP          TGGGTGCACACTTGGCCTAAAAT  6063 GG     G __  A  I
                           GTGCACA TT CC AAAA
                           IIIIIII II II IIII
                           CACGTGT AA GG TTTT
                           __     G CC A  I
GAM391  HDGF          ACATTTCCTAAAAAATGTG      6047  G  __       III
                           ACA TTCC AAAAATGT
                           III IIII IIIIIIII
                           TGT AAGG TTTTTACA
                            A  AT    CII
GAM391  IL13RA1       TGGTTGAAGACTACCAAAAATGT   6065 G  GCAC TT__     I
                           GGT  AG  CCAAAAATG
                           III  II  IIIIIIIII
                           CCA  TC  GGTTTTTAC
                           _  ACT_ TGAT      I
GAM391  IL13RA1       TGGTTGAAGACTACCAAAAATGT   6065 TG  GCAC TT__     GI
                           GGT  AG  CCAAAAATGT
                           III  II  IIIIIIIIII
                           CCA  TC  GGTTTTTACA
                           A_ ACT_ TGAT      II
GAM391  LCP1          GCATGGTTCCAAAAGTGTG       6049  CA    A II
                           GCA GTTCCAAAA TGT
                           III IIIIIIIII III
                           CGT CAAGGTTTT ACA
                            AC      C CI
GAM391  MYO6          TGGAAATTTCCAAAAATGT       6059 TGCACAG        II
                            TTCCAAAAATG
                            IIIIIIIIII
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                              AAGGTTTTTAC
                        ACCTTTA          AI
GAM391 NDN            GTACACTTTTCCAAAAATG      6053      AG        II
                        GTGCAC TTCCAAAAAT
                        |||||| ||||||||||
                        CATGTG AAGGTTTTTA
                          AA        CI
GAM391 NDN            GTACACTTTTCCAAAAATG      6053 TGGGTG  AG        T
                          CAC TTCCAAAAATG
                          ||| ||||||||||
                          GTG AAGGTTTTAC
                        _____    AA        T
GAM391 NR1I2         GCACAGTTCTCGAGAATGTG        6048        CAAA_   II
                        GCACAGTTC  AATGT
                        |||||||||  |||||
                        CGTGTCAAG  TTACA
                          AGCTC    CI
GAM391 REV3L        TGCACAGTTCCTCACAATG       6055        AAAAATII
                        TGCACAGTTCC
                        |||||||||||
                        ACGTGTCAAGG
                          AGTGTTAC
GAM391 REV3L        TGCACAGTTCCTCACAATG       6055 TGGGTGCA     AAA_
                          CAGTTCC  AATGT
                          |||||||  |||||
                          GTCAAGG  TTACG
                        _____       AGTG
GAM391 REV3L        TGCACAGTTTGATCAAAAT       6056      C___  AIII
                        TGCACAGTT  CAAAA
                        |||||||||  |||||
                        ACGTGTCAA  GTTTT
                          ACTA    AIII
GAM391 SCN1A         ACAGATTCCATAAAAATGTG      6046    _  __      III
                        ACAG TTCCA AAAATGT
                        |||| ||||| |||||||
                        TGTC AAGGT TTTTACA
                          T   AT    CII
GAM391 SLC9A1        TGGGAGCACAGTTCGAAAA      6064   T    C  ATGT
                        TGGG GCACAGTTC AAAA
                        |||| ||||||||| ||||
                        ACCC CGTGTCAAG TTTT
                          T    C   IIIG
GAM391 SLC9A1        TGGGAGCACAGTTCGAAAA      6064   T      CAAAII
                        TGGG GCACAGTTC
                        |||| |||||||||
                        ACCC CGTGTCAAG
                          T      CTTTTI
GAM391 TFCP2         TGGCTGCCCCAGGTTCCAAAA      6062  G  A_  _     ATGTG
                        TGG TGC CAG TTCCAAAA
                        ||| ||| ||| ||||||||
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                    ACC ACG  GTC AAGGTTTT
                     G  GG   C       IIIGT
GAM391 TFCP2        TGGCTGCCCCAGGTTCCAAAA    6062  G  A_  _      III
                    TGG TGC  CAG TTCCAAA
                    III III  III IIIIIII
                    ACC ACG  GTC AAGGTTT
                     G  GG   C       TII
GAM391 TJP1         GGTGCA---TTTAAAAAATGTG  6052      CAGTTCC   I
                    GGTGCA    AAAAATG
                    IIIIII    IIIIIII
                    CCACGT    TTTTTAC
                     AAAT___        A
GAM391 TRAP240      TGCACAGTTCCATCAAATG      6057          AAAATII
                    TGCACAGTTCCA
                    IIIIIIIIIIII
                    ACGTGTCAAGGT
                     AGTTTAC
GAM391 TRAP240      TGCACAGTTCCATCAAATG      6057 TGGGTGCA     A_   T
                    CAGTTCCA AAATG
                    IIIIIIII IIIII
                    GTCAAGGT TTTAC
                    _____     AG   T
GAM392 ATP1A2       GAACAGCCCTGCCACCTAA      6071 TGAAA  G      AGG
                    GGCCC GCCACCTAA
                    IIIII IIIIIIIII
                    TCGGG CGGTGGATT
                    TTG__   A     CII
GAM392 CORO2B       GAAAGGCCCAGCTCACCTGGAGG  6070 TG       _  AA  CI
                    AAAGGCCCGGC CACCT AGG
                    IIIIIIIIIII IIIII III
                    TTTCCGGGTCG GTGGA TCC
                    __      A   CC  CI
GAM392 IL16         AAGGAGAGGCCACCTATAAGC    6069 TGAAAGGCCC      A
                    GGCCACCTA AGGC
                    IIIIIIIII IIII
                    CCGGTGGAT TTCG
                    CTCT_____      A
GAM392 PML          AAGACCAGGGCCACCTAGAG     6068 TGAAAG  C_    A _
                    GCC GGCCACCTA AG G
                    III IIIIIIIIII II I
                    TGG CCGGTGGAT TC C
                    _____  TC     C T
GAM393 ACCN2        TGGGGGTGAACTTATAGGTATCAG 6085  A  __  C_     CTTI
                    TGGG GTG CTT AGGTATCAG
                    IIII III III IIIIIIIII
                    ACCC CAC GAA TCCATAGTC
                     C  TT  TA      IIIT
GAM393 ACCN2        TGGGGGTGAACTTATAGGTATCAG 6085 GAGT  C_    I
                    GG   GCTT AGGTATCA
                    II   IIII IIIIIIII
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                              CC   TGAA  TCCATAGT
                           ACT_   TA      I
GAM393 ADD1             GAGTGCTTCTGAAGGTTCATCAG  6076        ___   A  IIIC
                           GAGTGCTTC  AGGT TCA
                           ||||||||  |||| |||
                           CTCACGAAG  TCCA AGT
                             ACT   _  AGTC
GAM393 ARSB            GGAGTGTTGCAGATTTTATCAGCTT 6077 GAG  TTCAGG       I
                             TGC    TATCAGCT
                             |||    ||||||||
                             ACG    ATAGTCGA
                           ACA  TCTAAA      I
GAM393 ARSB            GGAGTGTTGCAGATTTTATCAGCTT 6077 TGGG   CTT   ___       II
                           AGTG  CAGGT  ATCAGCTT
                           ||||  |||||  ||||||||
                           TCAC  GTCTA  TAGTCGAA
                           ____  AAC   AAA     GA
GAM393 CARD10           GGGAGAAGGTGCAGGTATCAG   6079 __ _  TTC     I
                           GGAG TGC  AGGTATCA
                           |||| |||  |||||||||
                           CTTC ACG  TCCATAGT
                           CT  C ___      I
GAM393 CARD10           GGGAGAAGGTGCAGGTATCAG   6079 T __  TTC     CTT
                           GGGA GTGC  AGGTATCAG
                           |||| ||||  |||||||||
                           CTCT CACG  TCCATAGTC
                           C  TC ___       TII
GAM393 CDK10          TGGGAACTTGTGCTTCAGGT    6084   ____         ATCAGCT
                           TGGGA  GTGCTTCAGGT
                           |||||  |||||||||||
                           ACCCT  CACGAAGTCCA
                             TGAA      IIITTCG
GAM393 CDK10          TGGGAACTTGTGCTTCAGGT    6084   ____         IIIA
                           TGGGA  GTGCTTCAGG
                           |||||  ||||||||||
                           ACCCT  CACGAAGTCC
                             TGAA      AIII
GAM393 CPD           AGTGCTTCACAGATATAAGC     6074       __   C III
                           AGTGCTTCA GGTAT AG
                           ||||||||| ||||| ||
                           TCACGAAGT CTATA TC
                             GT   T GII
GAM393 CPD           AGTGCTTCACAGATATAAGC     6074 TGGGAGTGCTT     ___   T
                             CAGGTAT  CAGC
                             ||||||| ||||
                             GTCTATA GTCG
                           GAAGT_____      TTC  T
GAM393 DDX11          TGCTTCAGGTACATCAGGTT    6083       __   CTIII
                           TGCTTCAGGTA TCAG
                           ||||||||||| ||||
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                        ACGAAGTCCAT AGTC
                         GT   CAAII
GAM393 DDX11         TGCTTCAGGTACATCAGGTT      6083 TG  A   T    A A__ T
                        GG GTGC TCAGGT TC  GC
                        II IIII IIIIII II  II
                        TC CATG AGTCCA AG  CG
                         __ _   T    _ AAC I
GAM393 FOLR1         GGGATTTC--CAGGTATCAG      6080  GTGC        I
                        GGGA  TTCAGGTATC
                        IIII  IIIIIIIIII
                        CCCT  AGGTCCATAG
                         AA__      T
GAM393 FOLR1         GGGATTTC--CAGGTATCAG      6080 TG  GTGC         C
                         GGA  TTCAGGTATCAG
                         III  IIIIIIIIIIII
                         CCT  AGGTCCATAGTC
                         __ AA__        T
GAM393 PCDHA11      TGGGAGTGCCTCACTGT-TCAG     6087          G_ A  CTT
                        TGGGAGTGCTTCA GT TCAG
                        IIIIIIIIIIIII II IIII
                        ACCCTCACGGAGT CA AGTC
                          GA _   III
GAM393 PCDHA11      TGGGAGTGCCTCACTGT-TCAG     6087          G_ A  I
                        GGGAGTGCTTCA GT TCA
                        IIIIIIIIIII II III
                        CCCTCACGGAGT CA AGT
                          GA _  I
GAM393 PLD2        TGGGAGTGCCCTTTTCAGCTAT      6086         CAGGTA    T
                        TGGGAGTGCTT   TCAGCT
                        IIIIIIIIIII   IIIIII
                        ACCCTCACGGG   AGTCGA
                          AAA___    T
GAM393 PLD2        TGGGAGTGCCCTTTTCAGCTAT      6086        ____  G IIIA
                        TGGGAGTGCT   TCAG TA
                        IIIIIIIIII   IIII II
                        ACCCTCACGG   AGTC AT
                          GAAA   G AIII
GAM393 PPOX        AGTGCTTCA--AATCCGCT        6075         ATCA I
                        AGTGCTTCAGGT  GC
                        IIIIIIIIIIII  II
                        TCACGAAGTTTA  CG
                          GG__  A
GAM393 TCTA        GTCCTTCAGGTAATCAGCTT       6082 G       _  II
                        GT CTTCAGGTA TCAGCT
                        II IIIIIIIII IIIII
                        CA GAAGTCCAT AGTCGA
                         G    T   AI
GAM393 TH1L        TGGGAGTGC-TCA-GTCTCA       6088       T GTA  GC
                        TGGGAGTGCT CAG  TCA
                        IIIIIIIIII III  III
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                        ACCCTCACGA GTC  AGT
                         _    AG_  II
GAM393 TH1L        TGGGAGTGC-TCA-GTCTCA    6088        T GTATI
                        TGGGAGTGCT CAG
                        IIIIIIIIII III
                        ACCCTCACGA GTC
                         _     AGAGT
GAM393 UBE2V1         GTGACTTCAGGTAAGACGCTT    6081 _        TCA_  III
                        GTG CTTCAGGTA   GCT
                        III IIIIIIIII   III
                        CAC GAAGTCCAT   CGA
                         T      TCTG  AII
GAM393 ULBP2         GGAGC-CTTTTGGTATCAGCTT    6078 _  G  CA        I
                         GAGT CTT GGTATCAGCT
                        IIII III IIIIIIIIII
                        CTCG GAA  CCATAGTCGA
                        C  _  AA       I
GAM393 ULBP2         GGAGC-CTTTTGGTATCAGCTT    6078 TGGGAGT   CA_
                         GCTT GGTATCAGCTT
                         IIII IIIIIIIIIII
                         CGGA  CCATAGTCGAA
                        T_____  AAA
GAM394 FETUB        CAACATGCTGAGA-CCAAG    6095        GA   II
                        CAACATGCTG GCCAA
                        IIIIIIIIII IIIII
                        GTTGTACGAC TGGTT
                          TC   CI
GAM394 GUK1          ACATGCTG--GCCAAGGGC    6094       GA    TGI
                        ACATGCTG GCCAAG
                        IIIIIIII IIIIII
                        TGTACGAC CGGTTC
                           __    CCG
GAM394 HFE          ACCACATTTATGCAGCCAAGTGC  6091 CA   GC_ G      I
                        ACAT TG AGCCAAGTG
                        IIII II IIIIIIIII
                        TGTA AC TCGGTTCAC
                        G_   AAT G      I
GAM394 HOXA3         CATGCTGGAGCCAGAGGGC    6097          AGTGII
                        CATGCTGGAGCCA
                        IIIIIIIIIIIII
                        GTACGACCTCGGT
                         CTCCCG
GAM394 KEL          ACAAGCGGAAGCCAAGTGC    6093  T T      II
                        ACA GC GGAGCCAAGTG
                        III II IIIIIIIIII
                        TGT CG CTTCGGTTCAC
                         T  C     GI
GAM394 KRT3         GACAATCACAGGCTGGAGCC   6098 _  __       III
                        GACAA CAT GCTGGAGC
                        IIIII III IIIIIII
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                        CTGTT GTG  CGACCTCG
                          A  TC       GII
GAM394 LBR             GACTACCGGATGCTGGAGCAAA  6099  A ___        CAIII
                       GAC AC  ATGCTGGAGC
                       III II  IIIIIIIIII
                       CTG TG  TACGACCTCG
                         A GCC       TTTII
GAM394 PPP1R7          GACCACATGA-GGAGCCAAG  6101 _ A   CT     I
                        AC ACATG GGAGCCAA
                        II IIIII IIIIIIII
                        TG TGTAC CCTCGGTT
                         C G   T_      I
GAM394 SIRT3          CAACATGCT--AG--AAGTGC   6096          CCAAGI
                      CAACATGCTGGAG
                      IIIIIIIIIIII
                      GTTGTACGATCTT
                         CACGII
GAM394 SNX6          GACAACATGCGGCTGAG-GAAGTG  6100 A     TG__  CC  I
                       CAACATGC  GAG AAGT
                       IIIIIIII  III IIII
                       GTTGTACG  CTC TTCA
                       _      CCGA  C_  I
GAM394 UBE2I         ACAGCCAGCTGAGGCCAAGTGC   6092 CAA_ T  GA     I
                        CA GCTG GCCAAGTG
                        II IIII IIIIIIII
                        GT CGAC CGGTTCAC
                      GTCG _   TC     I
GAM394 XPC           TGACAAGG-GCTGGAGCCA   6102     CAT     I
                      TGACAA GCTGGAGCC
                      IIIIII IIIIIIIII
                      ACTGTT CGACCTCGG
                         CC_      T
GAM395 CRMP1         TCAGGCCACGCAGGGGCAGCCATC 6115   T T__  AT      I
                      TCAG CC  CGGG GGCAGCCATC
                      IIII II  IIII IIIIIIIIII
                      AGTC GG  GTCC CCGTCGGTAG
                        C TGC   __        I
GAM395 DIA1          CAGT--TCAGGATGGCAGACCA   6108 TCAGTCC        _ T
                       TCGGGATGGCAG CCA
                       IIIIIIIIIII III
                       AGTCCTACCGTC GGT
                      TCA____          T T
GAM395 EN2           TCAGTCCTCAGGGAGACCAGC   6111          AT _ CATC
                      TCAGTCCTCGGG GGC AGC
                      IIIIIIIIIII III III
                      AGTCAGGAGTCC CTG TCG
                        CT  G  IIIC
GAM395 FUT1          CATTCCT-GGG--GGCAGCCATC  6110 TCAG   C AT
                       TCCT GGG GGCAGCCAT
                       IIII III IIIIIIIII
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                                AGGA CCC  CCGTCGGTA
                              TA__    _  __
GAM395 ITGA6           TCAGTCCTCAGGGATTG-AGC   6112      _   GGC  CAT
                              TCAGTCCTC GGGAT  AGC
                              ||||||||| |||||  |||
                              AGTCAGGAG CCCTA  TCG
                                  T   AC_  |||
GAM395 LGTN            TCAGCCGT-GGG--GGCAGCCAT  6114     CTC  AT
                              TCAGTC GGG GGCAGCCAT
                              |||||| ||| |||||||||
                              AGTCGG CCC CCGTCGGTA
                                  CA_  __
GAM395 OXTR            CAGTTCCTCGGGATGTTCAGC   6106 TCAG      G_  CATC
                              TCCTCGGGATG CAGC
                              ||||||||||| ||||
                              AGGAGCCCTAC GTCG
                              TCA_         AA  C|||
GAM395 PCLO            AGTCCTGGAAAACTGGCAGCCA   6105 TCAG  C  ___      C
                              TCCT GGGA TGGCAGCCAT
                              |||| |||| ||||||||||
                              AGGA CCTT ACCGTCGGTG
                              ____   _  TTG      A
GAM395 PCSK1N          CAGTCCTGGTGGCGGGATGGC   6107 TC   _____    AGCCATC
                              AGTCCT  CGGGATGGC
                              ||||||  |||||||||
                              TCAGGA  GCCCTACCG
                              __    CCACC     C|||CTA
GAM395 PFKFB4          CAGTCCTCGTAAT-GCATCCA   6109 TC    GG  G G  T
                              AGTCCTCG ATG CA CCA
                              |||||||| ||| || |||
                              TCAGGAGC TAC GT GGT
                              __     AT  _ A  C
GAM395 SMAC            TCAGTCCTCCCGACCGGAGC    6113    GG  _ C  CAT
                              TCAGTCCTC GAT GG AGC
                              ||||||||| ||| || |||
                              AGTCAGGAG CTG CC TCG
                              GG  G  _  |||
GAM395 TIMM23          TCCTAGACGGGATGGCAGCC    6116 TCAGTCCT      AT
                              CGGGATGGCAGCC
                              |||||||||||||
                              GCCCTACCGTCGG
                              TCT_____      CC
GAM396 ACE2            TGA-ACAGAGTCA-TAGTTTT   6133  C     CC    CC
                              TGA ACAGAGTCA AGTTTT
                              ||| ||||||||| |||||
                              ACT TGTCTCAGT TCAAAA
                              _     A_  ||
GAM396 ATP5B           TGATACC-AGTCACCAGAATTTCC  6132  C AG    T_  G|
                              TGA AC AGTCACCAG TTTCC
                              ||| || ||||||||| |||||
```

```
                              ACT TG  TCAGTGGTC AAAGG
                               A  G_       TT   II
GAM396  BACH2          ACACAGAGTCA--GGTTTTCC   6126 TGAC        CCA
                          ACAGAGTCA GTTTTCC
                          IIIIIIIII IIIIIII
                          TGTCTCAGT CAAAAGG
                          ____        C__
GAM396  DEFA5          ACACAGAGTAAAATGTTTT    6122 TGAC     CACCA    CC
                          ACAGAGT  GTTTT
                          IIIIIII  IIIII
                          TGTCTCA  CAAAA
                          ____      TTTTA  AG
GAM396  DMXL1          ACACATGAAAAACCAGTTTTC    6119 TGAC  _  TC      CG
                          ACA GAG ACCAGTTTTC
                          III III IIIIIIIIII
                          TGT CTT TGGTCAAAAG
                          ____  A  TT        CG
GAM396  DNMT3B         ACACAGAG-CAGTAGCCAGTTTTC 6121 TGAC      CA___      CGI
                          ACAGAGT   CCAGTTTTC
                          IIIIIII   IIIIIIIII
                          TGTCTCG   GGTCAAAAG
                            ____      TCATC      TTI
GAM396  DNMT3B         CACCGAGCTTTGCAGTTTTCC    6127 TGACACA  CAC_      G
                             GAGT  CAGTTTTCC
                             IIII  IIIIIIIII
                             CTCG  GTCAAAAGG
                          G_____  AAAC      G
GAM396  DPYSL3         ACACCCACACACCAGTTTTC    6123 TGA  GAGT       C
                          CACA  CACCAGTTTTC
                          IIII  IIIIIIIIII
                          GTGT  GTGGTCAAAAG
                          TGG  ____       T
GAM396  FIGF           GACTCAGAGACTACAGTTTTCC   6129 TG A   TCAC      G
                          AC CAGAG  CAGTTTTCC
                          II IIIII  IIIIIIIII
                          TG GTCTC  GTCAAAAGG
                          __  A  TGAT        A
GAM396  GPX1           TGGCACAG-G----CAGTTTTCCG 6134  A   A TCAC
                          TG CACAG G  CAGTTTTCC
                          II IIIII I  IIIIIIIII
                          AC GTGTC C  GTCAAAAGG
                          C    _ ____
GAM396  KCNJ15         ACACAGAGT---CAGTTTTCC    6125 TGAC      CCA
                          ACAGAGTCA GTTTTC
                          IIIIIIIII IIIIII
                          TGTCTCAGT CAAAAG
                                     ____
GAM396  LMO7           ACAGAAAGGCTCACCAGTTT     6120 TGACAC AG      CC
                           AG TCACCAGTTTT
                           II IIIIIIIIIII
```

```
                              TC  AGTGGTCAAAG
                          TCTT__  CG        AI
GAM396 PPP2R2B        ACCCAGA---ACCAGTTTTC      6124 TGACA   GTC
                          CAGA   ACCAGTTTTC
                          ||||   |||||||||
                          GTCT   TGGTCAAAAG
                         G____      ___
GAM396 RALB          CACAGAGTCACAAATATTTTCC   6128 TGACAC     CAG___     GI
                          AGAGTCAC    TTTTCC
                          ||||||||    ||||||
                          TCTCAGTG    AAAAGG
                          _____      TTTATA    GG
GAM396 TGFB1          TGACACAGAGATCCGCAGT       6131       _ AC   TTTCC
                          TGACACAGAG TC  CAGT
                          |||||||||| ||  ||||
                          ACTGTGTCTC AG  GTCA
                              T GC   IIIGC
GAM396 TULP1          GACACAG-G--AGCAGTTTTCCG   6130 TG    _ TCAC
                          ACACAG AG   CAGTTTTCC
                          |||||| ||   |||||||||
                          TGTGTC TC   GTCAAAAGG
                          __      C ____
GAM397 AK1           GGGGCCCCGCACGCTTCGGG      6150      G TCCGIII
                          GGGGCCCCG AT
                          ||||||||| ||
                          CCCCGGGGC TG
                          G  CGAAGCC
GAM397 ARHGAP6        GGGGGCCCCTGGATCCAGG       6156       _   CGII
                          GGGGGCCCC GGATTC
                          ||||||||| ||||||
                          CCCCCGGGG CCTAGG
                          A     TCCI
GAM397 ATBF1          AGGGGG-CCCGGAGACAGGG      6146 _      C TTCCGGI
                          GGGGGCCC GGA
                          |||||||| |||
                          CCCCCGGG CCT
                          T     _ CTGTCCI
GAM397 BCAR1          GGGGCCCCGGCTCTCGCGGG      6151      A_ _ III
                          GGGGCCCCGG TTC CGG
                          |||||||||| ||| |||
                          CCCCGGGGCC GAG GCC
                          GA  C  CII
GAM397 BLK           GCCCACTGGATTCCGGGTC       6149  C__       III
                          GCCC  GGATTCCGGGT
                          ||||  |||||||||||
                          CGGG  CCTAAGGCCCA
                          TGA       GII
GAM397 CDK4          GGGGCCCCGGA-GCCGGTTC       6153 _      TT GTI
                          GGGCCCCGGA CCGG
                          |||||||||| ||||
```

```
                              CCCGGGGCCT GGCC
                            C       C_  AAI
GAM397 CPNE7        GGGGGCCCCAGA-GCCGGG    6158        TT  I
                            GGGGGCCCCGGA CCGG
                            |||||||||| ||||
                            CCCCCGGGGTCT GGCC
                                 C_  C
GAM397 CPT2        AAGGGGGCCCCAGCCTCCGCGT  6139        A   GGI
                            AGGGGGCCCCGG TTCCG
                            ||||||||||| |||||
                            TCCCCCGGGGTC GAGGC
                                   G  GCI
GAM397 DLG4        AGGGGGCCCTGACTTCTGG      6144     C GA  CGII
                            AGGGGGCCC G  TTC
                            ||||||||| |  |||
                            TCCCCCGGG C  AAG
                              A TG   ACCI
GAM397 GNA15       GGGGGCCCCAGGGAGGGCGGG    6155        __  TTC  III
                            GGGGGCCCC GGA  CGG
                            ||||||||| |||  |||
                            CCCCCGGGG CCT  GCC
                              TC  CCC  CII
GAM397 IFNGR2      GGGGCCCCG--CTCGGGGTC    6152      GA  C  I
                            GGGGCCCCG TTC GGG
                            ||||||||| ||| |||
                            CCCCGGGGC GAG CCC
                               __  C  A
GAM397 INHBB       GGGGGCCCCGCAGCCCCGGT    6159      GA_  GI
                            GGGGCCCCG TTCCGG
                            ||||||||| ||||||
                            CCCCGGGGC GGGGCC
                              GTC    II
GAM397 JPH3       AGTGGGCCCCGGCTTCCCTGGGGTC  6143 GGG    A  ___  I
                            GGCCCCGG TTCC  GGGT
                            |||||||| ||||  ||||
                            CCGGGGCC AAGG  CCCA
                            ___     G  GAC  I
GAM397 MAGEA3       TAAGGGATGCGGCCCCGGA     6160      ____     IIIT
                            TAAGGG  GGCCCCGG
                            ||||||  ||||||||
                            ATTCCC  CCGGGGCC
                              TACG     TIII
GAM397 MAP4        AAGGGGGCCAAGGA-CCCGGG    6138 _    CC  T  I
                            AGGGGGCC GGAT CCGG
                            |||||||| |||| ||||
                            TCCCCCGG CCTG GGCC
                            T    TT _  I
GAM397 MAPK1       AAGTGCTCCCCAAGGATTCCGG   6137 AGGGGG   __      I
                            CCCC GGATTCCG
                            |||| ||||||||
```

```
                        GGGG  CCTAAGGC
                        ACGA__   TT       I
GAM397 PTBP1            AGGAGCGCCCGCCTTCCGGGTC   6147 G    _   GA        I
                        GGGGC CCCG  TTCCGGGT
                        ||||| |||| |||||||||
                        CCTCG GGGC  AAGGCCCA
                         _    C   GG        I
GAM397 RDBP            GGGGGCCCCACGGTCTCCGG       6154       __  A     III
                        GGGGGCCCC  GG TTCCG
                        ||||||||| || |||||
                        CCCCCGGGG  CC GAGGC
                           TG  A    CII
GAM397 RFX1            AGGAGGGCCCCGGTCTTCCCTGTC  6140 G       A_   GG  I
                        GGGGCCCCGG  TTCC GT
                        |||||||||| |||| ||
                        TCCCGGGGCC  AAGG CA
                         _          AG   GA  I
GAM397 SLC12A7        GGGGGCCCC---TTCCCGG       6157       GGA
                        GGGGGCCCC  TTCCGG
                        ||||||||| ||||||
                        CCCCCGGGG  AGGGCC
                               A__
GAM397 SMARCD1        AGGAGGCCCCGGAGTTCCG       6142          _   II
                        AGGGGGCCCCGGA TTCC
                        ||||||||||||| ||||
                        TCCTCCGGGGCCT AAGG
                              C   CI
GAM397 ST14          AGGCGGCG--GGATTCCGGG       6145 _ G  CCC        I
                        GG GGC  GGATTCCGG
                        || ||| |||||||||
                        CC CCG  CCTAAGGCC
                         T  G  C__       I
GAM397 TBX1          AGGGGGCCCCCATGGCTTC       6141         GGATTIII
                        AGGGGGCCCC
                        ||||||||||
                        TCCCCCGGGG
                           GTACCGAA
GAM397 ZFP36L1       AGGGGGCTGCTGGTTCCGGGTC   6148      CCC_ A      I
                        GGGGGC  GG TTCCGGGT
                        |||||| || |||||||||
                        CCCCCG  CC AAGGCCCA
                         ACGA _      I
GAM398 ANXA1           AAAAATG---ATTTAAAGGC     6169 TGAAAAGATGGG
                              GATTTAAAGG
                              ||||||||||
                              CTAAATTTCC
                        TTA_____
GAM398 CEP1          TGAATGAGATGGGGAAAAAAATGC  6181    A_       TTT  G CI
                        TGAA AGATGGGGA  AAA GC
                        |||| |||||||| ||| ||
```

```
                    ACTT TCTACCCCT TTT CG
                     AC      TTT A II
GAM398 DBY          TGAAAAGATTTGTTTTTAAAG  6185      GGGGA     GCC
                    TGAAAAGAT   TTTAAAG
                    |||||||||   |||||||
                    ACTTTTCTA   AAATTTC
                        AACAA       III
GAM398 DTNA         TGAAAAG----GGATTTAATTGCC 6188   AGAT      AG
                    TGAAA  GGGGATTTAA GC
                    |||||  |||||||||| ||
                    ACTTT  TCCCTAAATT CG
                     ___          AA
GAM398 EDNRA        TGAAAAGATGTAG---TAAAGG   6187      GG ATT   C
                    TGAAAAGATG G  TAAAGG
                    ||||||||||  |  ||||||
                    ACTTTCTAC C  ATTTCC
                        AT ___    I
GAM398 EIF1A        GAAAAGAT-GGAATGTAAA      6175 TG    G T   G
                    AAAAGATGGG AT TAAAG
                    |||||||||| || |||||
                    TTTTCTACCT TA ATTT
                     __      _ C  I
GAM398 EIF2B1       TGAAAAGATGCTGAATTTA      6183      G_    AAGGC
                    TGAAAAGATG GGATTTA
                    ||||||||||  |||||||
                    ACTTTCTAC CTTAAAT
                        GA     IIICC
GAM398 FGD1         TGAAAAGAT---GAATTAAA     6184        GATTTAAAGG
                    TGAAAAGATGGG
                    |||||||||||
                    ACTTTCTACTT
                       AATTTIIICC
GAM398 FY           GAAAAGATGAGGAGGAAAAGG    6178 TG      TTT   CC
                    AAAAGATGGGGA AAAGG
                    |||||||||||  |||||
                    TTTTCTACTCCT TTTCC
                     __          CCT    TI
GAM398 GPR86        TGAATAGATCTATGTGGATTTAAA 6182   A GG____       GGCCI
                    TGAA AGAT    GGATTTAAA
                    |||| ||||    |||||||||
                    ACTT TCTA    CCTAAATTT
                     A  GATACA       IIICC
GAM398 JTB          GAAGAAGATGGGGA---AAAGG   6171 TGAA     TTT   C
                    AAGATGGGGA AAAGG
                    |||||||||| |||||
                    TTCTACCCCT TTTCC
                    TTC_       ___    C
GAM398 KLRC1        AAAAGGTGAA-ATTTAAAGGC    6167 TGAAAAGATG GG
                     G ATTTAAAGGC
                     | |||||||||||
```

```
                              C  TAAATTTCCG
                      TTCCA_____TT
GAM398  MAML1         GAAGAATATGGGGATTAATAGG   6172 TGAAAAG      TAA  CC
                          ATGGGGATT  AGG
                          ||||||||| |||
                          TACCCCTAA  TCC
                      TTCTTA_       TTA  TI
GAM398  MUC3B         GAGAAGATGGGG--TTACAGG   6180 TGAA      A  TAA  C
                         AAGATGGGG TT  AGG
                         ||||||||| || |||
                         TTCTACCCC AA  TCC
                     TC__      _ TG_  A
GAM398  MYO1B         AAATGATGCAATATTTAAAGG   6164 TGAAAA  G _      CC
                          GATG GG ATTTAAAGG
                          |||| || |||||||||
                          CTAC TT TAAATTTCC
                     TA____  G A      TA
GAM398  PRSS16        GAAAAGATGGTGAGTGAAGGG   6179 TG     G  TTTA  CC
                         AAAAGATGG GA   AAGG
                         ||||||||| ||   ||||
                         TTTTCTACC CT   TTCC
                     __       A  CAC_   CA
GAM398  RPL24         AAAAGATGGCGA---AAAG    6166 TGAA     G  TTT
                          AAGATGG GA   AAAG
                          ||||||| ||   ||||
                          TTCTACC CT   TTTC
                     ____      G  ___
GAM398  STS          TGGAAAACTGGGGATTTATAG   6186 T_   GA      A  GCC
                          GAAAA TGGGGATTTA AG
                          ||||| |||||||||| ||
                          CTTTT ACCCCTAAAT TC
                     AC   G_      A  III
GAM398  SULT1C1       GAATA-ATGGGGATTAAAA    6177 TGAAAA      TA
                         GATGGGGATT AAGG
                         |||||||||| ||||
                         TTACCCCTAA TTTT
                     TTA___       __
GAM398  TAC3          GAAAAGATGGAGAAGGAGTCAAAG  6174 TG      TTTA___  CI
                         AAAAGATGGGGA    AAGGC
                         ||||||||||||    |||||
                         TTTTCTACCTCT    TTTCG
                     __       TCCTCAG   II
GAM398  TNFRSF9       AAAAG-TGGTGCATTTTTAAAGGCC  6163 TGAA  A  GGA___      I
                         AAG TGG   TTTAAAGGCC
                         ||| |||   ||||||||||
                         TTC ACC   AAATTTCCGG
                     ____  _ ACGTAA      T
GAM398  TOP1          AAAAGATGGATATCTTAAAGG   6165 TGAA     GA_   CC
                         AAGATGGG TTTAAAGG
                         |||||||| ||||||||
```

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                              TTCTACCT  GAATTTCC
                              ____        ATA      CA
GAM398 TYK2          AAGCTGGGGGATTTAAGGGC    6170 TGAAAAGAT       A
                              GGGGATTTAA GGC
                              ||||||||| |||
                              CCCCTAAATT CCG
                         AC_____        C
GAM398 WASF3         GAAAAGATCTGGATTTAAA    6176 TG   GG     GGC
                              AAAAGAT GGATTTAAA
                              ||||||| |||||||||
                              TTTTCTA CCTAAATTT
                            __      GA     AII
GAM398 YWHAZ         AAAGAGGAAGGATTTTAAAGGC   6168 TGAAA AT   A      C
                              AG GGGG TTTAAAGGC
                              || |||| |||||||||
                              TC TCCT AAATTTCCG
                         C____ CT  A      T
GAM398 ZNF141        GAAAAGACTGAGGAAGATTTAAAG 6173 TG    ____        CCI
                              AAAAGAT  GGGGATTTAAAGG
                              |||||||  |||||||||||||
                              TTTTCTG  CTTCTAAATTTCT
                            __   ACTC        III
GAM399 CNTN3         ATATGTAAATTCCTTTGGTT    6192 TATAG    ATA   GA
                              GTAAATTCC  GGTT
                              ||||||||| ||||
                              CATTTAAGG  CCAA
                         ATA__      AAA   AI
GAM399 EFG1          TATACGATAAATTCCA-AGG    6193 _       T  TTGA
                              TATA GGTAAATTCCA AGG
                              |||| |||||||||| |||
                              ATAT CTATTTAAGGT TCC
                              G      _  IIIG
GAM399 GEM           TATAGGTAAAAACTTGCATATTTTGA 6194    TTC___  GG  GII
                              TATAGGTAAA    CATA TTGA
                              ||||||||||    |||| ||||
                              ATATCCATTT    GTAT AACT
                              TTGAAC  AA  III
GAM399 ILF1         AGGAAATCATTCCATAGGCTGA    6191 TATAGGTAA
                              ATTCCATAGGTTGAG
                              |||||||||||||||
                              TAAGGTATCCGACTT
                         TTTAG____
GAM399 LAMA2        TATAGGTAAAATATATTTGTT    6195     TTCCATAG GAG
                              TATAGGTAAA     GTT
                              ||||||||||     |||
                              ATATCCATTT     CAA
                              TATATAAA  III
GAM399 TACC1        TATGGAAAAATTCCAT--GTTG    6196 TATA T_    AG  A
                              GG AAATTCCAT GTTG
                              || ||||||||| ||||
```

```
                        CC  TTTAAGGTA  CAAC
                        ATA_ TT         __    I
GAM400  IGF1            TGAAGTACAAAGTCTGAAAA     6200        TTTTTATAAAAT
                        TGAAGTACAAA
                        IIIIIIIIII
                        ACTTCATGTTT
                        CAGACTTTTIII
GAM400  ZNF255         TGAAATA-AAATTTTTAATAAAA  6199      C      _    TA
                        TGAAGTA AAATTTTTA TAAAA
                        IIIIIII IIIIIIIII IIIII
                        ACTTTAT TTTAAAAAT ATTTT
                            _       T   II
GAM401  BLAME          CCAGAGCTTTTCTAGACAG      6206         T  II
                        CCAGAGCTTTTCTAG CA
                        IIIIIIIIIIIIII II
                        GGTCTCGAAAAGATC GT
                            T  CI
GAM401  BLAME          CCAGAGCTTTTCTAGACAG      6206 TAACCA       T  C
                        GAGCTTTTCTAG CAG
                        IIIIIIIIIII III
                        CTCGAAAAGATC GTC
                        _____         T  T
GAM401  FBXL3A         AATCAGAGCTTTTTACTATTTAG  6204 C         __   GTCAI
                        CAGAGCTTTT CTA
                        IIIIIIIIII III
                        GTCTCGAAAA GAT
                          _       AT  AAAII
GAM401  FBXL3A         AATCAGAGCTTTTTACTATTTAG  6204 TAAC       __   GTCAGCCI
                        CAGAGCTTTT CTA
                        IIIIIIIIII III
                        GTCTCGAAAA GAT
                        TA__       AT  AAATCTII
GAM401  NRF1           AACCAGAGCAACATTTTAATAGTCA 6203 TA      _____  TC    GCCII
                        ACCAGAGC   TTT TAGTCA
                        IIIIIIII   III IIIIII
                        TGGTCTCG   AAA ATCAGT
                          __       TTGTA  TT    AIIIC
GAM401  PTGFRN         CAGAGCTTTTAAAG-CAGC      6205      CT  T  I
                        CAGAGCTTTT AG CAG
                        IIIIIIIIII II III
                        GTCTCGAAAA TC GTC
                        TT _  G
GAM401  PTGFRN         CAGAGCTTTTAAAG-CAGC      6205 TAACCAGA   CT  T
                        GCTTTT AG CAG
                        IIIIII II III
                        CGAAAA TC GTC
                        _____       TT  _
GAM401  RECQL5         CCAGAGCTTTT-T--TCAGC     6208        C_  CAI
                        CCAGAGCTTTT TAGT
                        IIIIIIIIII IIII
```

```
                              GGTCTCGAAAA GTCG
                                 AA   III
GAM401  RECQL5         CCAGAGCTTTT-T--TCAGC   6208 TAACCA      CTAG
                              GAGCTTTT  TCAG
                              |||||||| ||||
                              CTCGAAAA  AGTC
                              _____     A___
GAM401  SIM1         CCAGAGAT---CTAGTCAGC   6207 _   CTTT
                              CAGAG   TCTAGTCAG
                              |||||   |||||||||
                              GTCTC   AGATCAGTC
                                G     T___
GAM401  SIM1         CCAGAGAT---CTAGTCAGC   6207 TAACCA  CTTT
                              GAG    TCTAGTCAG
                              |||    |||||||||
                              CTC    AGATCAGTC
                              _____    T___
GAM401  UBQLN1         TAACCAGAATCAGCTTTTCTA   6209      ____      GTCAGCC
                              TAACCAGA  GCTTTTCTA
                              ||||||||  |||||||||
                              ATTGGTCT  CGAAAAGAT
                                TAGT    IIICCGA
GAM401  UBQLN1         TAACCAGAATCAGCTTTTCTA   6209      ____      IIIT
                              TAACCAGA  GCTTTTCT
                              ||||||||  ||||||||
                              ATTGGTCT  CGAAAAGA
                                TAGT      TIII
GAM402  ABCA2          TGTCCTCCCTGGCCCAGCTCTGGGTGG6259        ___  GC_ C  III
                              TGTCCTCCCTG  CAGC  GG GTGG
                              |||||||||||  ||||  || ||||
                              ACAGGAGGGAC  GTCG  CC CACC
                                 CGG   AGA _   III
GAM402  ACAD8         TGCGCTCGCAC-TGGCGGGA    6256    G   C      GGC
                              TGCGC CGCAC TGGCGGGA
                              ||||| ||||| ||||||||
                              ACGCG GCGTG ACCGCCCT
                                  A     _    III
GAM402  ACAD8         TGCGCTCGCAC-TGGCGGGA    6256 _  G    C     I
                              GCGC CGCAC TGGCGGG
                              |||| ||||| |||||||
                              CGCG GCGTG ACCGCCC
                                A  A   _    I
GAM402  ACHE        GCGCCCAGCGAGGCGGGAGG    6226   G CCT_     II
                              GCGC CA  GGCGGGAG
                              |||| ||  ||||||||
                              CGCG GT  CCGCCCTC
                                 G CGCT      CI
GAM402  ADAM10         GCGCGCGCATGCGCGCGGGGGACG  6231 C    CC _   A I
                              GCGCGCA TG GCGGG GGC
                              ||||||| || ||||| |||
```

```
                          CGCGCGT GC CGCCC CTG
                          _     AC  G    C   I
GAM402 ADAM10        GCGCGCGCATGCGCGCGGGGGACG 6231 TG     CC _  A  I
                          CGCGCGCA TG GCGGG GGCG
                          |||||||| || ||||| ||||
                          GCGCGCGT GC CGCCC CTGC
                          __      AC  G    C   C
GAM402 BACE2         TGGGCGCGCACCGGGACCGGCGGCG 6254 C      T _ G A  II
                          TG GCGCGCACC GG C GG GGCG
                          || ||||||||| || | || ||||
                          AC CGCGCGTGG CC G CC CCGC
                          C      C T G G  II
GAM402 BACE2         TGGGCGCGCACCGGGACCGGCGGCG 6254 GC     T _ G A  I
                          GCGCGCACC GG C GG GGC
                          ||||||||| || | || |||
                          CGCGCGTGG CC G CC CCG
                          C_      C T G G  I
GAM402 C2           TGTCCTCCCT-AGGGGCGGCG  6261      CAGC    TG
                          TGTCCTCCCTG  GCGGCG
                          ||||||||||   ||||||
                          ACAGGAGGGAT  CGCCGC
                              CCC_     II
GAM402 CASP8        GCGTGAACC---CGGGAGGCG  6230 C  C__  TGG
                          GCG ACC  CGGGAGGC
                          ||| |||  ||||||||
                          CGC TGG  GCCCTCCG
                          _ ACT    ___
GAM402 CD7          TCCTCCCGGT-G-GCGGCGTGG  6251 TGTC    TGCAGC
                          CTCCC    GCGGCGTG
                          |||||    ||||||||
                          GAGGG    CGCCGCAC
                          ____     CCAC__
GAM402 CDKN3        CCTCCCTCTGCAGCGCCGGCG  6214 TGTCCT _     _  TGG
                          CC CTGCAGCGC GGCG
                          || ||||||||| ||||
                          GG GACGTCGCG CCGC
                          G_____ A    G  TGA
GAM402 CEBPA        GCCCGCGCACCT-CCGGGTCGCG  6242 _ G    GG  AG  I
                          C CGCGCACCT CGGG GC
                          | |||||||| |||| ||
                          G GCGCGTGGA GCCC CG
                          C G    G_ AG  I
GAM402 CEBPA        GCCCGCGCACCT-CCGGGTCGCG  6242 TG G    GG  AG
                          C CGCGCACCT CGGG GCG
                          | |||||||| |||| |||
                          G GCGCGTGGA GCCC CGC
                          __ G    G_ AG
GAM402 CHN1         TGTGCGCGCACCGGGCCCAGGGAG  6255 C     T ___  GCGI
                          TG GCGCGCACC GGC  GGGAG
                          || ||||||||| |||  |||||
```

```
                        AC CGCGCGTGG CCG  CCCTC
                        A      C  GGT  IIIG
GAM402 CHN1             TGTGCGCGCACCGGGCCCAGGGAG  6255 GCG      T  ___  I
                        CGCGCACC GGC  GGGA
                        IIIIIIII III  IIII
                        GCGCGTGG CCG  CCCT
                        ___     C  GGT  I
GAM402 COL5A1           GCGCTCGCCCACGGGCGGGAGG   6233 CG_  G  CT      I
                        CGC CAC  GGCGGGAG
                        III III  IIIIIIII
                        GCG GTG  CCGCCCTC
                        CGA  G  C_      I
GAM402 COL5A1           GCGCTCGCCCACGGGCGGGAGG   6233 T G  G  CT      CG
                        GC CGC CAC  GGCGGGAGG
                        II III III  IIIIIIIII
                        CG GCG GTG  CCGCCCTCC
                        G  A  G  C_      CI
GAM402 DGAT2            TCCTCCCTGCAATGGTGCATGG   6252 TGTC        CGCG
                        CTCCCTGCAG  GCGTGG
                        IIIIIIIIII  IIIIII
                        GAGGGACGTT  CGTACC
                        ____        ACCA
GAM402 FBP1            CGCGGG-ACCTGGCGGGAGG     6222 G  C_      I
                        CGCG ACCTGGCGGGAG
                        IIII IIIIIIIIIIII
                        GCGC TGGACCGCCCTC
                        _  CC        I
GAM402 FEZ1            TGACCTCC-TGCAGCGAGGC      6260 T  C    C GTG
                        TG CCTCC TGCAGCG GGC
                        II IIIII IIIIIII III
                        AC GGAGG ACGTCGC CCG
                        T   _    T III
GAM402 GAD2            GCGTGCGTGCCGTGTGGCGGGAGG  6235 C  C ACC_      I
                        GCG GC  TGGCGGGAG
                        III II  IIIIIIIII
                        CGC CG  ACCGCCCTC
                        _  A GCAC      I
GAM402 GAD2            GCGTGCGTGCCGTGTGGCGGGAGG  6235 TGC  C ACC_      CGI
                        GCG GC  TGGCGGGAGG
                        III II  IIIIIIIIII
                        CGC CG  ACCGCCCTCC
                        GCA  A GCAC      TII
GAM402 GALGT           GTCC-CACTGGCAGCGCGGGGAGG  6246 TGTCC  T___      CGT I
                        TCCC  GCAGCGCGG  GG
                        IIII  IIIIIIIII  II
                        AGGG  CGTCGCGCC  CC
                        _____      TGAC      CCT C
GAM402 GATA6           CCTCCCTGCCTCCTGGCGGCGTGG  6215 TGTCCT    AGC___      I
                        CCCTGC  GCGGCGTGG
                        IIIIII  IIIIIIIII
```

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                      GGGACG    CGCCGCACC
                 _____        GAGGAC        C
GAM402 GCK            TCCTCCCTGC-GCTTGCGGC    6248 TGTC      A __    GTG
                      CTCCCTGC GC GCGGC
                      |||||||| || |||||
                      GAGGGACG CG CGCCG
                 ____        _ AA    GTI
GAM402 HRB            TGCGCGCGCCGCCCGCGCCGGA   6253      A_  _ G  GGCG
                      TGCGCGCGC  CCTG GC GGA
                      ||||||||| |||| || |||
                      ACGCGCGCG  GGGC CG CCT
                       GC   G  G   IIIG
GAM402 HRB            TGCGCGCGCCGCCCGCGCCGGA   6253      _ A _  G  GI
                      GCGCGC GC CC TG CGG
                      |||||| || || || |||
                      CGCGCG CG GG GC GCC
                       G _  C  G  II
GAM402 HTR1E          CGCGAACC---CGGGAGGCG     6219 _  C  TGG
                      GCG ACC  CGGGAGGC
                      ||| |||  |||||||||
                      CGC TGG  GCCCTCCG
                      G   T   ___
GAM402 IFNAR2         CACCTGAACCCGGGAGGCG      6212       ___       III
                      CACCTGG  CGGGAGGC
                      ||||||| |||||||||
                      GTGGACT  GCCCTCCG
                       TGG       CII
GAM402 ILF1           GCGGGAGCACGCGCGGGCGGGAGG 6232 _      ACCT     I
                      GCGCGCGC  GGCGGGA
                      ||||||||  |||||||
                      CGTGCGCG  CCGCCCT
                       T    C___     C
GAM402 ILF1           GCGGGAGCACGCGCGGGCGGGAGG 6232 T____    ACCT       CGI
                      GCGCGCGC  GGCGGGAGG
                      ||||||||  |||||||||
                      CGTGCGCG  CCGCCCTCC
                  GCCCT     C___      TII
GAM402 IMPDH1        CCTCCCTGCAGCG-GTGGTGG     6218 TGTCCT        CGGC
                      CCCTGCAGCG  GTG
                      |||||||||| |||
                      GGGACGTCGC  CAC
                      _____        CAC_
GAM402 INPP1         GCGCGGCCC-GGCGGGAGG       6229  CA        I
                      GCGCG CCTGGCGGGAG
                      ||||| |||||||||||
                      CGCGC GGGCCGCCCTC
                       C_       C
GAM402 JAM2          GCGAGGAGCTGGGGGCGGGAGGCG  6228 CGC  ACCT        I
                      GC  GGCGGGAGGC
                      ||  |||||||||
```

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                              CG   CCGCCCTCCG
                              CCT  ACCC        I
GAM402  KIFC3          GCACG-GCCCCGTGGCGGGAGGC   6236    C  A  _        I
                          CGCG GC CC TGGCGGGAGG
                          |||| || || |||||||||||
                          GTGC CG GG ACCGCCCTCC
                           _  G  C        I
GAM402  KIFC3          GCACG-GCCCCGTGGCGGGAGGC   6236 TG   C  A  _        G
                          CGCG GC CC TGGCGGGAGGC
                          |||| || || |||||||||||
                          GTGC CG GG ACCGCCCTCCG
                          __  _ G  C       G
GAM402  LASS1         GCGCGCGCA---GGCGGCAGG      6239        CC     AI
                          GCGCGCGCA TGGCGGG
                          ||||||||| |||||||
                          CGCGCGCGT GCCGTCC
                                CC      II
GAM402  LASS1         GCGCGCGCA---GGCGGCAGG      6239 TG      CCT   G
                          CGCGCGCA  GGCGG AGG
                          ||||||||  ||||| |||
                          GCGCGCGT  CCGCC TCC
                          __      ___    G
GAM402  MADD          GTCGCTCCC--CAGCGCGGCG      6244 TG  _  TG       G
                          TC CTCCC  CAGCGCGGCGT
                          || |||||  ||||||||||||
                          AG GAGGG  GTCGCGCCGCG
                          __  C  __       I
GAM402  MCM4          TGCCCTGCTCCGCAGCGCGGACGT   6258     CC_     _ GGI
                          TGTCCT  CTGCAGCGCGG CGT
                          ||||||  |||||||||||| |||
                          ACGGGA  GGCGTCGCGCC GCA
                              CGA       T  III
GAM402  NCAM1         CCCCCCTGCAGCG-AGTGTGG      6217 TGTCCT      C C
                          CCCTGCAGCG GG GTG
                          |||||||||| || |||
                          GGGACGTCGC TC CAC
                          _____     _ A
GAM402  NOLA1         TCCTCCCTGACGCTGAGCCGTGG    6250 TGTC      CA  __ _  I
                          CTCCCTG GCGC GGC GTGG
                          ||||||| |||| ||| ||||
                          GAGGGAC TGCG TCG CACC
                          ____     __  AC  G  T
GAM402  NRXN2         GCGGGCGCATGGGGCGGGAGG      6240 C   CCT        I
                          CG GCGCA  GGCGGGAG
                          || ||||| |||||||||
                          GC CGCGT  CCGCCCTC
                          C  ACC        I
GAM402  NRXN2         GCGGGCGCATGGGGCGGGAGG      6240 TG  C   CCT       CG
                          CG GCGCA  GGCGGGAGG
                          || ||||| ||||||||||
```

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                         GC CGCGT  CCGCCCTCC
                         __  C  ACC       CI
GAM402 PACSIN3          GTCCTCCCTGGGCCCCTCGGCG  6245 TG     CA G___     TGG
                         TCCTCCCTG GC   CGGCG
                         IIIIIIIII II  IIIII
                         AGGAGGGAC CG   GCCGC
                         __         C_ GGGA    CII
GAM402 PCOLCE2           CGCGCGCACC-GCCGCGGGGCG  6223 _      T G _ A I
                         GCGCGCACC G CG GG GGC
                         IIIIIIIII I II II III
                         CGCGCGTGG C GC CC CCG
                         G     _ G G  _  I
GAM402 PCOLCE2           CGCGCGCACC-GCCGCGGGGCG  6223 TGCG     TG_  A_  G
                         CGCGCACC  GCGGG GGC
                         IIIIIIII  IIIII III
                         GCGCGTGG  CGCCC CCG
                         ____        CGG   CG  I
GAM402 PDGFB            CTCCGCGC-GCGCGGCGTG      6224 TGTCCTCCCT A
                         GC GCGCGGCGT
                         II IIIIIIIII
                         CG CGCGCCGCA
                         CG_____  _
GAM402 PODXL           TCCTCCCTGCCGCTGCAGC       6249 TGTC     A _    TG
                         CTCCCTGC GC GCGGCG
                         IIIIIIII II IIIIII
                         GAGGGACG CG CGTCGT
                         ____         G  A    CI
GAM402 PPP1CB          GCGCGCGCACACT--C-GGAGGC  6234 _      C  C GAI
                         GCGCGCGCAC TGG GG
                         IIIIIIIIII III II
                         CGCGCGTGTG GCC CC
                         G     A T GII
GAM402 PPP1CB          GCGCGCGCACACT--C-GGAGGC  6234 T       CTGGCG
                         GCGCGCGCAC    GGAGGC
                         IIIIIIIIII    IIIIII
                         CGCGCGTGTG    CCTCCG
                         G     AG____
GAM402 PPP2R5E         CGCTCACATTCCTGGCGGGCGGCG 6221 G   CA     A  I
                         CGCG CCTGGCGGG GGC
                         IIII IIIIIIIII III
                         GTGT GGACCGCCC CCG
                         A  AA     G  I
GAM402 PPP2R5E         CGCTCACATTCCTGGCGGGCGGCG 6221 TGCG  CA     A  I
                         CGCG CCTGGCGGG GGCG
                         IIII IIIIIIIII IIII
                         GTGT GGACCGCCC CCGC
                         GA__ AA    G  G
GAM402 PSMB2          CACTTGGGCCCGGGAGGCG       6213 C  ___      III
                         CAC TGG  CGGGAGGC
                         III III  IIIIIIII
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                            GTG ACC  GCCCTCCG
                             A  CGG      CII
GAM402 RB1              GCGCGCGCACGTCGGGGCACGC   6241       CTGG   AGGI
                           CGCGCGCAC   CGGG
                           |||||||||  ||||
                           GCGCGCGTG  GCCC
                             CA__   CGTG
GAM402 RB1              GCGCGCGCACGTCGGGGCACGC   6241 TG      CTGG  AG
                           CGCGCGCAC  CGGG GCG
                           |||||||||  |||| |||
                           GCGCGCGTG  GCCC TGC
                           __      CA__   CG
GAM402 S100A11           CTCTGTGC-GCGCGGCGTG       6225 TGTCCTCCC  A
                             TGC GCGCGGCGT
                             ||| |||||||||
                             ACG CGCGCCGCA
                           C_____  _
GAM402 SCAP1           GCGCGGGC-CCTGGTCGGGAGGCG  6238   C  A   _     I
                           CGCG GC CCTGG CGGGAGGC
                           |||| || ||||| ||||||||
                           GCGC CG GGACC GCCCTCCG
                            C  _   A     I
GAM402 SCAP1           GCGCGGGC-CCTGGTCGGGAGGCG  6238 TG   C  A   _      I
                           CGCG GC CCTGG CGGGAGGCG
                           |||| || ||||| |||||||||
                           GCGC CG GGACC GCCCTCCGC
                           __   C _  A      C
GAM402 SERPINB9         GCGTGAACC---CGGGAGGCG    6230 C  C__   TGG
                           GCG ACC  CGGGAGGC
                           ||| |||  ||||||||
                           CGC TGG  GCCCTCCG
                           _ ACT   ___
GAM402 SHOX           GCGCGCGCA---GGAGGGGGGCG    6243 _     CCT C  A
                           CGCGCGCA  GG GGG GGC
                           ||||||||  || ||| |||
                           GCGCGCGT  CC CCC CCG
                           C      ___ T  C
GAM402 SHOX           GCGCGCGCA---GGAGGGGGGCG    6243 TG     CCT C  A
                           CGCGCGCA  GG GGG GGC
                           ||||||||  || ||| |||
                           GCGCGCGT  CC CCC CCG
                           __     ___ T  C
GAM402 SLC25A1         CGGGCACCC--CGGGAGGCG      6220 _C     GG     I
                           G GCACCT CGGGAGGC
                           | |||||| ||||||||
                           C CGTGGG GCCCTCCG
                           G C   __    I
GAM402 SLC25A11         GCGCGCGCAACAGAGCGAG-GGCG  6237        _CT   A I
                           CGCGCGCA C  GGCGGG GGC
                           |||||||| |  |||||| |||
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                        GCGCGCGT G  TCGCTC CCG
                              T TC    _   I
GAM402  SLC25A11         GCGCGCGCAACAGAGCGAG-GGCG  6237 TG     _CT    A   I
                         CGCGCGCA C  GGCGGG GGCG
                         |||||||| |  |||||| ||||
                         GCGCGCGT G  TCGCTC CCGC
                          __      T TC    _   G
GAM402  SOX11            GCTCGC-CCAGAGCGGGAGGC   6227 CG  A  T_      I
                          CGC CC  GGCGGGAGG
                          ||| ||  |||||||||
                          GCG GG  TCGCCCTCC
                           GA  _  TC      I
GAM402  SOX11            GCTCGC-CCAGAGCGGGAGGC   6227 TGCGCG  A  T_
                          CGC CC  GGCGGGAGGC
                          ||| ||  ||||||||||
                          GCG GG  TCGCCCTCCG
                          _____ _ TC
GAM402  TAPBP          GCGTGAACC---CGGGAGGCG   6230 C  C__  TGG
                         GCG  ACC  CGGGAGGC
                         ||| |||  |||||||||
                         CGC  TGG  GCCCTCCG
                          _  ACT  ___
GAM402  TJP1          TCCTGAGCTCTGCAGCGCTGGGTGG  6247 TGTCCTCC     _  C  II
                          CTGCAGCGC GG GTGG
                          ||||||||| || ||||
                          GACGTCGCG CC CACC
                         GACTCGA_      A _  CG
GAM402  TNFRSF7         CCTCC-TGCAGCGCAGGCG    6216 TGTCCTC      _   T
                         CCTGCAGCGC GGCG
                         |||||||||| ||||
                         GGACGTCGCG CCGC
                         _____     T  G
GAM402  TPR          TGCGCGCGCAGCCGTTGGAAG    6257      C  GC   GCG
                         TGCGCGCGCA CTG  GGGAG
                         |||||||||| ||| |||||
                         ACGCGCGCGT GGC  CCTTC
                           C  AA   III
GAM402  TPR          TGCGCGCGCAGCCGTTGGAAG    6257      C  GC  I
                         GCGCGCGCA CTG  GGGA
                         ||||||||| ||| ||||
                         CGCGCGCGT GGC  CCTT
                           C  AA  I
GAM402  VIPR2          GCGTGAACC---CGGGAGGCG   6230 C  C__  TGG
                         GCG  ACC  CGGGAGGC
                         ||| |||  |||||||||
                         CGC  TGG  GCCCTCCG
                          _  ACT  ___
GAM403  AKAP13          CATGGCCGAAGCAGAGTCT    6266 T  C      II
                         CAT GCC AGGCAGAGTC
                         ||| ||| ||||||||||
```

```
                          GTA CGG TTCGTCTCAG
                           C   C        AI
GAM403 AKAP13          CATGGCCGAAGCAGAGTCT       6266 GTGCCATT  C
                          GCC AGGCAGAGTCT
                          ||| |||||||||||
                          CGG TTCGTCTCAGA
                       _____       C
GAM403 APOB48R         TGCTATGCTGCCCAGGCTG-GTCTC 6280 ___   CAT       AGA   I
                          GTGC TGCCCAGGC GTCTC
                          |||| ||||||||| |||||
                          TACG ACGGGTCCG CAGAG
                          CGA   ___       AC_   T
GAM403 APOB48R         TGCTATGCTGCCCAGGCTG-GTCTC 6280 _____ CAT       AGA   I
                           GC TGCCCAGGC GTCT
                           || ||||||||| ||||
                           CG ACGGGTCCG CAGA
                          GATA   ___       AC_   I
GAM403 ASL             TGTG---TTGCCCAGGCTGTGTC 6287    CCA       AGAI
                          TGTG TTGCCCAGGC
                          |||| ||||||||||
                          ACAC AACGGGTCCG
                             ___       ACAC
GAM403 ASL             TGTG---TTGCCCAGGCTGTGTC 6287    GCCAT     AGA
                          GTGT TGCCCAGGC GT
                          |||| ||||||||| ||
                          CACA ACGGGTCCG CA
                       _____        ACA
GAM403 CBFA2T1         GTGCGCC--TGCC-AGGCAGAG   6276     AT  C     T
                          GTGTGCC TGCC AGGCAGAG
                          ||||||| |||| ||||||||
                          CACGCGG ACGG TCCGTCTC
                             __  _      I
GAM403 CBFA2T1         GTGCGCC--TGCC-AGGCAGAG   6276 _   AT  C
                          TGTGCC TGCC AGGCAGA
                          |||||| |||| |||||||
                          ACGCGG ACGG TCCGTCT
                       C   __  _
GAM403 CDH5            GCCTTTGCCTCCAGGCAGA      6268 A  __    III
                          GCC TTGCC CAGGCAG
                          ||| ||||| ||||||||
                          CGG AACGG GTCCGTC
                           A  AG   TII
GAM403 CDH5            GCCTTTGCCTCCAGGCAGA      6268 GTG  ATTGC    GT
                          TGCC   CCAGGCAGA
                          ||||   |||||||||
                          ACGG   GGTCCGTCT
                       A__  A____     AT
GAM403 EIF2C1          TGTCATTGCCCAAAGCTGATTCTC 6281 GC      _ A G  I
                          CATTGCCCAG GC GA TCT
                          |||||||||| || || |||
```

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                              GTAACGGGTT CG CT AGA
                              A_        T  A  A   I
GAM403 EIF2C1         TGTCATTGCCCAAAGCTGATTCTC  6281 GTGC      _  A  G   I
                          CATTGCCCAG GC GA TCTC
                          |||||||||| || || ||||
                          GTAACGGGTT CG CT AGAG
                              CA__      T  A  A   A
GAM403 EPB42          TGTGCCAGGAGGCCCAGGCAG  6284     TT__      III
                          TGTGCCA  GCCCAGGCA
                          |||||||  |||||||||
                          ACACGGT  CGGGTCCGT
                            CCTC      CII
GAM403 EPB42          TGTGCCAGGAGGCCCAGGCAG  6284 GT   TT__      AGTC
                          GTGCCA  GCCCAGGCAG
                          ||||||  ||||||||||
                          CACGGT  CGGGTCCGTC
                          __       CCTC      CIII
GAM403 FZD4           GTGCCATTGCGCCCCAGCCTGGGT  6269 __  ATT  CA CAGI
                          GTGCC  GCC  GG
                          |||||  |||  ||
                          CGCGG  CGG  CC
                          AA    GGT  AC  AIII
GAM403 FZD4           GTGCCATTGCGCCCCAGCCTGGGT  6269 GTGT    _  A_  AGAGTCI
                          GCCATTGC CC GGC
                          |||||||| || |||
                          CGGTAACG GG TCG
                          ____        C  GG   GACCCAT
GAM403 IL2RA          TGCTATGCTGCCCAGGCTG-GTCTC  6280 ___  CAT    AGA   I
                          GTGC  TGCCCAGGC  GTCTC
                          ||||  |||||||||  |||||
                          TACG  ACGGGTCCG  CAGAG
                          CGA    ___      AC_  T
GAM403 IL2RA          TGCTATGCTGCCCAGGCTG-GTCTC  6280 ____  CAT    AGA   I
                          GC  TGCCCAGGC  GTCT
                          ||  |||||||||  ||||
                          CG  ACGGGTCCG  CAGA
                          GATA   ___      AC_   I
GAM403 IL6R          CATTGCCCAGGCTGA-TCTC     6267 _      A  G   I
                          ATTGCCCAGGC GA TCT
                          |||||||||||| || |||
                          TAACGGGTCCG CT AGA
                          G         A _  I
GAM403 IL6R          CATTGCCCAGGCTGA-TCTC     6267 GTGCCATT    A  G
                          GCCCAGGC GA TCT
                          |||||||| || |||
                          CGGGTCCG CT AGA
                          _____          A _
GAM403 MHC2TA          GTGTGAC-TT---CAGGCAGAG    6277     CCATT C_
                          GTGTG   GC CAGGCAGAG
                          |||||   || |||||||||
```

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                                CACAC    TG GTCCGTCTC
                                _____   AA
GAM403 MHC2TA          TGCCATTG-CAAGACACAG      6282      CC   GAI
                       TGCCATTGC AGGCA
                       ||||||||| |||||
                       ACGGTAACG TCTGT
                              T_  GTC
GAM403 MHC2TA          TGCCATTG-CAAGACACAG      6282 GT     CC   G TC
                        GCCATTGC AGGCA AG
                        |||||||| ||||| ||
                        CGGTAACG TCTGT TC
                         __       T_ G CI
GAM403 MHC2TA          TGCCATTG-CAAGACACAG      6282 GTGTGC    CC   G
                         CATTGC AGGCA AG
                         |||||| ||||| ||
                         GTAACG TCTGT TC
                        _____    T_  G
GAM403 MSX1            TGCCGCCGCGCAGGCAGAGT      6283 A    C       I
                       GCC TTGC CAGGCAGAG
                       ||| |||| |||||||||
                       CGG GGCG GTCCGTCTC
                          C   C       I
GAM403 MSX1            TGCCGCCGCGCAGGCAGAGT      6283 GT A    C       CT
                       GCC TTGC CAGGCAGAGT
                       ||| |||| ||||||||||
                       CGG GGCG GTCCGTCTCA
                        __ C   C       AI
GAM403 MSX1            TGCCGCCGCGCAGGCAGAGT      6283 GTGT ATT C
                       GCC  GC CAGGCAGAGT
                       |||  || ||||||||||
                       CGG  CG GTCCGTCTCA
                       G___ ___ C
GAM403 NPR2           GTG-GCCATTGCCCACCCAG       6275  T      GG AGT
                      GTG GCCATTGCCCA CAG
                      ||| |||||||||||| |||
                      CAC CGGTAACGGGT GTC
                       _        GG III
GAM403 NPR2           GTG-GCCATTGCCCACCCAG       6275 _ T      GG I
                       TG GCCATTGCCCA CA
                       || |||||||||||| ||
                       AC CGGTAACGGGT GT
                       C _       GG I
GAM403 OAS3           GTG-GCCATTGCCAAAGACTGAG    6273  T      C_ A TC
                      GTG GCCATTGCC AGGC GAG
                      ||| ||||||||| |||| |||
                      CAC CGGTAACGG TCTG CTC
                       _       TT A II
GAM403 OAS3           GTG-GCCATTGCCAAAGACTGAG    6273  T      C_ AGAI
                       TG GCCATTGCC AGGC
                       || ||||||||| ||||
```

```
                          AC CGGTAACGG  TCTG
                            _    TT    ACTI
GAM403  PNUTL2        GTGTGGATTTGCCCAGGCCAGACTC 6274    CCA       _ G II
                        GTGTG  TTGCCCAGGC AGA TC
                        IIIII  IIIIIIIIIII III II
                        CACAC   AACGGGTCCG TCT AG
                          CTA        G  G II
GAM403  PNUTL2        GTGTGGATTTGCCCAGGCCAGACTC 6274  CCA       _ GTI
                        GTG  TTGCCCAGGC AGA
                        III  IIIIIIIIIII III
                        CAC  AACGGGTCCG TCT
                         CTA      G  GII
GAM403  PNUTL2        TTGCCCAGGCCAGACTCTC       6288      _ G II
                        TTGCCCAGGC AGA TCT
                        IIIIIIIIII III III
                        AACGGGTCCG TCT AGA
                          G  G  GI
GAM403  RECQL5        TGCCATGTTGCCCAGGCTG-GTC  6278 G  __     AGAGTI
                         CCAT TGCCCAGGC
                         IIII IIIIIIIIII
                         GGTA ACGGGTCCG
                          _  CA       ACCAII
GAM403  RECQL5        TGCCATGTTGCCCAGGCTG-GTC  6278 GTGTGCCA     AGA
                           TTGCCCAGGC  GTC
                           IIIIIIIIII  III
                           AACGGGTCCG  CAG
                        GTAC____        AC_
GAM403  RECQL5        TGCCATGTTGCCCAGGCTG-GTCT 6279 G  __     AGA I
                          CCAT TGCCCAGGC  GTC
                          IIII IIIIIIIII  III
                          GGTA ACGGGTCCG  CAG
                          _ CA       AC_  I
GAM403  RECQL5        TGCCATGTTGCCCAGGCTG-GTCT 6279 GT  __     AGA  I
                          GCCAT TGCCCAGGC  GTCTC
                          IIIII IIIIIIIII  IIIII
                          CGGTA ACGGGTCCG  CAGAG
                          __ CA       AC_  I
GAM403  SLC4A8        ATTGCCCAGGC-TAGTCTC     6264      AG  I
                        ATTGCCCAGGC AGTCT
                        IIIIIIIIIII IIIII
                        TAACGGGTCCG TCAGA
                          A_    G
GAM403  TNFRSF1A      GTGC--TTGTCCAGGCAGAG     6271   CA C     TC
                        GTGC TTG CCAGGCAGAG
                        IIII III IIIIIIIIII
                        CACG AAC GGTCCGTCTC
                          __  A      II
GAM403  TNFRSF1A      GTGC--TTGTCCAGGCAGAG     6271 _ CA C     I
                        TGC TTG CCAGGCAGA
                        III III IIIIIIIII
```

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                                     ACG  AAC GGTCCGTCT
                                      C  __   A         I
GAM403 TNFRSF1A        TGTGC--TTGTCCAGGCAGAG    6286 _   CA   C        I
                         GTGC TTG CCAGGCAGA
                         |||| ||| |||||||||
                         CACG  AAC GGTCCGTCT
                            A  __   A         I
GAM403 TNFRSF1A        TGTGC--TTGTCCAGGCAGAG    6286 GT  CA   C        T
                         GTGC TTG CCAGGCAGAG
                         |||| ||| ||||||||||
                         CACG  AAC GGTCCGTCTC
                          __  __   A       C
GAM403 TNXB        GTGGCAGTGACGGGGCAGAGTC    6272   C  T CCCA       TC
                        GTG CA TG   GGCAGAGTC
                        ||| || ||   |||||||||
                        CAC GT AC   CCGTCTCAG
                         C   C TGCC       ||
GAM403 TNXB        GTGGCAGTGACGGGGCAGAGTC    6272   C  T CCCA      I
                        TG CA TG   GGCAGAGT
                        || || ||   ||||||||
                        AC GT AC   CCGTCTCA
                         C   C TGCC      I
GAM403 WSX1        ATTGCCCAGGCTG-GTCTC    6265        AGA   I
                        ATTGCCCAGGC  GTCT
                        |||||||||||  ||||
                        TAACGGGTCCG  CAGA
                           AC_   G
GAM403 XRCC3        GTGCCACGGCCCAGGCAGA    6270      T     GTCT
                        GTGCCAT GCCCAGGCAGA
                        ||||||| ||||||||||
                        CACGGTG CGGGTCCGTCT
                           C      IIIC
GAM403 XRCC3        GTGCCACGGCCCAGGCAGA    6270      T     II
                        GTGCCAT GCCCAGGCAG
                        ||||||| |||||||||
                        CACGGTG CGGGTCCGTC
                           C      TI
GAM403 XRCC3        TGTGCCACGGCCCAGGCAGA    6285      T    I
                        GTGCCAT GCCCAGGCAG
                        ||||||| |||||||||
                        CACGGTG CGGGTCCGTC
                           C      I
GAM403 XRCC3        TGTGCCACGGCCCAGGCAGA    6285 GT   T      GT
                        GTGCCAT GCCCAGGCAGA
                        ||||||| ||||||||||
                        CACGGTG CGGGTCCGTCT
                          __     C      GI
GAM404 AMT        CCTGGCAGAGTGGGAGAGATG    6291 TGTCCT    CTT _  C
                        GGCAGAG  GAG GATG
                        |||||||  ||| ||||
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                        CCGTCTC  CTC CTAC
                        _____       ACC  T  C
GAM404 DRD2       TGCCCTGGCAGAG--TGAGGGTG  6303      CT   ATGC
                        TGTCCTGGCAGAG TGAGG
                        |||||||||||| |||||
                        ACGGGACCGTCTC ACTCC
                             __     CACl
GAM404 MANBA       GTCCTGGCACAGATTCCAGGA   6296 TG    G C_ G  GC
                        TCCTGGCA AG  TT AGGAT
                        ||||||| || || |||||
                        AGGACCGT TC  AG TCCTG
                            __      G TA G   ||
GAM404 MAPK8IP1       TGTCCTGGCACTGGCCTGAGG    6302        GA_     ATGC
                        TGTCCTGGCA  GCTTGAGG
                        ||||||||||  ||||||||
                        ACAGGACCGT  CGGACTCC
                              GAC      |||C
GAM404 PER2       CTGGCAGAGGCCTGAAGCTGC   6293 TGTCCTGG   _    A
                        CAGAG CTTGAGG TGC
                        ||||| ||||||| |||
                        GTCTC GGACTTC ACG
                        _____      C   G
GAM404 PML       GTCAGGGCAGAGCTGTAAGGA   6295 TGTCCT     _    GC
                        GGCAGAGCT TGAGGAT
                        ||||||||| |||||||
                        CCGTCTCGA ATTCCTG
                        AGTC__      C   ||
GAM404 PML       TCCTGGCAGAGGCCTAGTGGA   6299 TGTC     _ A_ TGC
                        CTGGCAGAG CTTG GGA
                        ||||||||| |||| |||
                        GACCGTCTC GGAT CCT
                        ____      C  CA  CTI
GAM404 RXRA       GTCCTGGCAGGCCAGCTTCCAAGCATGC6294 TG      ___  __ G  |||
                        TCCTGGCAG  AGCTT GAG ATGC
                        |||||||||  ||||| ||| ||||
                        AGGACCGTC  TCGAA TTC TACG
                        __      CGG   GG  G  G||
GAM404 RXRA       TCCTGGCAGTGCCTG-GGA      6301 TGTC    A   A  T
                        CTGGCAG GCTTG GGA
                        ||||||| ||||| |||
                        GACCGTC CGGAC CCT
                        ____      A  _  C
GAM404 SHANK2       CTGGGCACAGAACT-GAGGATGC   6292 TGTCCTG     T
                        GCAGAGCT GAGGATGC
                        ||||||||| |||||||||
                        TGTCTTGA CTCCTACG
                        CG_____         _
GAM404 TACC1       GTCCAGTAAGAGCTTGAGGA   6298 TG  TGGC       TG
                        TCC  AGAGCTTGAGGA
                        |||    |||||||||||
```

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                                       AGG   TCTCGAACTCCT
                                        __   TCAT         TI
GAM404  TCF1         TCCTGGCAGTGC-TCAGGA       6300 TGTC    A   G
                              CTGGCAG GCTT AGGAT
                              ||||||| |||| |||||
                              GACCGTC CGAG TCCTG
                                 ____      A   _
GAM404  TIMM44         GTCCTGGCAGAGCTGGGGG       6297 TG       T A ATG
                              TCCTGGCAGAGCT G GG
                              ||||||||||||| | ||
                              AGGACCGTCTCGA C CC
                                __          _ C  CGI
GAM405  ARHGEF1          TCCCTGGGCTC----TGCAAGGCT 6310   A  ACCCAG
                              TCCC GGGC    TGCAAGGC
                              |||| ||||    ||||||||
                              AGGG CCCG    ACGTTCCG
                                A  AG____
GAM405  ASCL2           CCCAGGGCACGC-GTCCTAGG    6308 TC     CCA GCA  C
                              CCAGGGCAC GT AGG
                              ||||||||| || |||
                              GGTCCCGTG CA TCC
                                __      CG_ GGA A
GAM405  CD80          CCAGGGCACTTCCCAGGTGCAA    6307 TCCC    ___  _    CT
                              AGGGCA  CCCAG TGCAAGG
                              ||||||  ||||| |||||||
                              TCCCGT  GGGTC ACGTTTT
                                ____     GAA  C    II
GAM405  MADD         CAGGGCACCAA--GCAAGG       6306 TCCCAG    CAGT
                              GGCACC  GCAAGG
                              ||||||  ||||||
                              CCGTGG  CGTTCC
                              _____   TT__
GAM405  TP53BP1      TCCCAGGG--CCCGGGGCAAGG    6309       A CAGT   C
                              TCCCAGGGC CC  GCAAGG
                              ||||||||| ||  ||||||
                              AGGGTCCCG GG   CGTTCC
                                _ CCC_   I
GAM406  ATP2B2        GTACAGGGAAACCTGCGCCG    6325 TG      A  A CA
                              TACAGGGAGGC TGC CCG
                              ||||||||||| ||| |||
                              ATGTCCCTTTG ACG GGC
                                __      G  C  CI
GAM406  CKMT1         ACAGGGAGGGAGGATGCAACCG   6313 TGTAC    C  _  CAG
                              AGGGAGG ATGCA CCG
                              ||||||| ||||| |||
                              TCCCTCC TACGT GGC
                              CCC__    _  T CTA
GAM406  DVL1         ACAGGGGGCCTGTGCACCGCAG   6314 TGTACA  A  A__
                              GGG GGC  TGCACCGCAG
                              ||| |||  ||||||||||
```

```
                        CCC CCG   ACGTGGCGTC
                        _____  _  GAC
GAM406  EGLN1        CAGGGAGGCCGGCACCCCA      6323 TGTACAGG    AT    G
                        GAGGC  GCACC CA
                        |||||  ||||| ||
                        CTCCG  CGTGG GT
                                 GC   G
GAM406  FANCE        TGTAACAGGGAGGCAGTTGCA     6326   _     __   CCGCAG
                        TGTA CAGGGAGGCA  TGCA
                        |||| |||||||||| ||||
                        ACAT GTCCTCCGT  ACGT
                         T     CA   |||GAC
GAM406  GPR44        ACAGGGAGGC-TGGTCCGC       6316 TGTACA    A  CA
                         GGGAGGC TG  CCGC
                         |||||||| ||  ||||
                         CCCTCCG AC  GGCG
                         _____      _ CA
GAM406  GYG          TGTACAGGGTGCCACTGCA       6327       AG  ATG  C
                        TGTACAGGG GC  CAC GCA
                        ||||||||| ||   ||| |||
                        ACATGTCCC CG   GTG CGT
                         A_  ___   A
GAM406  ITGAL        ACAGGGAGGCAT-CACGGC       6317 TGTACA      G   C
                          GGGAGGCAT CAC GC
                          ||||||||| ||| ||
                          CCCTCCGTA GTG CG
                        _____       _ C
GAM406  ITIH4        TGTACAGGGTGG---GCACAGC    6328       A  CAT   C  A
                        TGTACAGGG GG   GCAC GC
                        ||||||||| ||   |||| ||
                        ACATGTCCC CC   CGTG CG
                         A ___   T |
GAM406  MB           ACAGGGAGGC--GCATCGC       6315 TGTACA     AT   C
                         GGGAGGC GCA CGC
                         ||||||| ||| |||
                         CCCTCCG CGT GCG
                        _____      __  A
GAM406  PABPC4       CACGGCCGCA-GCACCGCAG      6324 TGTACAGGGAG  T
                          GCA GCACCGCA
                          ||| |||||||||
                          CGT CGTGGCGT
                        CGG_____  _
GAM406  PDGFB        CAGGGAGGCAGGCAGGCCGC      6321 TGTA  G  A  A GCA
                         CAGG AGGC TGC CC
                         |||| |||| ||| ||
                         GTCC TCCG GCG GG
                         CTCC  G  _  A GII
GAM406  PRKCABP      CAGGGAGGCAGGCGCCCCA       6322 TGTACAGG    T  A  G
                         GAGGCA GC CC CA
                         |||||| || || ||
```

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                         CTCCGT CG GG GT
                   _____      C  C  G
GAM406  SERPIND1      ACAGGGAGGCA---ACAGCAG    6318 TGTACA      T  CC
                         GGGAGGCA GCA  GC
                         |||||||| ||| ||
                         CCCTCCGT TGT  CG
                   _____        _  __
GAM406  SLC29A1       ACAGGGAGGGAGGCA-GGCAG    6319 TGTAC      T __ GCA
                         AGGGAGGCA GCA  CC
                         ||||||||| ||| ||
                         TCCCTCCGT CGT  GG
                   CCC__        C  CA III
GAM406  WNT1          CAGGGAGGCATGGCTCACAGC    6320 TGTACAGG      CAC
                          GAGGCATG  CGCAG
                          |||||||| |||||
                          CTCCGTAC  GTGTC
                   _____        CGA
GAM407  APPL          AAGGGGGAAA-AAAGATCA      6336 TGAAAG    C    A
                          GGGGAAA AAAGA CA
                          ||||||| ||||| ||
                          CCCCTTT TTTCT GT
                   _____      _  A
GAM407  ATP6V1A1      AAACAGGGAAACAAATAACA     6331 TGAAAG       G  G
                          GGGGAAACAAA AACA
                          ||||||||||| ||||
                          TCCCTTTGTTT TTGT
                   TG____        A  G
GAM407  CASP2          GAAAGCAGGAA-CAAAGAAC    6347 TG  G   A    AG
                          AAAG GGGAA CAAAGAAC
                          |||| ||||| ||||||||
                          TTTC TCCTT GTTTCTTG
                   __  G  _   AI
GAM407  CCND1          TGGAAGGGGGAAAGAGCAAAG   6351 A      ___   AACAGC
                          TG AAGGGGGAAA  CAAAG
                          || |||||||||  |||||
                          AC TTCCCCCTTT  GTTTC
                   C      CTC  IIICGA
GAM407  CD1A          GAAAGGGGGGATCTAAATAACTGC 6346 TG    AAACAAAG_ A I
                          AAAGGGGG    AAC GC
                          ||||||||    ||| ||
                          TTTCCCCC    TTG CG
                   __      CTAGATTTA A T
GAM407  CDK2AP1       TGAAAAGG---AACAAAGAACA   6356       GAA      G
                          TGAAAGGGG ACAAAGAACA
                          ||||||||| ||||||||||
                          ACTTTTCCT TGTTTCTTGT
                   ___          I
GAM407  COL11A1       GAGAGGGGGAAAAAGTCAAAG    6345 TGAA     ____   AACAGC
                          AGGGGGAAA   CAAAG
                          |||||||||   |||||
```

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                      TCCCCCTTT  GTTTC
                    TC__        TTCA   CIIICG
GAM407 DPYSL3       AGGGGACGTGACAAAGAACAG    6339 TGAAAGGGGGAA      C
                        ACAAAGAACAG
                        ||||||||||
                        TGTTTCTTGTC
                    CTGCAC_____        T
GAM407 GBE1         TGAAAAAAAGAAACAAAGAA    6355          CAG
                        TGAAAGGGGGAAACAAAGAA
                        |||||||||||||||||||
                        ACTTTTTTTCTTTGTTTCTT
                                   III
GAM407 GBF1         AGTGGGAAACAAAGTGCAG     6340 TGAAAGGG        AA
                        GGAAACAAAG  CAG
                        ||||||||||  |||
                        CCTTTGTTTC  GTC
                        _____         AC
GAM407 HS2ST1       AAGGGGGAAAAAAAAATCAG    6335 TGAAA    C   A  C
                        GGGGGAAA AAAGA CAG
                        |||||||| ||||| |||
                        CCCCTTTT TTTTT GTC
                        _____     T   A  T
GAM407 KLHL3        GAATAGGGGGAAAGCACAAGAA  6341 TGAA      _ _    CAGC
                        AGGGGGAAA CA AAGAA
                        ||||||||| || |||||
                        TCCCCCTTT GT TTCTT
                    TTA_       C G   TIII
GAM407 NSD1         AAGGGGGAAAGAAAGAAAAG    6338 TGAAAG    C   C
                        GGGGAAA AAAGAA AG
                        ||||||| |||||| ||
                        CCCCTTT TTTCTT TC
                        _____    C   T
GAM407 NXF2         TGAAAAGAGGAAACAAAGA     6354          ACAG
                        TGAAAGGGGGAAACAAAGA
                        ||||||||||||||||||
                        ACTTTTCTCCTTTGTTTCT
                                   IIIC
GAM407 NXF5         TGAAAAGAGGAAACAAAGA     6354          ACAG
                        TGAAAGGGGGAAACAAAGA
                        ||||||||||||||||||
                        ACTTTTCTCCTTTGTTTCT
                                   IIIC
GAM407 PBX3         TGAA---GGGAAACAAAGA     6353 TGA A       AC
                        A GGGGGAAACAAAGA
                        | |||||||||||||
                        A TTCCCTTTGTTTCT
                        ___ C        II
GAM407 PCLO         TGGATGGTGGAAACAAAGGAGAAACAGC6352 TGAAA  G        ____    III
                        GG GGAAACAAAG  AACAGC
                        || |||||||||  ||||||
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                          CC CCTTTGTTTC   TTGTCG
                       ACCTA  A         CTCT      III
GAM407  PDCL           AAAAGGGACTACAAAGAACAGC   6332 TGAA    AA
                           AGGGGG  ACAAAGAACAGC

                           IIIIII  IIIIIIIIIII
                           TTCCCT  TGTTTCTTGTCG
                           ____         GA
GAM407  POLG            GGGGGACAGAACAAAGAACCAGC   6349 TGAAAGGG   A     _  I
                              GGAA CAAAGAAC AGC

                              IIII IIIIIIII III
                              TCTT GTTTCTTG TCG
                         TG_____  _     G  G
GAM407  PTPRJ           AAGGGGGAAAAAAAAAAAAG     6337 TGAAAG    C    C
                              GGGGAAA AAAGAA AG

                              IIIIIIII IIIIII II
                              CCCCTTT TTTTTT TC
                              _____     T   T
GAM407  RAP1           TGAGAAGGGCTCCAAAAAAAGAACAGC6350  A   ____   C      III
                              TGA AGGGG  GAAA AAAGAACAGC

                              III IIIII   IIII IIIIIIIIII
                              ACT TTCCC   TTTT TTTCTTGTCG
                               C  GAGG  _      III
GAM407  RNF4           GAAGGGGTTGGAAACAAAAGAGCAG  6343 TGA    ___    _ A CII
                              AAGGGG  GAAACAAA GA CAG

                              IIIIII  IIIIIIII II III
                              TTCCCC  CTTTGTTT CT GTC
                              ___     AAC    T C AII
GAM407  RORB           AAGGGGGAAA-AAAGGAAACAG   6334 T__         AAGAACAGC
                               GAAAGGGGGAAACA

                               IIIIIIIIIIIIII
                               CTTTTTTCCTTTGT
                         CCC           CTTTIIICG
GAM407  RRM2B            GAAATGGTGGGAAACAAAGA     6342 TGAAA _       ACAG
                              GG GGGAAACAAAGA

                              II IIIIIIIIIIII
                              CC CCCTTTGTTTCT
                         TTTA_  A         CIII
GAM407  TAT            GAAAGAAAGAAACAAAGAAAG   6348 TG  GG      C C
                              AAAG GGAAACAAAGAA AG

                              IIII IIIIIIIIIII II
                              TTTC TCTTTGTTTCTT TC
                              __   TT      T T
GAM407  TNFRSF17        AAGGGAGCTACAGAAAGAACAGC  6333 TGAAAG  AA __      I
                              GGGG ACA AAGAACAGC

                              IIII III IIIIIIII
                              CCTC TGT TTCTTGTCG
                              _____   GA  CT    G
GAM407  VAMP1           GAAAGGGGGATAGCAGAGACACA  6344 TG     AA_ A _ GCI
                              AAAGGGGGA  CA AGA ACA

                              IIIIIIIII  II III III
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                        TTTCCCCCT  GT TCT TGT
                        __    ATC  C  G  GII
GAM408  ALS2        CAAATCATTCCTTCTTTACAG      6363 TCAA_  GC      TGCT
                        ATTT  TCTTTACAGG
                        IIII IIIIIIIIII
                        TAAG  AGAAATGTCT
                        TTTAG  GA       IIIT
GAM408  ATP11B      CAAACT-GATCTTTACAGG      6365 TCAAAT  C      TG
                        TTG TCTTTACAGG
                        III IIIIIIIIII
                        GAC AGAAATGTCC
                        TTT___  T     TI
GAM408  ESR1        AAAATTG---TTTACAGGTGCT    6362 TCAAATTTGCTC
                        TTTACAGGTGC
                        IIIIIIIIIII
                        AAATGTCCACG
                        TTAAC_____
GAM408  F2R         TCTACTTTGCTCTTGAGGGCAGGT 6368 AAA      TA___    GCTI
                        TC TTTGCTCTT   CAGGT
                        II IIIIIIIII    IIIII
                        AG AAACGAGAA    GTCCA
                        ATG       CTCCC   IIIT
GAM408  FBXL7       AAATTTGCTTTGTTCAGGT      6361 TCAA     CTTTA   GC
                        ATTTGCT   CAGGT
                        IIIIIII    IIIII
                        TAAACGA   GTCCA
                        ____      AACAA    AA
GAM408  KIF5C       AAATTTGCTTTGCATTTTAACAGGTGC6360 TCAAA_  TC  _     III
                        TTTGC TTTA CAGGTGCT
                        IIIII IIII IIIIIIII
                        AAACG AAAT GTCCACGG
                        TAAACG  TA  T    TII
GAM408  KL          AAATTACTTCTCTTTACAG      6359 TCAA  G      GTGC
                        ATTT CTCTTTACAG
                        IIII IIIIIIIIII
                        TGAA GAGAAATGTC
                        TAA_   _      AGII
GAM408  MME         TGCTCTGTTTCTTACAGGTGCT    6371 TCAAATTTGC   T
                        TCTT ACAGGTGCT
                        IIII IIIIIIIII
                        AGAA TGTCCACGA
                        AA_____   _
GAM408  PCDHB12     TCAAAAATACTACTTTACAGG     6366    TT  _      TGCT
                        TCAAA TGCT CTTTACAGG
                        IIIII IIII IIIIIIIII
                        AGTTT ATGA GAAATGTCC
                        TT  T    IIIT
GAM408  PMCHL1      TCAACCTT-CTCTTTACAG       6369   ATTTG      GTG
                        TCAA  CTCTTTACAG
                        IIII   IIIIIIIIII
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                          AGTT    GAGAAATGTC
                          GGAA_         III
GAM408 PTGS2              TCAAACAAGCT-TTTACAGGTG  6370    TT  C      CT
                          TCAAAT GCT TTTACAGGTG
                          IIIIII III IIIIIIIIII
                          AGTTTG CGA AAATGTCCAC
                          TT  _        II
GAM408 SNX6              CAAGTGTTGTTCTTTACAG  6364 TCAAAT  C      GTGC
                          TTG TCTTTACAG
                          III IIIIIIIII
                          AAC AGAAATGTC
                          TTCAC_  A      GIII
GAM408 TRPC5            TCCATTTTGCTCTTCTCCAGG  6367 AAA       A_   TGCT
                          TC  TTTGCTCTTT CAGG
                          II  IIIIIIIIII IIII
                          AG  AAACGAGAAG GTCC
                           GTA        AG  IIIT
GAM409 BBS2            TGTGAT-C-CAA--AGCAAACCAG  6379    G T  TC
                          TGTGAT C CAA  AGCAAACCA
                          IIIIII I III  IIIIIIIII
                          ACACTA G GTT  TCGTTTGGT
                                  _ _  __
GAM409 BBS2            TGTGAT-C-CAA--AGCAAACCAG  6379 _   G T  TC
                           GTGAT C CAA  AGCAAACCA
                          IIIII I III  IIIIIIIII
                           CACTA G GTT  TCGTTTGGT
                          A   _ _  __
GAM409 CD3Z            TGCACCACCGGCAAACCAG      6377  TCA  A    II
                          TGC  ATC GCAAACCA
                          III  III IIIIIIII
                          ACG  TGG CGTTTGGT
                           TGG  C     CI
GAM409 GNS            GTGAAGTGCTCAATCTGAAA     6374  __       AGCAIII
                          GTGA TGCTCAATC
                          IIII IIIIIIIII
                          CACT ACGAGTTAG
                          TC      ACTTTII
GAM409 GNS            GTGAAGTGCTCAATCTGAAA     6374 TG __       AGCAAACCA
                          TGA TGCTCAATC
                          III IIIIIIIII
                          ACT ACGAGTTAG
                          __ TC       ACTTTAIII
GAM409 KRT15         GTGA-GTTC--TCAGCAAACC    6376 TGATGCTCAA
                              TCAGCAAAC
                              IIIIIIIII
                              AGTCGTTTG
                          CACTCAAG__
GAM409 KRT15         GTGA-GTTC--TCAGCAAACC    6376 TGTGATGCTCAA
                              TCAGCAAACC
                              IIIIIIIIII
```

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                              AGTCGTTTGG
                         ACTCAAG_____
GAM409  MICB         GTGAATGCCC--TCAGCAAACC   6375 T T      AA       A
                            G GATGCTC  TCAGCAAACC
                            | |||||||  ||||||||||
                            A TTACGGG  AGTCGTTTGG
                            _ C       __        A
GAM409  MICB         GTGAATGCCC--TCAGCAAACC   6375 T__     AA       I
                              GATGCTC  TCAGCAAAC
                              |||||||  |||||||||
                              TTACGGG  AGTCGTTTG
                         CAC       __        I
GAM409  RAB36        TGTGAAGCTTATGCCCAGCAAACC  6378    T CAA__       AGI
                           TGTGA GCT    TCAGCAAACC
                           ||||| |||    ||||||||||
                           ACACT CGA    GGTCGTTTGG
                             T ATACG        III
GAM409  RAB36        TGTGAAGCTTATGCCCAGCAAACC  6378 GTG____     CAAT     I
                             ATGCT   CAGCAAAC
                             |||||   ||||||||
                             TACGG   GTCGTTTG
                         CTTCGAA    ____     I
GAM410  ABCA3        CCTCTGGAGTGGGGCAGGGCA    6384 C _    __        III
                             CC CTGGA GGGGCAGGGC
                             || ||||| ||||||||||
                             GG GACCT CCCCGTCCCG
                           _ A  CA        TII
GAM410  ABL1         GGCCCCC--GAGGG-CAGGGCAG   6407      TGGA      I
                            GGCCCCC  GGGGCAGGGC
                            |||||||  ||||||||||
                            CCGGGGG  TCCCGTCCCG
                              C___        T
GAM410  ABL1         GGCCCCC--GAGGG-CAGGGCAG   6407 TG     TGGA
                             GCCCCC  GGGGCAGGGCA
                             ||||||  |||||||||||
                             CGGGGG  TCCCGTCCCGT
                           __      C___
GAM410  ACP1         GGTCACCTGGAGGGAGTAGGGC    6401 GCCC      _ C   I
                              CCTGGAGGG G AGGG
                              |||||||||| | ||||
                              GGACCTCCC C TCCC
                           AGT_        T A    I
GAM410  ACP1         GGTCACCTGGAGGGAGTAGGGC    6401 TGGCCC     _ C   AG
                              CCTGGAGGG G AGGGC
                              |||||||||| | |||||
                              GGACCTCCC C TCCCG
                           CAGT__       T A   CI
GAM410  ACPT         GGCCCCCTGGAGGGCCAGCAGGG   6400 GCC       G  GI
                              CCCTGGAGGG CAG
                              |||||||||| |||
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                          GGGACCTCCC GTC
                          ___         G  GT
GAM410 ACPT           GGCCCCCTGGAGGGCCAGCAGGG  6400 TG         ___      CAGI
                          GCCCCCTGGAGGG  GCAGGG
                          ||||||||||||  ||||||
                          CGGGGGACCTCCC  CGTCCC
                          __          GGT     AIII
GAM410 ACPT           TGACCATCTTGAGGGGCAG      6415    CC G      GGCA
                          TGGCC  CT GAGGGGCAG
                          ||||| || |||||||||
                          ACTGG  GA CTCCCCGTC
                          TA  A       IIIG
GAM410 ACPT           TGACCATCTTGAGGGGCAG      6415    CC G      II
                          TGGCC  CT GAGGGGCA
                          ||||| || ||||||||
                          ACTGG  GA CTCCCCGT
                          TA  A      CI
GAM410 ADRA1A         GGCCACATGAAGGGGCAGGGCA  6404   CCC           I
                          GCC  TGGAGGGGCAGGGC
                          |||  |||||||||||||
                          CGG  ACTTCCCCGTCCCG
                          TGT           I
GAM410 ADRA1A         GGCCACATGAAGGGGCAGGGCA  6404 TG  CCC           G
                          GCC  TGGAGGGGCAGGGCA
                          |||  ||||||||||||||
                          CGG  ACTTCCCCGTCCCGT
                          __  TGT           A
GAM410 ALPP          GGCCCCCTGGGGGGGGTACAGGG  6402 GC     A  __  I
                          CCCCTGG GGGG  CAGG
                          ||||||| |||| ||||
                          GGGGACC CCCC  GTCC
                          __     C  AT  I
GAM410 ALPP          GGCCCCCTGGGGGGGGTACAGGG  6402 TG     A  __  CAG
                          GCCCCCTGG GGGG  CAGGG
                          ||||||||| |||| |||||
                          CGGGGGACC CCCC  GTCCC
                          __     C  AT  CII
GAM410 ALPPL2        TGGGCCCCTAGGAGGGGCA      6412 T_   CT      GGGCA
                          GGCCCC GGAGGGGCA
                          |||||| |||||||||
                          CCGGGG CCTCCCCGT
                          AC     AT      IIIGA
GAM410 ALPPL2        TGGGCCCCTAGGAGGGGCA      6412 T_   CT      II
                          GGCCCC GGAGGGGC
                          |||||| ||||||||
                          CCGGGG CCTCCCCG
                          AC     AT      TI
GAM410 ARNT2         TGGCCCC----AAGGGCAGGGCAG  6417      CTGG
                          TGGCCCC AGGGGCAGGGCA
                          ||||||| |||||||||||
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```
                          ACCGGGG   TTCCCGTCCCGT
                               ___
GAM410  ARNT2        TGGCCCC----AAGGGCAGGGCAG  6417 _    CTGG
                         GGCCCC  AGGGGCAGGGCA
                         |||||| ||||||||||||
                         CCGGGG  TTCCCGTCCCGT
                         A       ____
GAM410  AXUD1        GGCCTCCTGGGCAAGGGGCAGG   6396  C   ___      III
                         GGCC CCTGG  AGGGGCAG
                         |||| |||||  ||||||||
                         CCGG GGACC  TCCCCGTC
                          A   CGT     CII
GAM410  AXUD1        GGCCTCCTGGGCAAGGGGCAGG   6396 TG  C   ___       GCAG
                         GCC CCTGG  AGGGGCAGG
                         ||| |||||  |||||||||
                         CGG GGACC  TCCCCGTCC
                         __  A   CGT     GIII
GAM410  CACNA1D      TGCCCATCTGGACAATGGGGCAGGGCAG6413 GGCCCC    ____        I
                         CTGGA  GGGGCAGGGCA
                         ||||| |||||||||||
                         GACCT  CCCCGTCCCGT
                      TA____   GTTA        I
GAM410  CACNA1D      TGCCCATCTGGACAATGGGGCAGGGCAG6413 TG   C_   ____        III
                         GCCC CTGGA  GGGGCAGGGCAG
                         |||| |||||  ||||||||||||
                         CGGG GACCT  CCCCGTCCCGTC
                         A_  TA  GTTA        III
GAM410  CALR         TGGCCCAGTCCTGG--GGGCAGGGGAG6411     ___    AG     C II
                         TGGCCC  CCTGG  GGGCAGGG AG
                         ||||||  ||||| ||||||||| ||
                         ACCGGG  GGACC  CCCGTCCC TC
                          TCA   __       C II
GAM410  CALR         TGGCCCAGTCCTGG--GGGCAGGGGAG6411     ___    AG     CAI
                         GCCC  CCTGG  GGGCAGGG
                         ||||  ||||| ||||||||
                         CGGG  GGACC  CCCGTCCC
                          TCA   __       CII
GAM410  CAPN10       GCCCCCTGGCAGGGCTGGG      6388      A   A II
                         GCCCCCTGG GGGGC GG
                         ||||||||| ||||| ||
                         CGGGGGACC TCCCG CC
                          G   A CI
GAM410  CAPN10       GCCCCCTGGCAGGGCTGGG      6388 TGGC    A   A C
                         CCCCTGG GGGGC GGG A
                         ||||||| ||||| ||| |
                         GGGGACC TCCCG CCC T
                         ___      G   A _
GAM410  CAPN7        TGGCCCCGCGCCGGGGCAGGGAAG  6418     C GA     CAI
                         GGCCCC TG GGGGCAGGG
                         ||||||  ||  |||||||||
```

```
                        CCGGGG GC  CCCCGTCCC
                           C  GG       TTI
GAM410  CAPN7           TGGCCCCGCGCCGGGGCAGGGAAG  6418       C  GA        C  I
                           TGGCCCC TG  GGGGCAGGG  AG
                           ||||||| ||  |||||||||| ||
                           ACCGGGG GC  CCCCGTCCC  TC
                              C  GG        T  I
GAM410  CHRM1           TGGGCCAGGCCTGTGTGGGGCAGGGC  6410 __    CCC  GA        I
                              GGCC  TG  GGGGCAGGG
                              |||| ||  |||||||||
                              CCGG  AC  CCCCGTCCC
                           GT    AC_  A_          I
GAM410  CHRM1           TGGGCCAGGCCTGTGTGGGGCAGGGC  6410 T_   C__   GA_      AGII
                              GGCC  CCTG  GGGGCAGGGC
                              |||| ||||  ||||||||||
                              CCGG  GGAC  CCCCGTCCCG
                           AC    TCC  ACA        IIIG
GAM410  CYP46           TGGCCCAGGGGACGGGGCAGGGGAG  6414      CCT  _      C  II
                           TGGCCC  GGA GGGGCAGGG AG
                           |||||| ||| |||||||| ||
                           ACCGGG  CCT CCCCGTCCC TC
                              TCC  G       C  II
GAM410  CYP46           TGGCCCAGGGGACGGGGCAGGGGAG  6414      CCT  _      CAI
                              GCCC  GGA GGGGCAGGG
                              |||| ||| ||||||||
                              CGGG  CCT CCCCGTCCC
                              TCC  G       CII
GAM410  DYRK1B            GGCCCCAGGGAGGGGGCAGGG    6398 GC  T_    _   I
                             CCCC  GGAGGGG CAGG
                             |||| ||||||| ||||
                             GGGG  CCTCCCC GTCC
                             __    TC    C  I
GAM410  DYRK1B            GGCCCCAGGGAGGGGGCAGGG    6398 TG   CT    _   CA
                             GCCCC  GGAGGGG CAGGG
                             ||||| ||||||| |||||
                             CGGGG  CCTCCCC GTCCC
                             __    TC    C  II
GAM410  EPHX1           GGGCCTGTGAGAGAGGCAGGGCAG   6395    CCCT           I
                             GCC   GGAGGGGCAGGGCA
                             |||   |||||||||||||||
                             CGG   TCTCTCCGTCCCGT
                              ACAC           I
GAM410  EPHX1           GGGCCTGTGAGAGAGGCAGGGCAG   6395 T   CCCT           I
                              GGCC   GGAGGGGCAGGGCAG
                              |||| |||||||||||||||
                              CCGG   TCTCTCCGTCCCGTC
                             _  ACAC           C
GAM410  HTR6             GCCCCCTGGAGGGGGCGGGC      6389          CA  I
                             CCCCCTGGAGGGG  GGG
                             |||||||||||| |||
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                    GGGGGACCTCCCC CCC
                        CG   I
GAM410 HTR6          GCCCCCTGGAGGGGGCGGGC    6389 TGGC      CA   A
                        CCCCTGGAGGGG GGGC

                        |||||||||||| ||||
                        GGGGACCTCCCC CCCG
                    ____        CG   C
GAM410 KCNK4        TGCCCGCCTGGAGGGGCCGGGC   6416 G    _     A   I
                        GCCC CCTGGAGGGGC GGG

                        |||| ||||||||||| |||
                        CGGG GGACCTCCCCG CCC
                        _   C       G  I
GAM410 KCNK4        TGCCCGCCTGGAGGGGCCGGGC   6416 TG   _     A   AG
                        GCCC CCTGGAGGGGC GGGC

                        |||| ||||||||||| ||||
                        CGGG GGACCTCCCCG CCCG
                        A_   C       G  II
GAM410 LIF          GCCCCCTGGA--AGCAAGACAG   6390      GG    I
                        GCCCCCTGGA GGCAGGGC

                        |||||||||| ||||||||
                        CGGGGGACCT TCGTTCTG
                        __        T
GAM410 LIF          GCCCCCTGGA--AGCAAGACAG   6390 TGGC    GG
                        CCCCTGGA GGCAGGGCA

                        |||||||| |||||||||
                        GGGGACCT TCGTTCTGT

                        ____       __
GAM410 LPIN1       GCCCCGGGGTGGGGCAGGGGAG    6391    CT A     CAI
                        CCCC GG GGGGCAGGG

                        |||| || |||||||||
                        GGGG CC CCCCGTCCC
                        CC  A      CTI
GAM410 LPIN1       GCCCCGGGGTGGGGCAGGGGAG    6391 TGGC CT A     C
                        CCC GG GGGGCAGGG AG

                        ||| || ||||||||| ||
                        GGG CC CCCCGTCCC TC
                        ____  CC  A     C
GAM410 MAP3K14      CCCTCTGGCCAGGGGCAGGGCAG  6382 __    CCCTGG       I
                        TGGCC    AGGGGCAGGGCAG

                        |||||    |||||||||||||
                        ACCGG    TCCCCGTCCCGTC
                        AG   _____      C
GAM410 MAP3K14      CCCTCTGGCCAGGGGCAGGGCAG  6382 CCC    __       I
                        CTGG AGGGGCAGGGCA

                        |||| |||||||||||
                        GACC TCCCCGTCCCGT
                        A__  GG      I
GAM410 MAX          GGCCACCTGG----GCAGGGCAG  6406  C  A_    GI
                        GGCC CCTGG GGGGCAG

                        |||| ||||| ||||||
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                        CCGG GGACC  TCCCGTC
                           T   CG      II
GAM410 MAX              GGCCACCTGG----GCAGGGCAG  6406 TG  C   A_      GCA
                          GCC CCTGG  GGGGCAGG
                          ||| ||||| |||||||||
                          CGG GGACC  TCCCGTCC
                          __  T   CG      III
GAM410 NDST1           GGCCTTCTGGGGGTGCAGGGCAG  6408   CC  A  _     I
                          GCC  CTGG GGG GCAGGGCA
                          ||| |||| ||| ||||||||
                          CGG  GACC CCC CGTCCCGT
                               AA  _  A     I
GAM410 NDST1           GGCCTTCTGGGGGTGCAGGGCAG  6408 TG  CC  A  _     I
                          GCC  CTGG GGG GCAGGGCAG
                          ||| |||| ||| |||||||||
                          CGG  GACC CCC CGTCCCGTC
                          __   AA  _  A     G
GAM410 NRXN2          GGCCCTCCCAGGAGGGGCAGCTGGCAG6392 GCC  T      __  I
                          CCC GGAGGGGCAG  GGCA
                          ||| |||||||||| ||||
                          GGG CCTCCCCGTC  CCGT
                          A__  T       GA  I
GAM410 NRXN2          GGCCCTCCCAGGAGGGGCAGCTGGCAG6392 TG   _  _       __  III
                          GCCC CCT GGAGGGGCAG  GGCAG
                          |||| ||| |||||||||| |||||
                          CGGG GGG CCTCCCCGTC  CCGTC
                          __    A T       GA  AII
GAM410 PDE4A          GGCCCCGTGGGTGGGGGCAGGG  6397 GC  C  A__     I
                          CCC TGG  GGGGCAGG
                          ||| |||  |||||||||
                          GGG ACC  CCCCGTCC
                          __  C  CAC     I
GAM410 PDE4A          GGCCCCGTGGGTGGGGGCAGGG  6397 TG   C  A__      CAG
                          GCCCC TGG  GGGGCAGGG
                          ||||| |||  |||||||||
                          CGGGG ACC  CCCCGTCCC
                          __    C  CAC      CII
GAM410 PDE4A          GCCCATGGGAGGGGGGCAGGGCA  6387 ___  CCCCCT A        I
                          TGG    GG GGGGCAGGGCAG
                          |||    || |||||||||||
                          ACC    CC CCCCGTCCCGTT
                          GGT  CT____  _       C
GAM410 PDE4A          GCCCATGGGAGGGGGGCAGGGCA  6387 CCCCCT_ A       I
                          GG GGGGCAGGGC
                          || ||||||||||
                          CC CCCCGTCCCG
                          GTACCCT  _       I
GAM410 PDGFRB          TGGCCTCCCTGGAGGCAGAGGGC  6409    _    _ C   AGI
                          TGGCC CCCTGGAGG GG AGGGC
                          ||||| ||||||||| || |||||
```

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                        ACCGG GGGACCTCC TC TCCCG
                          A        G  _     III
GAM410 PDGFRB       TGGCCTCCCTGGAGGCAGAGGGC  6409 G  _      _  C   I
                        GCC CCCTGGAGG GG AGGG
                        III IIIIIIIII II IIII
                        CGG GGGACCTCC TC TCCC
                          _  A        G  _   I
GAM410 PLXNA1       CCCCCTGGAGGGCCCTGGC      6383        G AG_ II
                        CCCCCTGGAGGG C  GG
                        IIIIIIIIIIII I  II
                        GGGGGACCTCCC G  CC
                            _ GGA  GI
GAM410 PLXNA1       CCCCCTGGAGGGCCCTGGC      6383 TGGCCC      G AG_  A
                          CCTGGAGGG C  GGC
                          IIIIIIIII I  III
                          GGACCTCCC G  CCG
                        _____         _ GGA  G
GAM410 PRKCD        GGCTCCCGTTGCAGGGGCAGG    6394  _  C_ G      III
                        GGC CCC  TG AGGGGCAG
                        III III  II IIIIIIII
                        CCG GGG  AC TCCCCGTC
                          A  CA G     CII
GAM410 PRKCD        GGCTCCCGTTGCAGGGGCAGG    6394 TG _  C_ G      GCAG
                        GC CCC  TG AGGGGCAGG
                        II III  II IIIIIIIII
                        CG GGG  AC TCCCCGTCC
                         __ A  CA G       GIII
GAM410 PTPRS        CCCGGGAGGGGCAGAGGCA      6385  T      _ II
                        CCC GGAGGGGCAG GGC
                        III IIIIIIIIII III
                        GGG CCTCCCCGTC CCG
                          C      T  TI
GAM410 RPN1        GGCCCCCTGGAGGATGC-GGGCAG  6399           _ A   I
                        GCCCCCTGGAGGG GC GGGCA
                        IIIIIIIIIIII II IIIII
                        CGGGGGACCTCCT CG CCCGT
                            A _  I
GAM410 RPN1        GGCCCCCTGGAGGATGC-GGGCAG  6399 TG         _ A   I
                        GCCCCCTGGAGGG GC GGGCAG
                        IIIIIIIIIIII II IIIII
                        CGGGGGACCTCCT CG CCCGTC
                           __        A _   C
GAM410 SCRT1       GGCACCCTGGAGGGG-AGGGGAG   6405 _ C       C  CAI
                        GC CCCTGGAGGGG AGGG
                        II IIIIIIIIIII IIII
                        CG GGGACCTCCCC TCCC
                          C T        _  CTI
GAM410 SCRT1       GGCACCCTGGAGGGG-AGGGGAG   6405 TG C       C  C
                        GC CCCTGGAGGGG AGGG AG
                        II IIIIIIIIIII IIII II
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                           CG GGGACCTCCCC TCCC TC
                           __  T          _   C
GAM410 SLC22A12            CCTGGAGGGACATGGGGAG    6386         _  CAII
                           CCTGGAGGGGCA GGG
                           IIIIIIIIIII III
                           GGACCTCCCTGT CCC
                                A   CTCI
GAM410 SLC22A12            CCTGGAGGGACATGGGGAG    6386 T_  CCCCT      AGGGCA
                                GGC   GGAGGGGC
                                III   IIIIIIII
                                CTG   CCTCCCCG
                           CC  TACC_      GTIIIG
GAM410 SLC22A12            GGCTCACCTGGAGGGGCAG    6393  CC_        II
                                GGC  CCTGGAGGGGCA
                                III  IIIIIIIIIII
                                CCG  GGACCTCCCCGT
                                 AGT        CI
GAM410 SLC22A12            GGCTCACCTGGAGGGGCAG    6393 TG CC_        GGCA
                                GC  CCTGGAGGGGCAG
                                II  IIIIIIIIIIII
                                CG  GGACCTCCCCGTC
                                __  AGT        GIII
GAM410 SNX9               GGTCCCCTGGAGGGACATGG    6403 GGC         GI
                                CCCCTGGAGGGGCA
                                IIIIIIIIIIIII
                                GGGGACCTCCCTGT
                                A__        AC
GAM410 SNX9               GGTCCCCTGGAGGGACATGG    6403 TGGC          _ CA
                                CCCCTGGAGGGGCA GGG
                                IIIIIIIIIIIII III
                                GGGGACCTCCCTGT CCC
                           CA__          A II
GAM411 ABCA3              TCCTGGAGAGGCAGGGAAGGC   6434 TATCATCCT  TC
                                GG  GCAGGGAAGGC
                                II  IIIIIIIIIII
                                TC  CGTCCCTTCCG
                           C_____   TC
GAM411 ARHGDIA            CAGCCCTGTC-CAGGGAAGG    6424 TATCAT   G G
                                CCTG TC CAGGGAAGG
                                IIII II IIIIIIIII
                                GGAC AG GTCCCTTCC
                           G_____   _ _
GAM411 ARHGDIA            TCCTGGCTGGGTCAGGGAAGGC  6433 TATCATC   TCG
                                CTGG  CAGGGAAGGC
                                IIII  IIIIIIIIII
                                GACC  GTCCCTTCCG
                           C_____    CA_
GAM411 ARHGEF12          ATCATCTTTGGACTGCAGGGAAG  6421 TA   C_  TC_       GCI
                                TCATC TGG  GCAGGGAAG
                                IIIII III  IIIIIIIII
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                              AGTAG ACC   CGTCCCTTC
                               __    AA  TGA       GII
GAM411  CCND1         CATCACAGG-CGCAGGGAAG      6423 TATCATCCT  T
                               GG CGCAGGGAAGG
                               || |||||||||||
                               CC GCGTCCCTTCT
                             GTGT_____  _
GAM411  CD7           CATGGTGGG-GCAGGGAAGG      6425 TATCATCC  TC
                               TGG GCAGGGAAGG
                               ||| ||||||||||
                               ACC CGTCCCTTCC
                             CC_____  C_
GAM411  CIT           TCATCCTCTGCAGGCAGGGAAG    6428 TATC   G_ C_      GC
                               ATCCT GT GCAGGGAAG
                               ||||| || |||||||||
                               TAGGA CG CGTCCCTTC
                             ____     GA TC      AC
GAM411  CMAR            TCCTGCGCCTCAGGGAAGG      6432 TATCATCCTG  G
                               GTC CAGGGAAGG
                               ||| ||||||||||
                               CGG GTCCCTTCC
                             G_____  A
GAM411  DBH            TCATCCTGGGCGTGCAGGG       6427 TATC   TC__   AAGG
                               ATCCTGG  GCAGGG
                               |||||||  ||||||
                               TAGGACC  CGTCCC
                             ____      CGCA   GAII
GAM411  DDEF2           TCCTGGGCTAGAAGGGAAGGC    6435 TATCATC  TCGC
                               CTGG  AGGGAAGGC
                               ||||  |||||||||
                               GATC  TCCCTTCCG
                             CC_____  T___
GAM411  IKBKG          TCATCCTGG--GCTAGGCAGGC    6431 TATC    TC A A
                               ATCCTGG GC GGG AGG
                               ||||||| || ||| |||
                               TAGGACC CG TCC TCC
                             ____      __ A G
GAM411  KRT4          ATCATCCTGG-GGCAGAGA        6422 TA      TC      AG
                               TCATCCTGG GCAGGGA
                               ||||||||| ||||||||
                               AGTAGGACC CGTCTCT
                             __      C_   CI
GAM411  LAMC3         TCAGTCCTGCTGGCAGGGAAG      6426 TATCA   GTC        C
                               TCCTG GCAGGGAAGG
                               ||||| ||||||||||
                               AGGAC CGTCCCTTCT
                             TC___  GAC      T
GAM411  LZTS1         TCAGCCCGCACTCAGGGAAGG      6430 TATCAT  GTCG       C
                               CCTG CAGGGAAGG
                               |||| |||||||||
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                        GGGC   GTCCCTTCC
                 TC____     GTGA      C
GAM411 SGT           TCCTTCGGGTCGGCCAGGGAAGG  6429 TATCA CT    __      CI
                 TC GGTCG  CAGGGAAGG
                 II IIIII  IIIIIIIII
                 AG CCAGC  GTCCCTTCC

                 GA___  C_  CG      TG
GAM412 ACRC          ACATGTGAAAAATATGGAACTCAA  6439 TGAC       TCT___    AI
                 ATGTGAAAA    GACTCAA
                 IIIIIIIII    IIIIIII
                 TACACTTTT    TTGAGTT

                 ____          TATACC     CA
GAM412 ACYP1         ACATTCAAAAATCTGACATTAAA  6441 TGACATGT       TCAAAI
                 GAAAATCTGAC
                 IIIIIIIIIII
                 TTTTTAGACTG

                 TAAG____         TAATTT
GAM412 AKAP2         ACA-GAGAAAATCTGGCTC      6442 TGACATGT     A  A
                 GAAAATCTG CTC
                 IIIIIIIII III
                 CTTTTAGAC GAG

                 TCT_____        C  A
GAM412 CNGB3         TGACATGTAGAGTCTGCCT      6446      AAAA_  A CAAA
                 TGACATGTG    TCTG CT
                 IIIIIIIII    IIII II
                 ACTGTACAC    AGAC GG

                 ATCTC  _  AIII
GAM412 FIGF          CATGTGTCTTAAATCTGACACA  6445 TGACA  GA_      T AA
                 TGT  AAATCTGAC CA
                 III  IIIIIIIII II
                 ACA  TTTAGACTG GT

                 C____  GAA     T CT
GAM412 M6PR          ACTTGTGAAAATGTGTTTAAAA  6444 TGACA       C ACTCAAA
                 TGTGAAAAT TG
                 IIIIIIIII II
                 ACACTTTTA AC

                 A____       C  AAATTTT
GAM412 PSG4          ACATGTGAAATTCTAATGACT   6440 TGAC     A ___   CAAA
                 ATGTGAAA TCT  GACT
                 IIIIIIII III  IIII
                 TACACTTT AGA  CTGA

                 ____     A TTA  CGII
GAM412 PSG7          ACATGTGAAATTCTAATGACT   6440 TGAC     A ___   CAAA
                 ATGTGAAA TCT  GACT
                 IIIIIIII III  IIII
                 TACACTTT AGA  CTGA

                 ____     A TTA  CGII
GAM412 RAD54B        TGACCGGCGAAAATCTGACAGAAA 6450    AT        TCAAAI
                 TGAC GTGAAAATCTGAC
                 IIII IIIIIIIIIIII
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                        ACTG  CGCTTTTAGACTG
                        GC        TCTTTI
GAM412 SLC4A7       TGTGCAAAAATCTGATTAAAA   6451 TGACATGT       CTCAAA
                        GAAAATCTGA
                        |||||||||||
                        TTTTTAGACT
                        _____        AATTTT
GAM412 SYT4        TGACAC---AAAACCTGACTCAAA  6449    GTG
                        TGACAT AAAATCTGACTCAAA
                        |||||| ||||||||||||||
                        ACTGTG TTTTGGACTGAGTTT
                           ___
GAM412 TNFAIP1        TGACAAG--AAAATCTGAC       6447    TGT      TCA
                        TGACA GAAAATCTGAC
                        ||||| |||||||||||
                        ACTGT CTTTTAGACTG
                          T__       III
GAM412 TNFRSF8       TGAAATGTGAAAA----ACCCAAA 6448   C     ATCT
                        TGA ATGTGAAA  GACTCAA
                        ||| |||||||||  |||||||
                        ACT TACACTTT  TTGGGTT
                          T     ____
GAM412 TOB1        ACATGTAAGACACTGACTCAAA   6443 TGAC     AAAT
                        ATGTGA  CTGACTCAAA
                        |||||| |||||||||||
                        TACATT  GACTGAGTTT
                        ____      CTGT
GAM412 ZNF236        ACATGAAGGAAAATCTGAC      6438 TGACATGT       TCAA
                        GAAAATCTGAC
                        |||||||||||
                        CTTTTAGACTG
                    TACTTC__       TAII
GAM413 A1BG        GACATTAAAAGGCATAGGCATATTA 6468 TG      __ A   G    II
                        ACATTAAAA CA GGG ATATTA
                        ||||||||| || ||| ||||||
                        TGTAATTTT GT TCC TATAAT
                          __      CC  A   G    CI
GAM413 BMP4        TGACAG-AAAACAA-GGCATAT  6471     TT     GGATATT
                        TGACA AAAACAAGG
                        ||||| |||||||||
                        ACTGT TTTTGTTCC
                          C_      GTATAII
GAM413 BMP4        TGACAG-AAAACAA-GGCATAT  6471     TT     GGATI
                        TGACA AAAACAAGG
                        ||||| |||||||||
                        ACTGT TTTTGTTCC
                          C_      GTATA
GAM413 CML66       ACATTAAAACTTAAGAGGTTA    6454        __   ATIII
                        ACATTAAAAC AAGGGG
                        ||||||||| |||||
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                         TGTAATTTTG TTCTCC
                          AA     AATII
GAM413 CML66        ACATTAAAACTTAAGAGGTTA    6454 TGAC      __   A  TA
                       ATTAAAAC AAGGGG TAT
                       |||||||| |||||| |||
                       TAATTTTG TTCTCC ATG
                            ____     AA   A  TI
GAM413 COL4A5        ACATTAAAACAGGGGGCATAT    6459 C      A   ATAI
                       ATTAAAACA GGGG
                       ||||||||| ||||
                       TAATTTTGT CCCC
                         _     C  GTAT
GAM413 COL4A5        ACATTAAAACAGGGGGCATAT    6459 TGAC     A  _  TA
                       ATTAAAACA GGGG ATAT
                       ||||||||| |||| ||||
                       TAATTTTGT CCCC TATA
                          ____     C  G  CC
GAM413 CRY2         GACATTTATAAAACAAGTGAATATT 6467 ACAT      G   I
                       TAAAACAAG GGATAT
                       ||||||||| ||||||
                       ATTTGTTC CTTATA
                        AAAT      A   I
GAM413 CRY2         GACATTTATAAAACAAGTGAATATT 6467 TG  ___      G   AII
                       ACAT  TAAAACAAG GGATATT
                       ||||  ||||||||| |||||||
                       TGTA  ATTTGTTC CTTATAA
                         __   AAT     A   GII
GAM413 DSC3         ACATTAAAAGAAGACGACTTTA    6462     C  G  ATTI
                       CATTAAAA AAGG GAT
                       |||||||| |||| |||
                       GTAATTTT TTCT CTG
                          C   G  AAAI
GAM413 DSC3         ACATTAAAAGAAGACGACTTTA    6462 TGAC    C   G  ATTA
                       ATTAAAA AAGG GAT
                       ||||||| |||| |||
                       TAATTTT TTCT CTG
                          ____     C  G  AAAT
GAM413 FBXL3A       ACATTAAAAAAAATTCGGAGATAT  6457 TGACATTAAAACAA    TAI
                          GGGGATAT
                          |||||||
                          CCTCTATA
                       TAATTTTTTTTAAG    CTI
GAM413 FGF2         GACATTTAAACATGTTAGGGGATATT 6469 ACATTA    ____      I
                       AAACA AGGGGATAT
                       ||||| |||||||||
                       TTTGT TCCCCTATA
                         AA____    ACAA     I
GAM413 FGF2         GACATTTAAACATGTTAGGGGATATT 6469 TG   A   ____      AII
                       ACATT AAACA AGGGGATATT
                       ||||| ||||| ||||||||||
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```
                        TGTAA TTTGT   TCCCCTATAA
                        __    A   ACAA       AII
GAM413 IKBKB            ACATTAAAATGCGGGAATCTTA   6463      CAA     ATTI
                            CATTAAAA  GGGGAT
                            IIIIIIII  IIIIII
                            GTAATTTT  CCCTTA
                              ACG    GAAI
GAM413 IKBKB            ACATTAAAATGCGGGAATCTTA   6463 TGAC     CAA     ATTA
                             ATTAAAA  GGGGAT
                             IIIIIII  IIIIII
                             TAATTTT  CCCTTA
                             ____       ACG     GAAT
GAM413 LILRB2          ATTAAAAAATGTAGGGATATTA    6464 TGACATTAAAACAA
                               GGGGATATTA
                               IIIIIIIIII
                               TCCCTATAAT
                          TTTTTACA_____
GAM413 LILRB2          ATTAAAAAATGTAGGGATATTA    6464 TTAAAACAA      I
                               GGGGATATT
                               IIIIIIIII
                               TCCCTATAA
                          TTTTTTACA        I
GAM413 MBL2            ACATTAAA--AAGGACATATT     6461      CA  G  I
                            ACATTAAAA AGGG ATA
                            IIIIIIIII IIII III
                            TGTAATTTT TCCT TAT
                              __   G  A
GAM413 MBL2            ACATTAAA--AAGGACATATT     6461 TGAC    CA  G
                             ATTAAAA AGGG ATATT
                             IIIIIII IIII IIIII
                             TAATTTT TCCT TATAA
                             ____    __  G
GAM413 MECP2          ACTTTAAAACAAGCGCAGGTATAT   6458 TGACA       ___ _   TAI
                            TTAAAACAAG  GGG ATAT
                            IIIIIIIIII  III IIII
                            AATTTTGTTC  TCC TATA
                        A____        GCG  A  TAI
GAM413 PCLO           ACATTAAA--AAGTGGATA        6460      CA  G  I
                            ACATTAAAA AG GGAT
                            IIIIIIIII II IIII
                            TGTAATTTT TC CCTA
                              __  A   T
GAM413 RABIF          ATTAAAACAATGAAATACTA       6466      G GG  I
                            TTAAAACAA G  ATATT
                            IIIIIIIII I  IIIII
                            AATTTTGTT C  TATGA
                             A TT    I
GAM413 RABIF          ATTAAAACAATGAAATACTA       6466 TGACATTA     G GG
                             AAACAA G  ATATT
                             IIIIII I  IIIII
```

```
                      TTTGTT C  TATGA
                      _____        A TT
GAM413 RNGTT          ACATTAAAACTCAGGTGAATAT   6455 CA      A_  _     I
                      TTAAAAC  AGG GGATA
                      ||||||| ||| |||||
                      AATTTTG  TCC CTTAT
                      __        AG  A   I
GAM413 RNGTT          ACATTAAAACTCAGGTGAATAT   6455 TGAC      A_  _    TA
                      ATTAAAAC  AGG GGATAT
                      |||||||| ||| ||||||
                      TAATTTTG  TCC CTTATA
                      ____        AG  A   TT
GAM413 SFPQ           TTAAAACAAAGGGGGCAATTA    6472        ATATTIII
                      TTAAAACAAGGGG
                      |||||||||||||
                      AATTTGTTTCCC
                      CCGTTAAT
GAM413 SLC20A1        ACATTAAAACATAATGGA-ATT   6456 TGAC      AG__   ATTA
                      ATTAAAACA   GGGAT
                      ||||||||| |||||
                      TAATTTTGT   CCTTA
                      ____        ATTA   ACTI
GAM413 SLC20A1        ACATTAAAACATAATGGA-ATT   6456         AG__   ATI
                      CATTAAAACA   GGGAT
                      ||||||||| |||||
                      GTAATTTTGT   CCTTA
                            ATTA    III
GAM413 SPAG8          TTAAAACAATGGCAT-TTA      6473     G  G  ATTI
                      TTAAAACAA GG AT
                      ||||||||| || ||
                      AATTTGTT CC TA
                      A  G  AATI
GAM413 TNFSF4         TAAACATAAGGGGATACTA      6470 TA    __        II
                      AAACA AGGGGATATT
                      ||||| ||||||||||
                      TTTGT TCCCCTATGA
                      A_    AT      TI
GAM413 VEGF           ATTAAAA--AGGG-ATATTA     6465 TTAAAAC
                      AAGGGGATATT
                      |||||||||||
                      TTTCCCTATAA
                      TAATT__
GAM414 ALDH3B2        TGGCAG-GCAGGATGCAGT      6488   T       AGA
                      TGGCAG GCAGGATGCAGT
                      |||||| |||||||||||||
                      ACCGTC CGTCCTACGTCA
                      _              III
GAM414 BIG1           CAGTGCAGGAAGAACTATAT     6477 TGGCAG      TGCAGTAGAT
                      TGCAGGA
                      |||||||
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                                    ACGTCCT
                               _____      TCTTGATATA
GAM414 COLQ          GGCACGGTGACAGCGGATGCAGT  6480 _____      GCA      AGATGI
                               TGGCAGT  GGATGCAGT
                               |||||||  |||||||||
                               ACTGTCG  CCTACGTCA
                           CGTGCC      ___         GIIIGT
GAM414 DGCR2          CAGCCCAGGATGCA-TCGATG   6478 TGGCAGTG      GTA
                               CAGGATGCA  GAT
                               ||||||||| |||
                               GTCCTACGT  CTA
                           GG_____         AG_
GAM414 FUT6          GGCAGTGCA--AAGCAGAAG    6483 TG      AT   T A
                               GCAGTGCAGG  GCAG  AG
                               |||||||||| |||| ||
                               CGTCACGTTT  CGTC  TC
                           __         __    T A
GAM414 GRM7          TGGCAGTGC-TGATGTCAGT    6486      AG  _   AGAT
                               TGGCAGTGC  GATG  CAGT
                               |||||||||  |||| ||||
                               ACCGTCACG  CTAC  GTCA
                               A_   A   IIIG
GAM414 MLPH          GCAGTGCAGGACTGAATGTCGCTG  6479 TGGC      GCA__  AGA  I
                               AGTGCAGGAT   GT  TG
                               ||||||||||   ||  ||
                               TCACGTCCTG   CA  AC
                           ____          ACTTA  GCG  A
GAM414 MNT           GGCACTGGCTCAGGATGCAG   6481 ____   AGTG      TAGAT
                               TGGC  CAGGATGCAG
                               ||||  ||||||||||
                               ACCG  GTCCTACGTC
                           CGTG  A___        CIIIG
GAM414 NOTCH2        TGCCAGGCCATGGATGCAGTA    6485 G  T A__      GATG
                               TG CAG GC  GGATGCAGTA
                               || ||| ||  ||||||||||
                               AC GTC CG  CCTACGTCAT
                               G  _  GTA        IIIG
GAM414 PITPNB        GGTATTGCA--ATGCAGTAG     6484 TGGCAG  GG      A
                               TGCA  ATGCAGTAG
                               ||||  ||||||||||
                               ACGT  TACGTCATC
                           CATA__   __        A
GAM414 STAU          CAGTGCAGGTTAATTCAGT      6476 TGGCAG    ATG___   AGAT
                               TGCAGG    CAGT
                               ||||||    ||||
                               ACGTCC    GTCA
                               _____      AATTAA  CGAI
GAM414 TCFL4         GGGACTGCAGGATGTCAGAAGA   6482 T AG       _  T  TG
                               GGC  TGCAGGATG CAG  AGA
                               |||  ||||||||| ||| |||
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                        CTG  ACGTCCTAC GTC TCT
                        C   __        A T CI
GAM414 XT3              TGGAA-TGAAGGATGCAGT      6487 C  C        AGA
                        TGG AGTG AGGATGCAGT
                        III IIII IIIIIIIIII
                        ACC TTAC TCCTACGTCA
                        _    T       III
GAM415 APAF1            GATCTATTCCCTTACCCTCT      6496 GAG CT       GTTGC
                        AT CCTTACCCTCT
                        II IIIIIIIIIII
                        TA GGAATGGGAGA
                        AGA AG      GGIII
GAM415 CAPN10          AGATCTGCTGCCCTACCCTCTG    6491 GA  ____       TTGCA
                        GATCT  CCTTACCCTCTG
                        IIIII  IIIIIIIIIIII
                        CTAGA  GGGATGGGAGAC
                        __   CGAC      CIIIA
GAM415 LPP             ATCTTTTT-CTCTCTGTTGCA    6495 GAGATCTCCTTACC
                        CTCTGTTGC
                        IIIIIIIII
                        GAGACAACG
                        AAAAAGA_____
GAM415 MAN1A2          GATCTCCTTCGACGCTTCTATTCCA 6497 GAGA     __ C _   G II
                        TCTCCTT AC CT CTGTT CA
                        IIIIIII II II IIIII II
                        AGAGGAA TG GA GATAA GT
                        ____     GC C A   G CT
GAM415 MANBA          TCTCCTTGTC-TCTGTTGC       6499 GAGATCTCCTTACC
                        CTCTGTTG
                        IIIIIIII
                        GAGACAAC
                        GAACA_____
GAM415 MB             AGATCTCCT---CCTC-ATTGCA   6493 GA      TAC   T
                        GATCTCCT  CCTC GTTGC
                        IIIIIIII  IIII IIIII
                        CTAGAGGA  GGAG TAACG
                        __      ___   _
GAM415 NKTR           GACCACCTTACCCTGTTTT       6498 GAGAT T     CT  GC
                        C CCTTACCCT GTT
                        I IIIIIIIIII III
                        G GGAATGGGA CAA
                        G____T      __ AA
GAM415 NR1I2          AGATCTCCTTATACTTCCTCCTTTGTTG6492 GA       C____   G CAIII
                        GATCTCCTTA   CCTCT TTG
                        IIIIIIIIII   IIIII III
                        CTAGAGGAAT   GGAGG AAC
                        __        ATGAA   A AACTI
GAM415 RARG           ATCTGTCCCTTTCACCCTCTGTT   6494 GAGA  C_        GCAI
                        TCTC TTACCCTCTGTT
                        IIII IIIIIIIIIIII
```

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                        AGGG  AGTGGGAGACAA
                        AC__   AA         GGAI
GAM416  ACP1           TGTCCGGAGGAGGAGGAGCTGCG   6508        ATTC_   G   ATI
                        TGTCCGGAG    GGAGC GCG
                        |||||||||    ||||| |||
                        ACAGGCCTC    CCTCG CGC
                          CTCCT    A   III
GAM416  ACP1           TGTCCGGAGGAGGAGGAGCTGCG   6508 G        ATTC_   G  I
                         TCCGGAG    GGAGC GC
                         |||||||    ||||| ||
                         AGGCCTC    CCTCG CG
                         _    CTCCT    A  I
GAM416  ALPPL2         GTCTGGAAGCAGTCGGAGAGCGGCGA 6507 TCC    AT_   __       I
                           GGAG   TCGGA  GCGGCG
                           ||||   ||||| ||||||
                           CTTC   AGCCT  CGCCGC
                           ___   GTC    CT    I
GAM416  ALPPL2         GTCTGGAAGCAGTCGGAGAGCGGCGA 6507 TGTCC   AT_   __       TII
                           GGAG   TCGGA  GCGGCGA
                           ||||   ||||| |||||||
                           CTTC   AGCCT  CGCCGCT
                          AGAC_   GTC   CT    CII
GAM416  APPBP2         CCGGAGGATTCGGAGGGGCG       6502      _      C  II
                        CCGGAG ATTCGGAG GGC
                        |||||| |||||||| |||
                        GGCCTC TAAGCCTC CCG
                            C     C  CI
GAM416  APPBP2         CCGGAGGATTCGGAGGGGCG       6502 TGTCC GA      C  A
                          G GATTCGGAG GGCG
                          | |||||||||| ||||
                          C CTAAGCCTC CCGC
                         _____ TC      C  C
GAM416  CD44           TGTCCGGAGCGAACGGAG-GGCG    6510        ATT_   C  AT
                        TGTCCGGAG    CGGAG GGCG
                        |||||||||    ||||| ||||
                        ACAGGCCTC    GCCTC CCGC
                          GCTT    _   II
GAM416  CD44           TGTCCGGAGCGAACGGAG-GGCG    6510        ATT_   C  I
                         GTCCGGAG    CGGAG GGC
                         ||||||||    ||||| |||
                         CAGGCCTC    GCCTC CCG
                          GCTT    _  I
GAM416  CDX2           GGGGACTCGAGGAGCGGCG        6506 _ A   __       III
                          GG GATTC  GGAGCGGC
                          || ||||| |||||||||
                          CC CTGAG  CCTCGCCG
                           C _   CT    CII
GAM416  CDX2           GGGGACTCGAGGAGCGGCG        6506 TGTCCGGAGATTC       A
                            GGAGCGGCG
                            |||||||||
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                              CCTCGCCGC
                         GAGCT_____         C
GAM416 ENTPD3            TGTGCGGAGCCGATTCGGAGAAGGCGA6509  C   ___       C_   TIII
                         TGT CGGA  GATTCGGAG GGCGA
                         ||| |||| ||||||||| |||||
                         ACA GCCT  CTAAGCCTC CCGCT
                           C  CGG      TT   IIIT
GAM416 ENTPD3            TGTGCGGAGCCGATTCGGAGAAGGCGA6509 GTCC  ___      C_  I
                            GGA  GATTCGGAG GGCG
                            ||| ||||||||| ||||
                            CCT  CTAAGCCTC CCGC
                           ___    CGG      TT  I
GAM416 GAL              CCGG-G-TTCGGAGCGTCG      6504   AGA       GCI
                         CCGG  TTCGGAGCG
                         ||||  |||||||||
                         GGCC  AAGCCTCGC
                           C__       AGC
GAM416 GAL              CCGG-G-TTCGGAGCGTCG      6504 TGTCCGGAGA      G
                              TTCGGAGCG CG
                              ||||||||| ||
                              AAGCCTCGC GC
                         CC_____          A
GAM416 NAP1L3           CGGAGGTG-GCAGCGGCGAT    6505 _ ATTC _     I
                              GGAG  GG AGCGGCGA
                              ||||  || |||||||||
                              CCTC  CC TCGCCGCT
                           G   CA__  G       I
GAM416 PPP4R1           CCGGGGCTACATGGAGCGGCG   6503   AG__ TC      III
                         CCGG  AT GGAGCGGC
                         ||||  || |||||||||
                         GGCC  TG CCTCGCCG
                           CCGA TA      CII
GAM416 PPP4R1           CCGGGGCTACATGGAGCGGCG   6503 TGTCC AG TC     AT
                            GG AT GGAGCGGCG
                            || || |||||||||
                            CC TG CCTCGCCGC
                         C____ GA TA      GC
GAM416 SNRP70           TGTCCGGAGGCTCGCGGCGGC   6513       AT GA   GAT
                         TGTCCGGAG TCG GCGGC
                         ||||||||| ||| |||||
                         ACAGGCCTC AGC CGCCG
                           CG GC   III
GAM416 SNRP70           TGTCCGGAGGCTCGCGGCGGC   6513       AT GA  I
                          GTCCGGAG TCG GCGG
                          |||||||| ||| ||||
                          CAGGCCTC AGC CGCC
                           CG GC  I
GAM416 TEM8            TGTCCGGAG----GGAGCAGGCG   6511       ATTC  _ A
                         TGTCCGGAG  GGAGC GGCG
                         |||||||||  ||||| ||||
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                              ACAGGCCTC   CCTCG CCGC
                                   ___     T   I
GAM416  TEM8          TGTCCGGAG----GGAGCAGGCG  6511 _      ATTC    _
                          GTCCGGAG   GGAGC GGC
                          IIIIIIII   IIIII III
                          CAGGCCTC   CCTCG CCG
                              A      ___     T
GAM416  TJP1          TGTCTGGTT-TTCGGAGCGG     6512  C AGA      CGA
                          TGTC GG  TTCGGAGCGG
                          IIII II  IIIIIIIIII
                          ACAG CC  AAGCCTCGCC
                           A AA_       III
GAM416  TJP1          TGTCTGGTT-TTCGGAGCGG     6512 _ C AGA      I
                           GTC GG  TTCGGAGCG
                           III II  IIIIIIIII
                           CAG CC  AAGCCTCGC
                            A A AA_      I
GAM417  CEP1          GAAAGACCTAGGCTGAAGAAG    6525 TGA  TA  _        CC
                           GA  GCC AGGCTGAAGAAG
                           II  III IIIIIIIIIII
                           TT  TGG TCCGACTTCTTC
                           ___  TC  A       AI
GAM417  DYRK2         GATAGTTTCCCAGGCTGAGAGAA  6526 TGAGATAG      _  G I
                            CCAGGCTGA AGAA CC
                            IIIIIIIII IIII II
                            GGTCCGACT TCTT GG
                          TCAAAG__      C  _ A
GAM417  EGLN3         AGAGAGCCAAGTGAGCTGAAGAA  6518 TGAGAT    ____       CCI
                           AGCCA   GGCTGAAGAAG
                           IIIII   IIIIIIIIIII
                           TCGGT   TCGACTTCTTT
                           TC____   TCAC        CII
GAM417  GJA5          GAGTTCAGCCAGGCT-AAGGAG   6522 TGAGA       A AGCC
                            TAGCCAGGCTGA GA
                            IIIIIIIIIIII II
                            GTCGGTCCGATT CT
                          TCAA_        C CCII
GAM417  IL13          TGAGGTCGGCTAGGCTGAAGA    6528   ATA_ C       AGCC
                           TGAG  GC AGGCTGAAGA
                           IIII   II IIIIIIIII
                           ACTC   CG TCCGACTTCT
                           CAGC  A       IIIC
GAM417  LDHB          AGATAG--AG-CTGAAGAAG     6521 TGAG   CCA
                           ATAG  GGCTGAAGAAG
                           IIII  IIIIIIIIIII
                           TATC  TCGACTTCTTC
                           ____   __
GAM417  MFAP2         GAGGTGGCCACAGGCTGAAGGAG  6523 TGAGATA  __     A CCI
                           GCCA  GGCTGAAG AG
                           IIII  IIIIIIII II
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                          CGGT  CCGACTTC TC
                    TCCAC__    GT     C CII
GAM417 NPEPPS       AGAAAGGCCTGGCTGAAGA      6517 TGAGATA A      AGC
                        GCC GGCTGAAGA
                        ||| |||||||||
                        CGG CCGACTTCT
                    TTTC___   A      AGI
GAM417 PRKY         TGAGA-AGCACAGGCTGAA       6527  T  _      GAAG
                        TGAGA AGC CAGGCTGAA
                        ||||| ||| |||||||||
                        ACTCT TCG GTCCGACTT
                    _   T     IIIC
GAM417 RFP          GAGGAAGCCAGGCTGAGCCAAGAAGC 6524 TG  AT         ____    CII
                        AG AGCCAGGCTGA  AGAAGC
                        || |||||||||||  ||||||
                        TC TCGGTCCGACT  TCTTCG
                    __  CT      CGGT    AII
GAM417 SUV39H1      AGATATGCAGCCCTGAAGAAG     6519 TGAGA   AGG     CC
                        TAGCC  CTGAAGAAG
                        ||||| |||||||||
                        GTCGG  GACTTCTTC
                    TATAC    ___       TC
GAM417 TNFRSF10C    AGATAGAGCCAGGCTGGAGA      6516 TGAGAT      A AGC
                        AGCCAGGCTG AGA
                        |||||||||| |||
                        TCGGTCCGAC TCT
                    TATC__      C GTI
GAM417 UMOD         AGA-AGGCAGGCTGAACAA       6520 TGAGAT C      G
                        AG CAGGCTGAA AAG
                        || ||||||||| |||
                        TC GTCCGACTT TTT
                    T_____ C      G
GAM418 ABCB11       TAAAATATTAACATTCTTCT      6538      TA_ G   ATTT
                        TAAAATATT AT CTTCT
                        ||||||||| || |||||
                        ATTTTATAA TA GAAGA
                    TTG A    IIIA
GAM418 ADH4         TATAATATTTAAAGC-TCT-TTTA 6546 A      T   CTAI
                        AATATTTAA GCTT
                        ||||||||| ||||
                        TTATAAATT CGAG
                    A      T  AAAI
GAM418 ADH4         TATAATATTTAAAGC-TCT-TTTA 6546 TAA      T   CTATTTA
                        AATATTTAA GCTT
                        ||||||||| ||||
                        TTATAAATT CGAG
                    ATA      T  AAAATII
GAM418 ARHGEF7      TATAATAAATAATACATTCTATTTA 6540 AA   TT    _    I
                        AATA  TAATGC TTCTATTT
                        ||||  |||||| ||||||||
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                    TTAT ATTATG AAGATAAA
                    A_   TT     T    I
GAM418  ARHGEF7      TATAATAAATAATACATTCTATTTA 6540 TAA   TT    _      II
                    AATA TAATGC TTCTATTTA
                    IIII IIIIII IIIIIIIII
                    TTAT ATTATG AAGATAAAT
                    ATA  TT     T      II
GAM418  C18orf1      TAATATATAATAATGCTTCCTTCTTTA6536  T_       ATTTI
                    ATAT TAATGCTTCT
                    IIII IIIIIIIIII
                    TATA ATTACGAAGG
                    TT        AAGII
GAM418  C18orf1      TAATATATAATAATGCTTCCTTCTTTA6536 TAAA  T_       A AIII
                    ATAT TAATGCTTCT TTT
                    IIII IIIIIIIIII III
                    TATA ATTACGAAGG AGA
                    ATTA TT        A AATI
GAM418  CCR9         AAGTAATTAATGCTTCATAT     6534 AAA  T      TAII
                    TA TTAATGCTTC
                    II IIIIIIIIII
                    AT AATTACGAAG
                    TTC T       TATA
GAM418  CCR9         AAGTAATTAATGCTTCATAT     6534 TAAAA T      TATTT
                    TA TTAATGCTTC
                    II IIIIIIIIII
                    AT AATTACGAAG
                    C____ T       TATAT
GAM418  COL19A1      TAAAATATTTA--GCTT-TAT    6542       AT  CI
                    TAAAATATTTA GCTT
                    IIIIIIIIIII IIII
                    ATTTTATAAAT CGAA
                          __ AT
GAM418  COL19A1      TAAAATATTTA--GCTT-TAT    6542       AT  CTATT
                    TAAAATATTTA GCTT
                    IIIIIIIIIII IIII
                    ATTTTATAAAT CGAA
                          __ ATAII
GAM418  CSF2         TAAAATATTCCCATTCTTCT     6537       AATG_ ATTT
                    TAAAATATTT   CTTCT
                    IIIIIIIIII   IIIII
                    ATTTTATAAG   GAAGA
                      GGTAA   IIIA
GAM418  EHF          AAAACATTTAATGCCCTCTGATTT 6532       _ ATTI
                    ATATTTAATGCT TCT
                    IIIIIIIIIIII III
                    TGTAAATTACGG AGA
                      G CTII
GAM418  EHF          AAAACATTTAATGCCCTCTGATTT 6532 TA       _ _ AI
                    AAATATTTAATGCT TCT ATTT
                    IIIIIIIIIIII III IIII
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                    TTTGTAAATTACGG AGA TAAA
                    __      G  C  AI
GAM418 ERBB4        TAAAATATTTCTTGCTTAAATT   6543      AA    CTATTTA
                    TAAAATATTT TGCTT
                    |||||||||| |||||
                    ATTTTATAAA ACGAA
                         GA    TTTAAII
GAM418 ERBB4        TAAAATATTTCTTGCTTAAATT   6543      AA    CTATI
                    AAAATATTT TGCTT
                    ||||||||| |||||
                    TTTTATAAA ACGAA
                         GA    TTTAI
GAM418 ETF1         TAAAGTATTTT-TGCTTCTATGTA  6545   A  AA      TTAI
                    TAAA TATTT TGCTTCTAT
                    |||| ||||| |||||||||
                    ATTT ATAAA ACGAAGATA
                         C  A_      CATI
GAM418 ETF1         TAAAGTATTTT-TGCTTCTATGTA  6545 AAA_   AA      TI
                    TATTT TGCTTCTAT
                    ||||| |||||||||
                    ATAAA ACGAAGATA
                    TTTC   A_     CI
GAM418 GLRA3        TAAAGTCTTTTAATGCTCTTATTTA 6535 AAAATA      TC    I
                    TTTAATGCT TATTT
                    ||||||||| |||||
                    AAATTACGA ATAAA
                    TTCAGA       GA    I
GAM418 GLRA3        TAAAGTCTTTTAATGCTCTTATTTA 6535 TAAAATA_      TC    II
                    TTTAATGCT TATTTA
                    ||||||||| ||||||
                    AAATTACGA ATAAAT
                    ATTTCAGA      GA    II
GAM418 IFNGR1       TAAAAAATATACACGTTCTATTTA 6539 _      TTA C     I
                    AAAATAT ATG TTCTATTT
                    ||||||| ||| ||||||||
                    TTTTATA TGC AAGATAAA
                    T    TG_  A      I
GAM418 IFNGR1       TAAAAAATATACACGTTCTATTTA 6539 T__     TTA C     II
                    AAAATAT ATG TTCTATTTA
                    ||||||| ||| |||||||||
                    TTTTATA TGC AAGATAAAT
                    ATT    TG_  A     II
GAM418 ITGA1        TAAAATATTTCATTTCTCCATTT  6544        A GC     AI
                    TAAAATATTT AT TTCTATTT
                    |||||||||| || |||||||||
                    ATTTTATAAA TA GAGGTAAA
                         G  AA     II
GAM418 MYO1D        AAAATAAGATTTAATGCTT-TATT  6531 AAAT         CTAI
                    ATTTAATGCTT
                    |||||||||||
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                         TAAATTACGAA
                     ATTC        ATAI
GAM418  MYO1D      AAAATAAGATTTAATGCTT-TATT  6531 TAAAAT_        C   TAI
                        ATTTAATGCTT TATT
                        ||||||||||| ||||
                        TAAATTACGAA ATAA
                     TTTATTC       _   CII
GAM418  PDK4       AAAATAGTTGA-GCTTCTATT     6533 AAATATTTAAT      I
                             GCTTCTAT
                             ||||||||
                             CGAAGATA
                        TTTTATCAACT      I
GAM418  PDK4       AAAATAGTTGA-GCTTCTATT     6533 TAAAATATTTAAT      T
                             GCTTCTATT
                             |||||||||
                             CGAAGATAA
                     TTTATCAACT___        T
GAM418  SMARCC1      TAAAATATTTAGCACTATCTACTT  6541         AT _    AI
                     TAAAATATTTA GCT TCTATTT
                     ||||||||||| ||| |||||||
                     ATTTTATAAAT TGA AGATGAA
                         CG   T   II
GAM418  SMARCC1      TAAAATATTTAGCACTATCTACTT  6541 A       AT _   I
                       AAATATTTA GCT TCTATT
                       ||||||||| ||| ||||||
                       TTTATAAAT TGA AGATGA
                     _     CG  T   I
GAM419  MAML1       CCATTGTTT-TCCG-CGCTA       6549 TAACCA    CT _ CG
                        TTGTTT CG GC CT
                        |||||| || || ||
                        AACAAA GC CG GG
                     _____      AG G AT
GAM420  CD53       CCCCAGAACTCCCTTCAACTAGTCTC 6558     CA___      AA CII
                        CCCCAG   CCTTCAACTA CTC
                        ||||||   |||||||||| |||
                        GGGGTC   GGAAGTTGAT GAG
                        TTGAG      CA III
GAM420  CREBL2      CAGCACCTTCTCCTGGACTCC      6556 CCCCAG     AA AA
                        CACCTTC CT ACTCC
                        ||||||| || |||||
                        GTGGAAG GA TGAGG
                     _____    AG CC
GAM420  FKBP1A      CAGCACCTTCAATTGAAACT       6554 CCCCAG      CT_  C
                        CACCTTCAA AAACT
                        ||||||||| |||||
                        GTGGAAGTT TTTGA
                     _____     AAC  C
GAM420  GLRA3       CAGCACCTTAGAC--AGCTCC      6555 CCCCAG    CA TAAA
                        CACCTT AC  CTC
                        |||||| ||  |||
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                              GTGGAA TG   GGG
                     _____        TC  TCGA
GAM420  PAG          AGCAC-TTCAACTAGGCTCC    6552 CCCCAGCAC      AA
                              CTTCAACTA CTC
                              ||||||||| |||
                              GAAGTTGAT GAG
                     _____        CC
GAM420  PRDM4        CCAGCACCTGC--CGAAACT    6557 CCCC    TCAA  _
                              AGCACCT   CT AAACT
                              |||||||   || |||||
                              TCGTGGA   GG TTTGA
                     ___       C___ C
GAM420  RAD54L       CCCCAGCACCTCTC-TCTCAAC   6559          _____    TAAACTCC
                              CCCCAGCACCT    TCAAC
                              |||||||||||    |||||
                              GGGGTCGTGGA    AGTTG
                              GAGAG    IIICCTCA
GAM420  SORCS1       CAGCACCTTGCCTCACTAATCTCC  6553 CCCCAG    CA___   A   I
                              CACCTT   ACTAA CTCC
                              ||||||   ||||| ||||
                              GTGGAA   TGATT GAGG
                     _____        CGGAG    A   A
GAM420  TSLP         CCCCAGT---TTCACACTAAACTC  6560    CACC  _    C
                              CCCCAG   TTCA ACTAAACTC
                              ||||||   |||| |||||||||
                              GGGGTC   AAGT TGATTTGAG
                                A___   G        I
GAM421  APC4         CCGGCAGACTAACACGGCCCC    6571 TCC  _   C      TTTC
                              CAG CTGAC ACGGCCCC
                              ||| ||||| |||||||||
                              GTC GATTG TGCCGGGG
                              CC_ T   _   TCII
GAM421  BCL11B       CCCAGCTGAATCACCAGCTCCTTT  6578 TC     C_ _ C  CI
                              CCAGCTGA CAC GGC CCTTT
                              |||||||| ||| ||| |||||
                              GGTCGACT GTG TCG GGAAA
                              __     TA  G  A   AI
GAM421  BCL2         TCCCACC---CCACGGCCCC    6588   G TGA      TT
                              TCCCA C  CCACGGCCCC
                              ||||| |  ||||||||||
                              AGGGT G  GGTGCCGGGG
                                G ___       II
GAM421  BCR          CCAGACTCTGGCCACGGCCCC    6569 TCCCAG  A     CTTT
                              CTG CCACGGCCC
                              ||| |||||||||
                              GAC GGTGCCGGG
                              TCTGA_  C    CGII
GAM421  CARD4        TCCCGCCTGCGCA-GGCCCCTTT   6590   AG  AC C     C
                              TCCC CTG CA GGCCCCTTT
                              |||| ||| || |||||||||
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                    AGGG  GAC  GT CCGGGGAAA
                     CG   GC  _       I
GAM421  DDX11       TCCCAGCTGACCACAGCCCCTTTC  6592                I
                   TCCCAGCTGACCACGGCCCCTTTC
                   IIIIIIIIIIIIIIIIIIIIIIII
                   AGGGTCGACTGGTGTCGGGGAAAG
                              I
GAM421  DUSP4      TCCCAGCTGCTCA-GTCCCAACTTTC 6587      ACCA  _  __   II
                   TCCCAGCTG  CGG CCC CTTTC
                   IIIIIIIII  III III IIIII
                   AGGGTCGAC  GTC GGG GAAAG
                        GA__  A  TT   II
GAM421  EPB72     AGCTGACCAGCTTCCTCTTTC    6563 TC   GA A____   CCCTTTC
                    CCAGCT CC   CGGC
                    IIIIII II   IIII
                    GGTCGA GG   GTCG
                   CT   A_ AGAAA  TIIICTT
GAM421  HEXA       CCAGC--ACC--GGCCCCTTTC   6576 TCCC  TGACCA
                      AGC   CGGCCCCTT
                      III   IIIIIIIII
                      TCG   GCCGGGGAA
                   ____    TG____
GAM421  HMGB3      CCAGCTGACC----CCCCTTT    6575 TCCC      ACGG
                      AGCTGACC  CCCCTT
                      IIIIIIII  IIIIII
                      TCGACTGG  GGGGAA

GAM421  HSD17B2     AGCAGCCC-CAGCCCCTTTC    6565 TCCCAGCTGA A
                       CC CGGCCCCTTT
                       II IIIIIIIIII
                       GG GTCGGGGAAA
                   CG_____  _
GAM421  INPP1     CCGGC-GACGCACGGCCCC      6572 TCCCA T _     TT
                    GC GAC CACGGCCCC
                    II III IIIIIIIII
                    CG CTG GTGCCGGGG
                   C____ _ C    CG
GAM421  KCNA5     CCCAGCTGAC--CGGCTCC      6580 TC     AC _ TT
                    CCAGCTGACC GGC CCC
                    IIIIIIIIII III III
                    GGTCGACTGG CCG GGG
                   __       __ A  II
GAM421  LDOC1     CCAGGCTGA--ACGGCCCCTT    6570 TCCCA    CC
                    GCTGA ACGGCCCCTTT
                    IIIII IIIIIIIIII
                    CGACT TGCCGGGGAAG
                   TC___   __
GAM421  LIMK1     TCCCAGCTGAGGGCCACCTCCC   6583      CCAC  _ TT
                    TCCCAGCTGA  GGCC CCT C
                    IIIIIIIIII  IIII III  I
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                       AGGGTCGACT   CCGG GGA  G
                          C___   T  GG
GAM421 LRRC2           CCACCACACC-CGGCCCCTTT    6574 TC  GCTG  A
                          CCA   ACC CGGCCCCTTT
                          |||   ||| ||||||||||
                          GGT   TGG GCCGGGGAAA
                          T_  G___   _
GAM421 MAPK12          CCCAGGCTGCGCACGGCCCCT    6577 TC  _ AC      TC
                          CCAG CTG  CACGGCCCCTT
                          |||| ||| |||||||||||
                          GGTC GAC  GTGCCGGGGAG
                          __  C  GC       ||
GAM421 MBTPS2          CAGCTGACCGCGCGCGCCTT     6567 TCCCAG    A _ C  T
                          CTGACC CG GC CCTT
                          |||||| || || ||||
                          GACTGG GC CG GGAA
                          _____      C  G  C  T
GAM421 NEU1            CAGCTGACC-CGGACCCTTT     6568 TCCCAG    A  C
                          CTGACC CGG CCCTTT
                          |||||| ||| ||||||
                          GACTGG GCC GGGAAA
                          _____      _  T
GAM421 PAX5            CTGACCATCGCGGCCCCTT      6581 TCCCAGCTGACCA      T
                             CGGCCCCTT
                             |||||||||
                             GCCGGGGAA
                       TAGC_____         T
GAM421 POV1            CAGCTGGCACCTCAGGCCCCTTTC  6566 TCCCAG  __  A _     |
                          CTG  ACC C GGCCCCTTTC
                          |||  ||| | |||||||||||
                          GAC  TGG G CCGGGGAAAG
                          _____   CG  A T      G
GAM421 RBP3            AGCTCAGCA-GGCCCCTTT       6564 TCC   TGACCAC
                          CAGC    GGCCCCTT
                          ||||    ||||||||
                          GTCG    CCGGGGAA
                          ___   T_____
GAM421 RFXANK          TCCCTGCGTCTCACACAGCCCCTTTC 6582    A TGAC__         ||
                          TCCC GC    CACGGCCCCTTTC
                          |||| ||     |||||||||||||
                          AGGG CG     GTGTCGGGGAAAG
                          A CAGAGT            ||
GAM421 SH3GL1          TCCCAGCTGGCCTCTGTCCC     6589       A ACGG_ CTTT
                          TCCCAGCTG CC   CCC
                          ||||||||| ||    |||
                          AGGGTCGAC GG   GGG
                          C AGACA  |||C
GAM421 SLC13A3         TCCCAGCTGGCCAAGCGCTCCT   6585       A CG_ C TTC
                          TCCCAGCTG CCA  GC CCT
                          ||||||||| |||  || |||
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                         AGGGTCGAC GGT  CG GGA
                              C  TCG  A  III
GAM421 SLC4A1        TCCCAGCTG--CACGGCTCAGTTC 6591       AC     CCCTTTC
                         TCCCAGCTG CACGGC
                         ||||||||| ||||||
                         AGGGTCGAC GTGCCG
                              __        AGTCAAG
GAM421 SMAC          CCAGCTCCCC-CGGCCCCTT   6573 TCCC  GA A
                           AGCT CC CGGCCCCTTT
                           |||| || |||||||||
                           TCGA GG GCCGGGGAAG
                           ____    GG _
GAM421 TCF8          TCCCAGCTGCCCA--GCCC       6586     A A   CTT
                         TCCCAGCTG CC CGGCCC
                         ||||||||| || ||||||
                         AGGGTCGAC GG GTCGGG
                              _ _      III
GAM421 TPS1          CCCAGCTGACCACGCCCGCCT   6579 TC        G _ TTC
                          CCAGCTGACCACG CC CCT
                          |||||||||||| || |||
                          GGTCGACTGGTGC GG GGA
                          __           G C CII
GAM421 XRCC3         TCCCAGCTGTGCCACGGCCC   6584     A_     CTTT
                         TCCCAGCTG CCACGGCCC
                         ||||||||| |||||||||
                         AGGGTCGAC GGTGCCGGG
                              AC       IIIC
GAM422 ABCA3        GTGCTGGTCC-ACTC----GCTAC 6604      ACAC GI
                         GTGCTGGTCCG  CTG
                         ||||||||||   |||
                         CACGACCAGGT  GAT
                           GAGC  GI
GAM422 ABCA3        GTGCTGGTCC-ACTC----GCTAC 6604      ACACCTGG
                         GTGCTGGTCCG    GCTA
                         ||||||||||     ||||
                         CACGACCAGGT    CGAT
                           GAG_____
GAM422 ATP8A2      GTGCTGGTCTGTTAACACCT   6602       C___     GGGCTA
                         GTGCTGGTC GACACCT
                         ||||||||| |||||||
                         CACGACCAG TTGTGGA
                           ACAA      IIICAT
GAM422 ATP8A2      GTGCTGGTCTGTTAACACCT   6602       C___     III
                         GTGCTGGTC GACACC
                         ||||||||| ||||||
                         CACGACCAG TTGTGG
                           ACAA   AII
GAM422 CACNB3       TGCTCTGAGTCCTGGGCTA      6610 G C CA     II
                         TG TC GA CCTGGGCT
                         || || || ||||||||
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                              AC AG CT  GGACCCGA
                              G  A  CA      TI
GAM422  CACNB3           TGCTCTGAGTCCTGGGCTA      6610 GTGCTGGTCC  CA
                              GA  CCTGGGCTA
                              II  IIIIIIII
                              CT  GGACCCGAT
                         GA_____  CA
GAM422  DGCR2            GCAGGTCAGAGGGCACCTGGGCT  6597 CTG  C ___       I
                              GTC GA  CACCTGGGC
                              III II  IIIIIIII
                              CAG CT  GTGGACCCG
                         ___  T CCC      I
GAM422  DGCR2            GCAGGTCAGAGGGCACCTGGGCT  6597 GTGCT   C ___       ACI
                              GGTC GA  CACCTGGGCT
                              IIII II  IIIIIIIII
                              CCAG CT  GTGGACCCGA
                         T____  T CCC      GAI
GAM422  FLRT2            GCTGGTCTGGAACTCCTGGGCTA  6595 ___   TCC  A      I
                              CTGG  GAC CCTGGGCT
                              IIII  III IIIIIIII
                              GACC  TTG GGACCCGA
                         CCA  ___  A      I
GAM422  FLRT2            GCTGGTCTGGAACTCCTGGGCTA  6595 GTGC    C__  A      CI
                              TGGTC  GAC CCTGGGCTA
                              IIIII  III IIIIIIIII
                              ACCAG  TTG GGACCCGAT
                         ____     ACC  A      TT
GAM422  GAB2            TGCTGGTCCTTGACTCCCTGGG  6606          __  A_  III
                              TGCTGGTCC GAC CCTGG
                              IIIIIIIII III IIIII
                              ACGACCAGG CTG GGACC
                              AA  AG   CII
GAM422  GAB2            TGCTGGTCCTTGACTCCCTGGG  6606 GT      __  A_  CTAC
                              GCTGGTCC GAC CCTGGG
                              IIIIIIII III IIIIII
                              CGACCAGG CTG GGACCC
                              __     AA  AG    AIII
GAM422  HIRA           TGCTGGCCCCAGGGCACCTGGGC  6607 GCT   GA___      I
                              GGTCC   CACCTGGG
                              IIIII   IIIIIIII
                              CCGGG   GTGGACCC
                              ___   GTCCC   I
GAM422  HIRA           TGCTGGCCCCAGGGCACCTGGGC  6607 GT      GA___      TACI
                              GCTGGTCC   CACCTGGGC
                              IIIIIIII   IIIIIIIII
                              CGACCGGG   GTGGACCCG
                              __      GTCCC    TIII
GAM422  IGHMBP2         TGGTCTGCCAGCGCCCTGGGCTAC  6609 G  CGACA       I
                              GTC   CCTGGGCTA
                              III   IIIIIIIII
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                                 CGG    GGACCCGAT
                              A  TCGCG            I
GAM422 IGHMBP2        TGGTCTGCCAGCGCCCTGGGCTAC  6609 G  TG  CCGACA        I
                              TGC GT    CCTGGGCTAC
                              ||| ||    ||||||||||
                              ACG CG    GGACCCGATG
                              G  GT CG____        G
GAM422 ISG20         GCTGCTCCATCTCCTGGGCTAC  6599   G  ACA      I
                              CTG TCCG  CCTGGGCTA
                              ||| ||||  |||||||||
                              GAC AGGT  GGACCCGAT
                                G  AGA        I
GAM422 ISG20         GCTGCTCCATCTCCTGGGCTAC  6599 GTGC G  ACA
                              TG TCCG  CCTGGGCTAC
                              || ||||  ||||||||||
                              AC AGGT  GGACCCGATG
                              ____  G  AGA
GAM422 ITCH          GCTGGTCTTTAACTCCTGGGCTA  6596 CT  C__  A      I
                              GGTC  GAC CCTGGGCT
                              ||||  ||| |||||||||
                              CCAG  TTG GGACCCGA
                              __  AAA  A      I
GAM422 ITCH          GCTGGTCTTTAACTCCTGGGCTA  6596 GTGC  C__  A      CI
                              TGGTC  GAC CCTGGGCTA
                              |||||  ||| ||||||||||
                              ACCAG  TTG GGACCCGAT
                              ____      AAA  A       TT
GAM422 OSR1         GTGCTGTTCC---ACCTGGGC   6603    G  GAC      T
                              GTGCTG TCC  ACCTGGGC
                              |||||| |||  |||||||||
                              CACGAC AGG  TGGACCCG
                                 A  ___      I
GAM422 OSR1         GTGCTGTTCC---ACCTGGGC   6603 _   G  GAC
                              TGCTG TCC  ACCTGGG
                              ||||| |||  ||||||||
                              ACGAC AGG  TGGACCC
                                 C  A  ___
GAM422 PXF         GTGCTGGTCAGTGAACACCT    6601       C___      GGGCTA
                              GTGCTGGTC  GACACCT
                              ||||||||| |||||||
                              CACGACCAG  TTGTGGA
                                TCAC      IIICAT
GAM422 PXF         GTGCTGGTCAGTGAACACCT    6601       C___      III
                              GTGCTGGTC  GACACC
                              ||||||||| ||||||
                              CACGACCAG  TTGTGG
                                TCAC    AII
GAM422 RLN1        TGCTGTGGCCTACACACCTGGGC  6605 G_  C   CG_       ACI
                              TG TGGTC  ACACCTGGGCT
                              || |||||  |||||||||||
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                              AC ACCGG  TGTGGACCCGG
                              CG _  ATG        III
GAM422  RLN1        TGCTGTGGCCTACACACCTGGGC   6605 GC    CG_       I
                              TGGTC  ACACCTGGG
                              IIIII  IIIIIIIII
                              ACCGG  TGTGGACCC
                              C_  ATG        I
GAM422  SURF5       GCGGGACCCAC-CCTGGGCTA    6598 CT_ T G A      I
                              GG CC AC CCTGGGCT
                              II II II IIIIIIII
                              CC GG TG GGACCCGA
                              CGC T G _       I
GAM422  SURF5       GCGGGACCCAC-CCTGGGCTA    6598 GTGCT T G A
                              GG CC AC CCTGGGCTA
                              II II II IIIIIIII
                              CC GG TG GGACCCGAT
                              C____ T G _
GAM422  SYNGR1       TGCTGGTCC--CATGTGGCCAC   6608 _     GA CC     I
                              GCTGGTCC CA TGGGCTA
                              IIIIIIII II IIIIIII
                              CGACCAGG GT ACCCGGT
                              A      __ AC      I
GAM422  SYNGR1       TGCTGGTCC--CATGTGGCCAC   6608 GT     GA CC
                              GCTGGTCC CA TGGGCTAC
                              IIIIIIII II IIIIIIII
                              CGACCAGG GT ACCCGGTG
                              __      __ AC
GAM422  TCF2        GTGCTGGTCAGGTCA-CTGGGCT   6600       CGA_ C   AC
                              GTGCTGGTC  CAC TGGGCT
                              IIIIIIIII  III IIIIII
                              CACGACCAG   GTG ACCCGA
                              TCCA _     II
GAM422  TCF2        GTGCTGGTCAGGTCA-CTGGGCT   6600       CGA_ C   I
                              TGCTGGTC  CAC TGGGC
                              IIIIIIII  III IIIII
                              ACGACCAG   GTG ACCCG
                              TCCA _   I
GAM423  ADD2        CTTAGCTATCTCCGGTCGGC     6616 TAACTTGGATA     ATG
                              CCGGTCGGC
                              IIIIIIIII
                              GGCCAGCCG
                              TCGATAGA___      GTG
GAM423  CARKL       GCTCTTCGCC-CAGGGGGGCGG   6618 GTGC      AGAAGTT
                              TCTTCGCC    GGCGG
                              IIIIIIII    IIIII
                              AGAAGCGG    CCGCC
                              ____      GTCCCC_
GAM423  CMAR        GCTCTTCGCCTCCAAG-TGGAGG  6617 GTGC     AG_ T C
                              TCTTCGCC  AAGT GG GG
                              IIIIIIII  IIII II II
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                        AGAAGCGG  TTCA CC CC
                   ____        AGG   _  T
GAM423 ESR2         TGCTCTTCGCCCTGCAAGTT    6622 GT       AG__     GGCG
                        GCTCTTCGCC  AAGTT
                        |||||||||| |||||
                        CGAGAAGCGG  TTCAA
                          __      GACG   A|||
GAM423 LGALS3BP       GTGCTCTTCG--AGCTGTTGG    6621      CC AA   CG
                        GTGCTCTTCG AG GTTGG
                        |||||||||| || |||||
                        CACGAGAAGC TC CAACC
                          __ GA   ||
GAM423 MUC4           CTCTGAGCGTGAAGTTGGC    6615 GTGCTCTTC CA      GGC
                          GC GAAGTTGGCG
                          || ||||||||||
                          CG CTTCAACCGT
                     ACT_____  CA
GAM423 PRX           AATTTGGATACC-TTCAGCTTGG    6613 TAAC      GG    A
                        TTGGATACC TCGGC TGG
                        ||||||||| ||||| |||
                        AACCTATGG AGTCG ACC
                     TA__        A_   A
GAM423 PRX           ACCTGG-TAC---TCGGCATGG    6614 TAACT  A  CGG
                        TGG TAC  TCGGCAT
                        ||| |||  |||||||
                        ACC ATG  AGCCGTA
                     G____  _  ___
GAM423 RNMT          GTGCTCTTCCTGGCCCGACGGTGG    6619      ___   AGAAGT   I
                        GTGCTCTTC GCC    TGGCGG
                        ||||||||| |||    ||||||
                        CACGAGAAG CGG    GCTGCC
                           GAC _____   A
GAM423 ZNF76         GTGCACTCAGACATGAAGTTGGC    6620 __ TG  TTC CA      GGI
                        G CTC  GC GAAGTTGGC
                        | ||| || ||||||||||
                        C GAG  TG CTTCAACCG
                     CA GT  TC_  TA      |||
GAM424 ABCB9         TGCAGGCCTGG-GCTCGGAGGGC    6665 TT      ___  T AGAGC
                        GCAGGCCTGG  TGG GGG
                        ||||||||||  ||| |||
                        CGTCCGGACC  GCC CCC
                          __      CGA  T  GTIII
GAM424 ADAM11        TGCAGACCCCGTGGTGGGAG    6662 TT     G     AG
                        GCAGGCCT GTGGTGGGAG
                        |||||||| ||||||||||
                        CGTCTGGG CACCACCCTC
                          __     G     GI
GAM424 ADAM11        TTGC---CCTGGTGGTAGAAG    6671 AGG       A
                        TTGC CCTGGTGGTGGGAG
                        |||| ||||||||||||||
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                          AACG  GGACCACCATCTTC
                                      I
GAM424  ALDH3B1        GCAGGCGCGATGGTGGGAGA     6656 TTGC   C
                          AGGC TGGTGGTGGGAGAG
                          IIII IIIIIIIIIIIII
                          TCCG GCTACCACCCTCTT
                          ____      C
GAM424  B29            CCCTCCTTCTTCCCTCATG-CCA   6643        G  C  A  T
                       CCCTCCTTCTTC TTC TG CCA
                       IIIIIIIIIII III II III
                       GGGAGGAAGAAG GAG AC GGT
                             G  T  _  I
GAM424  B29            CCCTCCTTCTTCCCTCATG-CCA   6643 _      G  C  A  I
                        CCTCCTTCTTC TTC TG CC
                        IIIIIIIIII III II II
                        GGAGGAAGAAG GAG AC GG
                        G        G  T  _  I
GAM424  BLTR2          CCCTCCTTCTTTG-TCCAGCCC    6642        C  T  TGA  AT
                       CCCTCCTTCTT GT CC  CC
                       IIIIIIIIII II II   II
                       GGGAGGAAGAA CA GG  GG
                             A  _  TCG II
GAM424  BLTR2          CCCTCCTTCTTTG-TCCAGCCC    6642 _      C  CTGACI
                        CCTCCTTCTT GTTC
                        IIIIIIIIII IIII
                        GGAGGAAGAA CAGG
                        G       A  TCGGII
GAM424  CA11           CCCTCCTTCTGGGACCCTGTCC    6641       TCGT   A  AT
                        CCCTCCTTCT   TCCTG CC
                        IIIIIIIIII   IIIII II
                        GGGAGGAAGA   GGGAC GG
                           CCCT    A  II
GAM424  CA11           CCCTCCTTCTGGGACCCTGTCC    6641       TCGT   ACI
                        CCTCCTTCT   TCCTG
                        IIIIIIIII   IIIII
                        GGAGGAAGA   GGGAC
                           CCCT   AGI
GAM424  CAPNS1         TGCAGGGCCTGGTGGGAATGGGGAGA 6661 TT    _    T____    GCII
                        GCAGG CCTGGTGG   GGGAGA
                        IIIII IIIIIIII   IIIIII
                        CGTCC GGACCACC   CCCTCT
                        __   C    CTTAC   GIII
GAM424  CASR           CCCTCCTTCCACTCTCCTG     6635       TCG    ACCA
                       CCCTCCTTCT TTCCTG
                       IIIIIIIIII IIIIII
                       GGGAGGAAGG GAGGAC
                            TGA    IIIT
GAM424  CASR           CCCTCCTTCCACTCTCCTG     6635       TCG    II
                        CCTCCTTCT TTCCT
                        IIIIIIIII IIIII
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                              GGGAGGAAGG  GAGGA
                                  TGA    CI
GAM424  DMD              CTCCTTCTTCATCTGTCATGAC    6650            CCTGAIII
                              CTCCTTCTTCGTT
                              IIIIIIIIIIII
                              GAGGAAGAAGTAG
                                  ACAGTACT
GAM424  DMD              CTCCTTCTTCATCTGTCATGAC    6650 CCCT        ___  C   CAT
                            CCTTCTTCGT  TC TGAC
                            IIIIIIIIII  II IIII
                            GGAAGAAGTA  AG ACTG
                            ____           GAC  T   ACI
GAM424  DVL3             TTTCAGGCCTGGAGGTGAGATGAGC  6669 TTG      T     _   II
                            CAGGCCTGG GGTGGGA GAGC
                            IIIIIIIII IIIIIII IIII
                            GTCCGGACC CCACTCT CTCG
                            AAA       T      A  II
GAM424  ELF3             TTGCAGGCCTCGAGTGGTCCGTGAG  6668      __    GG__  AGCII
                            TTGCAGGCCT GGTGGT   GAG
                            IIIIIIIIII IIIIII   III
                            AACGTCCGGA TCACCA   CTC
                              GC     GGCA  IIICG
GAM424  EPHB2             AGGCCTGGTGGCAGGTGGGAG    6626 TTGCA CT   TG   AGC
                              GGC GGTGG GGAG
                              III IIIII IIII
                              CCG CCACC CCTC
                            GACCA  T_   CT  CII
GAM424  F2RL3            GGCCTGGTGGGGCCACAGC       6660 TTGCA  _   GG  GAGAG
                              GGCC TGGT TGG
                              IIII IIII III
                              CCGG GTCG ACC
                            CCACC   T  TA  IIICG
GAM424  FGFR1            GCAGTGCCTGGTGGCAGGGAG     6651 TTGCAG        _   AGC
                              GCCTGGTGGT GGGAG
                              IIIIIIIIII IIIII
                              CGGACCACCG CCCTC
                            TCA___        T  CCI
GAM424  FOXD2            GCAGTGGTTGGTGGTGGGGGA     6652 TTGCA CC       A GC
                              GG TGGTGGTGGG GA
                              II IIIIIIIIIII II
                              CC ACCACCACCC CT
                            TCA__ A_      C AA
GAM424  GAB2             CCTTCCTTCTTCCTCCACTGGACC  6634       G  _  ACI
                              TCCTTCTTC TTC CTG
                              IIIIIIIII III III
                              AGGAAGAAG AGG GAC
                                G  T  CII
GAM424  GAB2             CCTTCCTTCTTCCTCCACTGGACC  6634 C      G  _  _  ATI
                              CC TCCTTCTTC TTC CTG ACC
                              II IIIIIIIII III III III
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                              GG AGGAAGAAG AGG GAC TGG
                               A      G T  C   III
GAM424  HIPK2              CCCTCCTTCTCTCCCTCCT    6633      _ G    GACCA
                              CCCTCCTTCT TC TTCCT
                              IIIIIIIIII II IIIII
                              GGGAGGAAGA AG GAGGA
                                 G G    IIITA
GAM424  HIPK2              CCCTCCTTCTCTCCCTCCT    6633      _ G   II
                              CCCTCCTTCT TC TTCC
                              IIIIIIIIII II IIII
                              GGGAGGAAGA AG GAGG
                                 G G   AI
GAM424  HOXB1            CAGGCCTGG-GTTGGGAGAGC    6628 TTGCAG    TGG
                               GCCTGG  TGGGAGAG
                               IIIIII  IIIIIIII
                               CGGACC  ACCCTCTC
                              _____     CA_
GAM424  HPSE          CCTTCGCTTCCTTGCTTCCTGACCAT 6629  C _    C _     II
                              CC TC CTTCTT GTT CCTGACCAT
                              II II IIIIII III IIIIIIIII
                              GG AG GAAGGA CGA GGACTGGTA
                                A C   A A     II
GAM424  HPSE          CCTTCGCTTCCTTGCTTCCTGACCAT 6629 CC _    C _    I
                              TC CTTCTT GTT CCTGACCA
                              II IIIIII III IIIIIIII
                              AG GAAGGA CGA GGACTGGT
                              __ C    A A     I
GAM424  IGFBP5         TGCAGCCGAGAGGGTGGGAGA     6664 TT  G T T_      C
                              GCAG CC GG  GGTGGGAGAG
                              IIII II II  IIIIIIIIII
                              CGTC GG TC  CCACCCTCTT
                              __ _ C TC      I
GAM424  KAI1          GCAGGCCTGGAGGAGGGAG       6655 TTGC    T T  AG
                              AGGCCTGG GG GGGAG
                              IIIIIIII II IIIII
                              TCCGGACC CC CCCTC
                              ____      T T  GG
GAM424  KCNK3             CCCTCCTTCTTTCTGTCCTG    6631        _GT  ACCA
                              CCCTCCTTCTT C TCCTG
                              IIIIIIIIIII I IIIII
                              GGGAGGAAGAA G AGGAC
                                 A AC   IIIT
GAM424  KCNK3             CCCTCCTTCTTTCTGTCCTG    6631        _GT  II
                              CCCTCCTTCTT C TCCT
                              IIIIIIIIIII I IIII
                              GGGAGGAAGAA G AGGA
                                 A AC  CI
GAM424  KCNMB3         CCCTCCTTCTCCTCCTCTCTGGCCA 6632          G_ _ A TII
                              CCCTCCTTCTTC TTC CTG CCA
                              IIIIIIIIII III III III
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                         GGGAGGAAGAGG  GAG GAC GGT
                            AG   A   C   III
GAM424  KCNMB3           CCCTCCTTCTCCTCCTCTGGCCA 6632 CC      G_  _ A I
                        TCCTTCTTC  TTC CTG CC
                        |||||||||  ||| ||| ||
                        AGGAAGAGG  GAG GAC GG
                            __      AG   A   C   I
GAM424  LOXL1           AGGCCTGGTGGACAGAGAG     6627 TTGCAGGC    TG
                          CTGGTGG  GGAGAG
                          |||||||  ||||||
                          GACCACC  TCTCTC
                        _____        TG
GAM424  LZTR1          TGCGGG---GGTGGTGGG-GAGC  6666 TT A CCT      A
                       GC GG   GGTGGTGGG GAG
                       || ||   ||||||||| |||
                       CG CC   CCACCACCC CTC
                       __  C  ___      _
GAM424  MAP3K8         TGCAGGCCT----GTGGGAG    6663 TT     GGTG
                       GCAGGCCT   GTGGGAG
                       ||||||||   |||||||
                       CGTCCGGA   CACCCTC
                        __      ____
GAM424  MN1           CCCTCCTTCTTC---CCTG     6637        G CCT
                      CCCTCCTTCTTC TT
                      |||||||||||| ||
                      GGGAGGAAGAAG GA
                            G  CII
GAM424  MN1           CCCTCCTTCTTC---CCTG     6637        GTT  AC
                      CCCTCCTTCTTC  CCTG
                      ||||||||||||  ||||
                      GGGAGGAAGAAG  GGAC
                            ___    II
GAM424  NDUFS2        CCTCCTTCTTGGCTTCTCACC   6648      C  C  G  I
                      CTCCTTCTT GTT CT AC
                      ||||||||| ||| || ||
                      GAGGAAGAA CGA GA TG
                         C   A  G   I
GAM424  NDUFS2        CCTCCTTCTTGGCTTCTCACC   6648 CC     C  C  G  AT
                       CTCCTTCTT GTT CT ACC
                       ||||||||| ||| || |||
                       GAGGAAGAA CGA GA TGG
                        __    C   A  G  AI
GAM424  NHLH1        TTGAAAGC-TGGTGGTGGGAG    6670 C  C       AG
                    TTG AGGC TGGTGGTGGGAG
                    ||| |||| |||||||||||||
                    AAC TTCG ACCACCACCCTC
                      T   _        II
GAM424  NLGN2       GCAGGCGCGTGGTGGTGGTGAAGAGC 6654 TTGC  C__      _ _ II
                    AGGC  TGGTGGTGG GA GAGC
                    ||||  ||||||||| || ||||
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                          TCCG   ACCACCACC CT CTCG
                          ____      CGC       A  T   AG
GAM424  NR4A2         GGTCGGGTAGGGGTGGGAGAGC   6659 TTGCA  CCT  T
                          GG  GG GGTGGGAGAGC
                          ||  || ||||||||||
                          CC  CC CCACCCTCTCG
                          _____    AT_  _
GAM424  PFKFB3         CCCAACATCTACGTTCCTGA      6638   TCCT  T      CCA
                          CCC   TCT CGTTCCTGA
                          |||   ||| |||||||||
                          GGG   AGA GCAAGGACT
                           TTGT  T       |||
GAM424  PFKFB3         CCCAACATCTACGTTCCTGA      6638  TCCT  T      I
                          CC   TCT CGTTCCTG
                          ||   ||| ||||||||
                          GG   AGA GCAAGGAC
                           TTGT  T      I
GAM424  PYGM          AGGCCCTCGGCGGTGGGAGA      6625 TTGCAGG  _
                          CCT GGTGGTGGGAGAG
                          ||| |||||||||||||
                          GGA CCGCCACCCTCTT
                          _____   G
GAM424  RAB7L1        CCCTCCTTCTGCATTCCAGA      6639       T   T CCA
                          CCCTCCTTCT CGTTCC GA
                          |||||||||| |||||| ||
                          GGGAGGAAGA GTAAGG CT
                             C    T |||
GAM424  RAB7L1        CCCTCCTTCTGCATTCCAGA      6639       T   TGI
                          CCTCCTTCT CGTTCC
                          ||||||||| ||||||
                          GGAGGAAGA GTAAGG
                             C    TCI
GAM424  SEPN1         CCTTCCTTCTTCCT--CTG-CCA   6644   _      G TC  A
                          CCT CCTTCTTC T  CTG CC
                          ||| |||||||| |  ||| ||
                          GGA GGAAGAAG A  GAC GG
                             A       G__   _
GAM424  SEPN1         CCTTCCTTCTTCCT--CTG-CCA   6644  C      G TC  A
                          CC TCCTTCTTC T  CTG CCA
                          || |||||||| |  ||| |||
                          GG AGGAAGAAG A  GAC GGT
                             A       G__   _
GAM424  SIGLEC11        GCAGGAAGCCTGGTGGAGGG      6653 TTGC       T  AGAG
                          AGGCCTGGTGG GGG
                          ||||||||||| |||
                          TTCGGACCACC CCC
                          TCC_      T  CGII
GAM424  SLC10A2        CCTCCTGCCACCTCCCTGACCAT   6649   T TCG       I
                          CTCCT CT  TTCCTGACCA
                          ||||| ||  |||||||||||
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                        GAGGA GG  AGGGACTGGT
                          C TGG         I
GAM424 SLC10A2        CCTCCTGCCACCTCCCTGACCAT  6649 CC    T TCG        I
                        CTCCT CT  TTCCTGACCAT
                        |||| || ||||||||||
                        GAGGA GG  AGGGACTGGTA
                        __   C TGG        C
GAM424 SLC19A1        GCTGCCCTTAGGGTGGGAGAG   6658 TTGCAG  __ T     C
                          GCCT GG GGTGGGAGAG
                          |||| || ||||||||||
                          CGGG TC CCACCCTCTC
                        A_____ AA _     T
GAM424 SLC6A8         CCCTCCTTC--CCTTCCTCAC   6640        CG  G CA
                        CCCTCCTTCTT TTCCT AC
                        ||||||||||| ||||| ||
                        GGGAGGAAGGG AAGGA TG
                               __  G II
GAM424 SLC6A8         CCCTCCTTC--CCTTCCTCAC   6640        CG  GI
                        CCCTCCTTCTT TTCCT
                        ||||||||||| |||||
                        GGGAGGAAGGG AAGGA
                               __  GT
GAM424 SMG1          TTGCAGGCCATGGTGTTGGG     6667        _  G  AGAG
                        TTGCAGGCC TGGTG TGGG
                        ||||||||| ||||| ||||
                        AACGTCCGG ACCAC ACCC
                              T  A  IIIC
GAM424 SOX13          GCAGGGCTGG--GTGGGAGAG    6657 TTGC  C  TG
                          AGG CTGG  GTGGGAGAG
                          ||| ||||  ||||||||||
                          TCC GACC  CACCCTCTC
                          ____  C  __
GAM424 SYN3          TTGGAGGCCTGGT-TTGGG-GAGC  6672  C      GG  A
                        TTG AGGCCTGGT TGGG GAGC
                        ||| ||||||||| |||| ||||
                        AAC TCCGGACCA ACCC CTCG
                          C     A_  _
GAM424 TAF7L          CCTCTTGCTCCCTCTCCTGACCA  6646 CC____      TTCGT      I
                        CTCCTTC  TCCTGACCAT
                        |||||||  |||||||||||
                        GAGGGAG  AGGACTGGTG
                        GAGAAC       _____      I
GAM424 TRC8          CCCTCCTTCCTC--TCCTG      6636        GT  ACC
                        CCCTCCTTCTTC TCCTG
                        |||||||||||| |||||
                        GGGAGGAAGGAG AGGAC
                                  __  III
GAM424 TRC8          CCCTCCTTCCTC--TCCTG      6636        GT  I
                        CCCTCCTTCTTC TCCT
                        |||||||||||| ||||
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                              GGGAGGAAGGAG  AGGA
                                __     C
GAM424  TRHDE        CCTCCTTCTTCTTCTTCCT    6645        G__    III
                     CCTCCTTCTTC  TTCC
                     |||||||||||  ||||
                     GGAGGAAGAAG  AAGG
                          AAG   AII
GAM424  TRHDE        CCTCCTTCTTCTTCTTCCT    6645 CC        G__    GACCA
                      CTCCTTCTTC  TTCCT
                      ||||||||||  |||||
                      GAGGAAGAAG  AAGGA
                        __       AAG    GIIIT
GAM424  TRIM39       CCTC-TCCTTCCTTCCTGACC    6647 _  C      G      I
                      CTC TTCTTC TTCCTGAC
                      ||| |||||| |||||||||
                      GAG AGGAAG AAGGACTG
                        G _    G     I
GAM424  TRIM39       CCTC-TCCTTCCTTCCTGACC    6647 CC      TCG      A
                       CTCCTTCT TTCCTGACC
                       |||||||| |||||||||
                       GAGGAAGG AAGGACTGG
                        GA     ___      G
GAM424  VASP         CCCTCCTTCCTTCCCCCTTCCTG  6630         ____ G    ACCATI
                      CCCTCCTTCT  TC TTCCTG
                      ||||||||||  || ||||||
                      GGGAGGAAGG  GG AAGGAC
                         AAGG  G    IIITAC
GAM424  VASP         CCCTCCTTCCTTCCCCCTTCCTG  6630         ____ G    IIIC
                      CCCTCCTTCT  TC TTCCT
                      ||||||||||  || |||||
                      GGGAGGAAGG  GG AAGGA
                         AAGG  G    CIII
GAM425  CENTD2       GGAATCCTAGAGCCAAGGAT      6676 TGGC      A  C_   TT
                       ATCCTAGAG CC  GGAT
                       |||||||||| || ||||
                       TAGGATCTC GG  CCTA
                      CT__        _ TT   CI
GAM425  CSH2         TGGGATCCTAGAG--CCGG       6677  C       AC   ATT
                      TGG ATCCTAGAG  CCGG
                      ||| ||||||||| ||||
                      ACC TAGGATCTC  GGCC
                        C      __   III
GAM425  RAB6A        CAGCCTAGAGACCTCCCGGA      6675 TGGCAT       ___      T
                       CCTAGAGA  CCCGGATT
                       ||||||||  ||||||||
                       GGATCTCT  GGGCCTGG
                      _____       GGA      C
GAM425  RNASE6       TGGCATCCTAGGCACTCGAATT    6678        AG  C   TA
                      TGGCATCCTAG AC CGGATT
                      ||||||||||| || ||||||
```

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                    ACCGTAGGATC  TG GCTTAA
                       CG  A      II
GAM426  ARF4L          GGACTGCCAGCCTCTTCTCC    6692     A   A   I
                       GACTGCCA CCTCT CTC
                       IIIIIIII IIIII III
                       CTGACGGT GGAGA GAG
                          C    A  I
GAM426  ARF4L          GGACTGCCAGCCTCTTCTCC    6692 GAAGGA   A   A
                         CTGCCA CCTCT CTCC
                         IIIIII IIIII IIII
                         GACGGT GGAGA GAGG
                       _____      C   A
GAM426  CACNB2         CTTCCCACCTTCTACTCCC     6689 CTG A  _     II
                         CC ACCT CTACTCC
                         II IIII IIIIIII
                         GG TGGA GATGAGG
                       GAA  G   A    GI
GAM426  CORO2B         AAGGACTGCAGAAACTTTA      6681       CAACCTCTII
                       AAGGACTGC
                       IIIIIIIII
                       TTCCTGACG
                         TCTTTGAAAT
GAM426  CRYZ          AGGACTGCCACACCT-T-CTCC    6685 _      _  _ ACTCI
                       GGACTGCCA ACCT CT
                       IIIIIIIII IIII II
                       CCTGACGGT TGGA GA
                       T     G   A  GIIIC
GAM426  CRYZ          AGGACTGCCACACCT-T-CTCC    6685 GAAG      _ CTA
                       GACTGCCA ACCT  CTCC
                       IIIIIIII IIII  IIII
                       CTGACGGT TGGA  GAGG
                       ____      G   A__
GAM426  F8A           GAAG-ACAGCCATGTCCTCTACTC  6691 AA   T  A__     I
                       GGAC GCCA  CCTCTACT
                       IIII IIII  IIIIIIIII
                       TCTG CGGT  GGAGATGA
                       __    T  ACA     I
GAM426  F8A           GAAG-ACAGCCATGTCCTCTACTC  6691 GA   T  A__     CCI
                       AGGAC GCCA  CCTCTACTC
                       IIIII IIII  IIIIIIIIII
                       TTCTG CGGT  GGAGATGAG
                       C_   T  ACA      III
GAM426  GNAZ          AGGACTGCCA--CTC-ACTCC     6686 _      AC  T
                       GGACTGCCA CTC ACTC
                       IIIIIIIII III IIII
                       CCTGACGGT GAG TGAG
                       T         __  _
GAM426  GNAZ          AGGACTGCCA--CTC-ACTCC     6686 GAAG     AC  T
                       GACTGCCA CTC ACTC
                       IIIIIIII III IIII
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                    CTGACGGT GAG TGAG
                    ____      __  _
GAM426  HOXD1       AGGACTGCCGCCGTCTGCGCC    6687      AA _ ACTCI
                    GGACTGCC CC TCT
                    ||||||| || |||
                    CCTGACGG GG AGA
                        C_ C CGCGI
GAM426  HOXD1       AGGACTGCCGCCGTCTGCGCC    6687 GAAG    AA _ ACT C
                    GACTGCC CC TCT  CC
                    ||||||| || ||| ||
                    CTGACGG GG AGA  GG
                    ____      C_ C CGC C
GAM426  HSPB3       CTGCCAACCTTCCACTGCC     6688        _ _ II
                    CTGCCAACCT CTACT CC
                    |||||||||| ||||| ||
                    GACGGTTGGA GGTGA GG
                         A   C II
GAM426  IRAK4       ACTGC-AACCTCTACCTCCC    6684   C     _ II
                    ACTGC AACCTCTAC TCC
                    ||||| ||||||||| |||
                    TGACG TTGGAGATG AGG
                      _      G  GI
GAM426  RAB7L1      ACTGC-AACCTCTAACTCCC    6683   C     _ II
                    ACTGC AACCTCTA CTCC
                    ||||| |||||||| ||||
                    TGACG TTGGAGAT GAGG
                      _      T  GI
GAM426  SORCS3      CTTCCAACCTCTTTAACTCC    6690 CTG      ___ III
                    CCAACCTCT ACTC
                    ||||||||| ||||
                    GGTTGGAGA TGAG
                    GAA     AAT GII
GAM426  ZNF265      AAGGCATGC--ACCTCTACT    6682 _ AC CA     I
                    AGG TGC ACCTCTAC
                    ||| ||| ||||||||
                    TCC ACG TGGAGATG
                    T  GT __    I
GAM426  ZNF265      AAGGCATGC--ACCTCTACT    6682 GA AC CA     C
                    AGG TGC ACCTCTACT
                    ||| ||| |||||||||
                    TCC ACG TGGAGATGA
                    __  GT __     T
GAM427  AQP6        TCAGTTCTTCTCAAGGGTG     6708      C TIII
                    TCAGTTCTTC CAGG
                    |||||||||| ||||
                    AGTCAAGAAG GTTC
                        A   CCAC
GAM427  AQP6        TCAGTTCTTCTCAAGGGTG     6708 TATC   C __ AACA
                    AGTTCTTC CA GGTG
                    |||||||| || ||||
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                              TCAAGAAG GT  CCAC
                    ____          A  TC    CCII
GAM427 CAPN9        TCA-TTCTTCCCAGATCAA      6709 TATCA        G  C
                        GTTCTTCCCAGGT AA
                        ||||||||||| ||
                        TAAGAAGGGTCTA TT
                    _____              G  C
GAM427 CAPN9        TCA-TTCTTCCCAGATCAA      6709 TCA         GAI
                        GTTCTTCCCAGGT
                        ||||||||||||
                        TAAGAAGGGTCTA
                    AG_          GTT
GAM427 CD80       CTTCCCAGGTGCAAAACAG      6705         AACAIII
                       CTTCCCAGGTG
                       ||||||||||
                       GAAGGGTCCAC
                          GTTTGT
GAM427 CLU        TCTGTTCTTCCCA--TGAGCAG  6712 CA      GG  AI
                        GTTCTTCCCA TGA
                        |||||||||| |||
                        CAAGAAGGGT ACT
                    GA        __  CG
GAM427 CLU        TCTGTTCTTCCCA--TGAGCAG  6712 TATCA      GG  A
                        GTTCTTCCCA TGA CA
                        |||||||||| ||| ||
                        CAAGAAGGGT ACT GT
                    A____          __  C
GAM427 CREBL2     AGTTCTTCCCTATTTAACAG    6696        AGGTG  I
                       GTTCTTCCC   AACA
                       |||||||||   ||||
                       CAAGAAGGG   TTGT
                         ATAAA    I
GAM427 CREBL2     AGTTCTTCCCTATTTAACAG      6696 TATCAGTT    AGGTG
                        CTTCCC   AACA
                        ||||||   ||||
                        GAAGGG   TTGT
                    _____        ATAAA
GAM427 DISC1     ATGAGTTCTTAGCCAGGTGAACA  6698 TATC    C_      I
                       AGTTCTT CCAGGTGAACAG
                       ||||||| |||||||||||
                       TCAAGAA GGTCCACTTGTT
                    AC__       TC        I
GAM427 DISC1     ATGAGTTCTTAGCCAGGTGAACA  6698 TC      C_      I
                       AGTTCTT CCAGGTGAAC
                       ||||||| ||||||||||
                       TCAAGAA GGTCCACTTG
                    C_     TC      I
GAM427 FEN1      TCAGCTGATTGCCAGGTGAACA   6707 C   C_  C      I
                       AGTT TT CCAGGTGAAC
                       |||| || ||||||||||
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                              TCGA  AA GGTCCACTTG
                               _    CT C        I
GAM427  FEN1            TCAGCTGATTGCCAGGTGAACA   6707 TATC   C_ C        G
                              AGTT  TT CCAGGTGAACA
                              |||| || |||||||||||
                              TCGA  AA GGTCCACTTGT
                              ____    CT C         A
GAM427  GGA1            AGTTCTTCCAAGGCTACACAG   6695 G    C  GA_   I
                              TTCTTCC AGGT  ACA
                              ||||||| ||||  |||
                              AAGAAGG TCCG  TGT
                               _      T  ATG I
GAM427  GGA1            AGTTCTTCCAAGGCTACACAG   6695 TATCAGTT   C  GA_
                              CTTCC AGGT  ACAG
                              ||||| ||||  ||||
                              GAAGG TCCG  TGTC
                              _____   T  ATG
GAM427  GNAZ           TCATTTGCTCCCAGGTGAA   6710  G C        II
                              TCA TT TTCCCAGGTGA
                              ||| || |||||||||||
                              AGT AA GAGGGTCCACT
                               A  C        TI
GAM427  GNAZ           TCATTTGCTCCCAGGTGAA   6710 TATCAGTTC        CA
                              TTCCCAGGTGAA
                              ||||||||||||
                              GAGGGTCCACTT
                              TAAAC____         TC
GAM427  MAPRE1        TCTGTT-TTCC-AGGTGAAC   6711 CA_  C  C     I
                              GTT TTCC AGGTGAA
                              ||| |||| |||||||
                              CAA AAGG TCCACTT
                               AGA  _   _     I
GAM427  MAPRE1        TCTGTT-TTCC-AGGTGAAC   6711 TATCA  C   C
                              GTT TTCC AGGTGAAC
                              ||| |||| ||||||||
                              CAA AAGG TCCACTTG
                               A____  _   _
GAM427  MC1R           CAGTTCTTCCCCTCCAGGTG   6701 TATCAG     _     AACA
                              TTCTTC CCAGGTG
                              |||||| |||||||
                              AAGGGG GGTCCAC
                              AAG___    A    AGGI
GAM427  MC1R           CAGTTCTTCCCCTCCAGGTG   6701           ____  IIIC
                              CAGTTCTTCCC  AGGT
                              |||||||||||  ||||
                              GTCAAGAAGGG  TCCA
                               GAGG   CIII
GAM427  MLPH          ATCAGTAAA-CCCAGGTGAGCAG   6700 _  TCTT      ACAI
                              TCAGT  CCCAGGTGA
                              |||||  |||||||||
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                        AGTCA   GGGTCCACT
                    T    TTT_        CGTI
GAM427 MLPH         ATCAGTAAA-CCCAGGTGAGCAG  6700 TA   TCTT      A
                        TCAGT   CCCAGGTGA CAG
                        |||||   ||||||||| |||
                        AGTCA   GGGTCCACT GTC
                         __    TTT_         C
GAM427 NR1I2        CAGTTGTCTTCAGGTGAACA  6704   C CC      I
                        AGTT TT CAGGTGAAC
                        |||| || |||||||||
                        TCAA AG GTCCACTTG
                          C AA       I
GAM427 NR1I2        CAGTTGTCTTCAGGTGAACA   6704 TATCA T  CC
                        GT CTTC AGGTGAACA
                        || |||| |||||||||
                        CA GAAG TCCACTTGT
                    AA___ _  __
GAM427 OGG1         CAGTTCTTCACCTTGTGAA   6702    _ AG  II
                        CAGTTCTTC CC GTGA
                        ||||||||| || ||||
                        GTCAAGAAG GG  CACT
                          T AA   TI
GAM427 OGG1         CAGTTCTTCACCTTGTGAA   6702 TATCAG   _ AG   CA
                        TTCTTC CC GTGAA
                        |||||| || |||||
                        AAGAAG GG  CACTT
                    _____     T AA   AG
GAM427 OVOL1        TCTTCCCAGGCTCAGAACAG   6715        ___    III
                        TCTTCCCAGGT GAACA
                        ||||||||||| |||||
                        AGAAGGGTCCG  CTTGT
                          AGT   CII
GAM427 OVOL1        TCTTCCCAGGCTCAGAACAG    6715 TA__  TTCTT CA  GAACA
                        TCAG   CC GGT
                        ||||   || |||
                        AGTC   GG  CCG
                        TCCG   TTGTC AG  IIIGA
GAM427 PCDHGA8      TCTTCCAGTAGGTGAACAG    6713    C__     III
                        TCTTCC AGGTGAACA
                        |||||| |||||||||
                        AGAAGG TCCACTTGT
                          TCA      CII
GAM427 PIP5K1B      CAGTTCTTCACAGTTCAGCA   6703    C GTGAACI
                        AGTTCTTC CAG
                        |||||||| |||
                        TCAAGAAG GTC
                          T AAGTCGI
GAM427 PIP5K1B      CAGTTCTTCACAGTTCAGCA   6703 TAT____   TTCC   GAACA
                        CAGTTC CAGGT
                        |||||| |||||
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                        GTCAAG   GTTCG
                     AAGAAGT   TC__    IIIGA
GAM427  PLCG2        TCTTCCCAGAGTGTGAATAG   6714        ___    CAIII
                        TCTTCCCAG  GTGAA
                        IIIIIIIII  IIIII
                        AGAAGGGTC  CACTT
                          TCA    ATCII
GAM427  PPP1R12B     ATCAAATCATTCCAGGTGAA   6699    T TTC      I
                        TCAG TC  CCAGGTGA
                        IIII II  IIIIIIII
                        AGTT AG  GGTCCACT
                          T TAA      I
GAM427  PPP1R12B     ATCAAATCATTCCAGGTGAA   6699 TA  T TTC       CA
                        TCAG TC  CCAGGTGAA
                        IIII II  IIIIIIIII
                        AGTT AG  GGTCCACTT
                        __   T TAA       TI
GAM427  TAF4B        TCAGCTTCTTCCTCAGGTGAACA   6706 CAG      _       I
                        TTCTTCC  CAGGTGAAC
                        IIIIIII  IIIIIIIII
                        AAGAAGG  GTCCACTTG
                          CG_    A      I
GAM427  TAF4B        TCAGCTTCTTCCTCAGGTGAACA   6706 TATCAG      _       GI
                         TTCTTCC  CAGGTGAACA
                         IIIIIII  IIIIIIIIII
                         AAGAAGG  GTCCACTTGT
                         TCG___   A        GT
GAM427  TNNI1        ATCATTTGCATCCCAGGTGA   6697   GTTCT_      II
                        ATCA    TCCCAGGTG
                        IIII    IIIIIIIII
                        TAGT    AGGGTCCAC
                         AAACGT       TI
GAM427  TNNI1        ATCATTTGCATCCCAGGTGA   6697 TA  GTTCT_       ACA
                        TCA    TCCCAGGTGA
                        III    IIIIIIIIII
                        AGT    AGGGTCCACT
                        __   AAACGT       AII
GAM428  ACOX1        GAGTTGCACACAGGC-GCTT   6726 _         TGTCA  I
                        AGTTGCACAC   GCT
                        IIIIIIIIII   III
                        TCAACGTGTG   CGA
                        C       TCCG_  I
GAM428  ACOX1        GAGTTGCACACAGGC-GCTT   6726 TGAGAG      TGTCA
                        TTGCACAC   GCTT
                        IIIIIIII   IIII
                        AACGTGTG   CGAA
                        _____       TCCG_
GAM428  ATSV         AGAGTCTGCACACTGGCAG    6718    _       T II
                        AGAGT TGCACACTG CA
                        IIIII IIIIIIIII II
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                          TCTCA ACGTGTGAC GT
                            G        C CI
GAM428  ATSV          AGAGTCTGCACACTGGCAG      6718 TGAG  _      T  CTT
                          AGT TGCACACTG CAG
                          ||| ||||||||| |||
                          TCA ACGTGTGAC GTC
                          ____   G        C  CAI
GAM428  CALM3         TGAGTGTTGCCCACTGTCAG      6728  A  A      CTT
                          TGAG GTTGC CACTGTCAG
                          |||| ||||| |||||||||
                          ACTC CAACG GTGACAGTC
                             A    G       |||
GAM428  CALM3         TGAGTGTTGCCCACTGTCAG      6728  A  A      I
                          GAG GTTGC CACTGTCA
                          ||| ||||| ||||||||
                          CTC CAACG GTGACAGT
                            A    G      I
GAM428  CSN10          GAGTTGG-C-CTGTCAGCT      6725     CACA    I
                          GAGTTG  CTGTCAGC
                          ||||||  ||||||||
                          CTCAAC  GACAGTCG
                             CG__      A
GAM428  CSN10          GAGTTGG-C-CTGTCAGCT      6725 TGAGAGTTGCACA
                                 CTGTCAGCT
                                 |||||||||
                                 GACAGTCGA
                          AACCG_____
GAM428  GOSR1         AGAGTC-CATCACTGTCAGTCTTG  6720 G  G  _     _  I
                          AGTT CA CACTGTCAG CTT
                          |||| || ||||||||| |||
                          TCAG GT GTGACAGTC GAA
                          _  _ A    A  I
GAM428  GOSR1         AGAGTC-CATCACTGTCAGTCTTG  6720 TGAG   G  _     _  I
                          AGTT CA CACTGTCAG CTTG
                          |||| || ||||||||| ||||
                          TCAG GT GTGACAGTC GAAC
                          ____   _  A    A  G
GAM428  IFI27        AGAGTTGCAACAAT-TCATCTT     6719     C  TG_  G I
                          GAGTTGCA AC  TCA CT
                          |||||||| ||  ||| ||
                          CTCAACGT TG  AGT GA
                           _ TTA  A I
GAM428  IFI27        AGAGTTGCAACAAT-TCATCTT     6719 TGAG    C  TG_  G G
                          AGTTGCA AC  TCA CTT
                          ||||||| ||  ||| |||
                          TCAACGT TG  AGT GAA
                          ____    _ TTA  A A
GAM428  KIF3C         GAGCAGATGCCCAACACTGTCAG   6722 _  T  ___       IIIC
                          GAG AG TGC  ACACTGTCA
                          ||| || |||  |||||||||
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                        CTC TC ACG  TGTGACAGT
                        G T  GGT      CIII
GAM428  KIF3C           GAGCAGATGCCCAACACTGTCAG  6722 TG_ _ GC       CTTGI
                        AGA GTT  ACACTGTCAG
                        III III  IIIIIIIIII
                        TCT CGG  TGTGACAGTC
                        TCG  A  GT      CIIIG
GAM428  MFAP4           GAGAGTGGCTCCTGGCTGTCAGCT  6723 AGA  GCACA       I
                        GTT   CTGTCAGC
                        III   IIIIIIIII
                        CGA   GACAGTCG
                        CAC  GGACC    I
GAM428  MFAP4           GAGAGTGGCTCCTGGCTGTCAGCT  6723 TG  T ACA___       TGI
                        AGAGT GC   CTGTCAGCT
                        IIIII II   IIIIIIIII
                        TCTCA CG    GACAGTCGA
                        __  C AGGACC       CII
GAM428  PTGIR           AGAGAT-CACAGGGTCAGCTTG   6721 _ TTG  CT     I
                        GAG  CACA  GTCAGCTT
                        III  IIII  IIIIIIIII
                        CTC  GTGT  CAGTCGAA
                        T TA_  CC     I
GAM428  PTGIR           AGAGAT-CACAGGGTCAGCTTG   6721 TGAG  TTG   CT
                        AG  CACA  GTCAGCTTG
                        II  IIII  IIIIIIIII
                        TC  GTGT  CAGTCGAAC
                        ____  TA_  CC
GAM428  PTPN1           GAGAGTTGCTCCCTG-CAGATT   6724       ACA T CI
                        AGAGTTGC  CTG CAG
                        IIIIIIII  III III
                        TCTCAACG  GAC GTC
                        AGG _ TA
GAM428  PTPN1           GAGAGTTGCTCCCTG-CAGATT   6724 TG     ACA T C G
                        AGAGTTGC  CTG CAG TT
                        IIIIIIII  III III II
                        TCTCAACG  GAC GTC AA
                        __   AGG _ T G
GAM428  TCP11           TGAGTTGTTGCACACGGACAGCT  6727   A_     TGT  TGI
                        TGAG GTTGCACAC  CAGCT
                        IIII IIIIIIIII  IIIII
                        ACTC CAACGTGTG  GTCGA
                        AA     CCT III
GAM428  TCP11           TGAGTTGTTGCACACGGACAGCT  6727 GAGA     TGT I
                        GTTGCACAC  CAGC
                        IIIIIIIII  IIII
                        CAACGTGTG  GTCG
                        TCAA     CCT I
GAM429  CDK7            AAACCAGAAT-TAAATTTTTA    6738 GGAAT    GC
                        CTAGAA TAAATTTTTA
                        IIIIII IIIIIIIIII
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                              GGTCTT ATTTAAAAAT
                             T____      A_
GAM429  CDK7          AAACCAGAAT-TAAATTTTTA    6738 TGGAAT     GC
                             CTAGAA TAAATTTTT
                             |||||| |||||||||
                             GGTCTT ATTTAAAAA
                             _____      A_
GAM429  CNTNAP2       AATCTAGAAACTTGAATTCAATTTA 6735 GGAA        A_   TTAII
                             TCTAGAAGCT AATTT
                             |||||||||| |||||
                             AGATCTTTGA TTAAG
                             ____       AC   TTAAA
GAM429  CREBL2        ATTTGGAAGCTAAATATTT     6741 GGAATCTA        T
                              GAAGCTAAAT TTT
                              |||||||||| |||
                              CTTCGATTTA AAA
                             AC_____        T
GAM429  CREBL2        ATTTGGAAGCTAAATATTT     6741 TGGAATCTA        T
                              GAAGCTAAAT TTT
                              |||||||||| |||
                              CTTCGATTTA AAA
                             C_____       T
GAM429  CRYGB         GAAAC-ACAAGCTAAATATTTTA  6743 GGAATC G      T AI
                              TA AAGCTAAAT TTT
                              || ||||||||| |||
                              GT TTCGATTTA AAA
                             TTT___  G      T AT
GAM429  CRYGB         GAAAC-ACAAGCTAAATATTTTA  6743 TGGAATC G       T A
                              TA AAGCTAAAT TTT
                              || ||||||||| |||
                              GT TTCGATTTA AAA
                             TT_____  G     T A
GAM429  DAZL          AATCTAGAAACAATGCTAACTTTT 6733 GGAA        TA____     II
                              TCTAGAAGC   AATTTTTA
                              |||||||||   ||||||||
                              AGATCTTTG   TTGAAAAT
                             ____         TTACGA     TI
GAM429  DMD           TACGATGTCAG---TACTTCCAAT 6750 AA_ T  CAA
                              GAT TTAG  TACTTCCAA
                              ||| ||||  |||||||||
                              CTA AGTC  ATGAAGGTT
                             ATG  C   ___
GAM429  DMD           TACGATGTCAG---TACTTCCAAT 6750 TAA  T   CAA
                              GAT TTAG  TACTTCCAAT
                              ||| ||||  ||||||||||
                              CTA AGTC  ATGAAGGTTA
                             ATG  C   ___
GAM429  DSCR1         TGAATTGTATAAGCTAAATT     6751 TG  CTAG_      TTT
                              GAAT   AAGCTAAATT
                              ||||   ||||||||||
```

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                              CTTA    TTCGATTTAA
                          A_    ACATA        III
GAM429  GPR48          GGAATCAAGTA---AAATTTTTA   6749     TAG  CT
                          GGAATC  AAG  AAATTTTTA
                          IIIIII  III  IIIIIIIII
                          CCTTAG  TTC  TTTAAAAAT
                              ___      AT
GAM429  LECT2          AAGTTTGAATGAATACTTCC     6732 TAAGATTTTAGC       AA
                                  AATACTTCC
                                  IIIIIIIII
                                  TTATGAAGG
                          TCAAACTTAC__       AI
GAM429  LNK          GGAAATTCTAGAAGCAAAAATTT  6746   __       T_    TTAI
                          GGAA  TCTAGAAGC  AAATTT
                          IIII  IIIIIIIII  IIIIII
                          CCTT  AGATCTTCG  TTTAAA
                            TA       TT    IIIA
GAM429  LNK          GGAAATTCTAGAAGCAAAAATTT  6746 T   _       T_    TTAI
                          GGAAT CTAGAAGC  AAATTT
                          IIIII IIIIIIII  IIIIII
                          CTTTA GATCTTCG  TTTAAA
                            _    A    TT    CIII
GAM429  LUZP1         AAGCTTTCCGTCAATACTTCC    6731 TA A  AG_       AAT
                          AG TTTT  CAATACTTCC
                          II IIII  IIIIIIIIII
                          TC AAAG  GTTATGAAGG
                            __ G   GCA        CII
GAM429  LUZP1         AAGCTTTCCGTCAATACTTCC    6731 AGA  AG_       I
                             TTTT  CAATACTTC
                             IIII  IIIIIIIII
                             AAAG  GTTATGAAG
                          CG_  GCA        I
GAM429  MEN1         ATTTCATCCCCACTTCCAAT      6742     GCAA       I
                          TTTTA  TACTTCCAA
                          IIIII  IIIIIIIII
                          AAAGT  GTGAAGGTT
                            AGGG       I
GAM429  MEN1         ATTTCATCCCCACTTCCAAT      6742 TAAGATTTTAGCAA
                                  TACTTCCAA
                                  IIIIIIIII
                                  GTGAAGGTT
                          GTAGGG_____
GAM429  P23          AATGT-GAAG-TAAATTTTT     6737 GGAATCTA   C
                             GAAG TAAATTTTT
                             IIII IIIIIIIII
                             CTTC ATTTAAAAA
                          ACA_____   _
GAM429  P23          AATGT-GAAG-TAAATTTTT     6737 TGGAATCTA   C
                             GAAG TAAATTTTT
                             IIII IIIIIIII
```

```
                              CTTC ATTTAAAA
                    CA_____      _
GAM429  PSCDBP          AATCTAGAAAATAAATATT     6736 GGAA     C    TTTT
                           TCTAGAAG TAAAT
                           |||||||| |||||
                           AGATCTTT ATTTA
                    ____        T    TAAT
GAM429  SEL1L           GGAAGCTGGGGGCTAAATTTGTA   6748  T  AGAA     TTAI
                           GGAA CT   GCTAAATTT
                           |||| ||   |||||||||
                           CCTT GA   CGATTTAAA
                           C  CCCC      CATI
GAM429  SLC22A12        GAGTTTAGCAATCATTTCC      6745  T       ACTTCII
                           GA TTTAGCAAT
                           || |||||||||
                           CT AAATCGTTA
                           C       GTAAAGG
GAM429  SLC22A12        GAGTTTAGCAATCATTTCC      6745 TAAGAT      AC_   AA
                           TTTAGCAAT  TTCC
                           |||||||||  ||||
                           AAATCGTTA  AAGG
                    _____        GTA   AA
GAM429  SMARCA3        AATCT-GACTGCTAAATTTCTA    6734 GGAA  A  A_
                           TCT GA  GCTAAATTTTTA
                           ||| ||  |||||||||||
                           AGA CT  CGATTTAAAGAT
                    ____      _  GA
GAM429  SMARCA3        AATCT-GACTGCTAAATTTCTA    6734 TGGAATCTA  A_
                           GA  GCTAAATTTTTA
                           ||  |||||||||||
                           CT  CGATTTAAAGAT
                    GA_____    GA
GAM429  TAF5         GAACATGGAAGCTAAATTT        6744 GGAATCTA          T
                           GAAGCTAAATTTT
                           |||||||||||||
                           CTTCGATTTAAAG
                    TTGTAC__          I
GAM429  TAF5         GAACATGGAAGCTAAATTT        6744 TGGAATCTA
                           GAAGCTAAATTTTT
                           ||||||||||||||
                           CTTCGATTTAAAGA
                    TGTAC____
GAM429  TCF12        ATCTAGAAGCTTGAAAAGTCTT     6740 GGAATC       AAATTTTTAI
                           TAGAAGCT
                           ||||||||
                           ATCTTCGA
                    _____        ACTTTTCAGA
GAM429  TRIM34         AGTTTGTACCTGATACTTCCA    6739 TAAGATTTTAGCA       AT
                           ATACTTCCA
                           |||||||||
```

```
                              TATGAAGGT
                        AAACATGGAC___        CC
GAM429  ZNF264          GGGATCTATACGCTGAAAATTTTTA 6747 _  A   GAA  __       II
                        GGA TCTA  GCT  AAATTTTTA
                        ||| ||||  |||  |||||||||
                        CCT AGAT  CGA  TTTAAAAAT
                        C  _  ATG  CT      II
GAM429  ZNF264          GGGATCTATACGCTGAAAATTTTTA 6747 T  A   GAA  __       II
                        GGA TCTA  GCT  AAATTTTTA
                        ||| ||||  |||  |||||||||
                        CCT AGAT  CGA  TTTAAAAAT
                        _  _  ATG  CT      TI
GAM430  DLG5            GGATTTCAACCTCCTTGTTGGC   6754 TGGG        ____       CAGG
                        GTTTCAACT   TGTTGGC
                        |||||||||   |||||||
                        TAAAGTTGG   ACAACCG
                        ____        AGGA      AGII
GAM430  EPB41           TGAGGTT----CTTGTTGGCC   6758      TCAA       A
                        TGGGGTT  CTTGTTGGCC
                        |||||||  ||||||||||
                        ACTCCAA  GAACAACCGG
                         ____          I
GAM430  GOLGA4          GGTTTTCAACTTGCTAGTCA   6756 TGGGG       C
                        TTTCAACTTGTTGG CAG
                        |||||||||||||| |||
                        AAAGTTGAACGATC GTT
                        A____        A
GAM430  PSD             TGGGGTTTCA-CTACGTTGGCCAGG 6757      ACT       I
                        TGGGGTTTCA TGTTGGCCAGG
                        |||||||||| |||||||||||
                        ACCCCAAAGT GCAACCGGTCC
                            GAT        I
GAM430  SULT2A1         GGGTTTCAAC-TG-TAGCCA   6755 TGGG     T T
                        GTTTCAACT GT GGCCA
                        ||||||||| || |||||
                        CAAAGTTGA CA TCGGT
                            ____      _ _
GAM431  ARHC            TGTCCGGGGGGCTTTGCACA   6764       _ CG    TCAT
                        TGTCCGGGGG C TGTACA
                        |||||||||| | ||||||
                        ACAGGCCCCC G ACGTGT
                            C AA     IIIG
GAM431  ARHC            TGTCCGGGGGGCTTTGCACA   6764       _ CG    II
                        TGTCCGGGGG C TGTAC
                        |||||||||| | |||||
                        ACAGGCCCCC G ACGTG
                            C AA    TI
GAM431  ARHGAP6         CGGGGGCCGCTTGT-CATC    6762        GTA_  II
                        CGGGGGCCGT  CAT
                        ||||||||||  |||
```

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                      GCCCCCGGCG   GTA
                    AACA   GI
GAM431 ARHGAP6      CGGGGGCCGCTTGT-CATC      6762 TGTCCGGG    GTA_  A
                    GGCCGT   CATC
                    ||||||   ||||
                    CCGGCG   GTAG
                    _____    AACA   G
GAM431 HD           TGGCCGGGGGCCCTGTCCACCA   6765  T     G  A   TG
                    TG CCGGGGGCC TGT CATCA
                    || ||||||||| ||| |||||
                    AC GGCCCCGG ACA GTGGT
                      C    G  G  ||
GAM431 HD           TGGCCGGGGGCCCTGTCCACCA   6765 GT     G  A   I
                      CCGGGGGCC TGT CATC
                      ||||||||| ||| ||||
                      GGCCCCGG ACA GTGG
                      CC     G  G  I
GAM431 MAPT         CGGGGGCCGGGT-CATTAT      6763      T  A  CAI
                    CGGGGGCCG GT CAT
                    ||||||||| || |||
                    GCCCCCGGC CA GTA
                        C _ ATA
GAM431 MAPT         CGGGGGCCGGGT-CATTAT      6763 TGTCCGGG   T  A  CA
                      GGCCG GT CAT
                      ||||| || |||
                      CCGGC CA GTA
                    _____      C _ AT
GAM431 PSME3        CCGGGCCGGGCCGTGTCCGATC   6761    ___     ACATIIIG
                    CCGGG GGCCGTGT
                    ||||| |||||||||
                    GGCCC CCGGCACA
                      GGC     GGCTAGII
GAM431 PSME3        CCGGGCCGGGCCGTGTCCGATC   6761 TGTCCGG    AC_ ATG
                      GGGCCGTGT ATC
                      ||||||||| |||
                      CCCGGCACA TAG
                    CCGG___      GGC  GAG
GAM432 ALDH1A3      CTGCAGCTA--GGATCGGAATTCC 6779   G CC TC
                    CTGCAG TA GG CGGAATTCC
                    |||||| || || |||||||||
                    GACGTC AT CC GCCTTAAGG
                      G __ TA
GAM432 ALDH1A3      CTGCAGCTA--GGATCGGAATTCC 6779 _   G CC TC    I
                     TGCAG TA GG CGGAATTC
                    |||||| || || |||||||||
                     ACGTC AT CC GCCTTAAG
                      G  G __ TA   I
GAM432 ATP1B1       GCAGCTGCCGCGGTCCGGA      6780  __ AC      III
                    GCAG GT CGGTCCGG
                    |||| || ||||||||
```

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                         CGTC CG  GCCAGGCC
                           GA  GC       TII
GAM432 ATP1B1          GCAGCTGCCGCGGTCCGGA    6780 __    AGGTAC      ATTC
                         CTGC    CGGTCCGGA
                         ||||    |||||||||
                         GACG    GCCAGGCCT
                           TC  GC____      CCII
GAM432 CNTN1          TGC-GGCACAG--CCGGAATTC   6787 _ A   C T
                         GC GGTAC GG CCGGAATT
                         || ||||| || ||||||||
                         CG CCGTG TC GGCCTTAA
                           A _    _ _
GAM432 CNTN1          TGC-GGCACAG--CCGGAATTC   6787 CT A   C T
                         GC GGTAC GG CCGGAATT
                         || ||||| || ||||||||
                         CG CCGTG TC GGCCTTAA
                           __ _    _ _
GAM432 FCN2          TGCAGGTACGCGGGCCTGGGAA   6785      _ T _ AIII
                         TGCAGGTAC CGG CC GG
                         ||||||||| ||| || ||
                         ACGTCCATG GCC GG CC
                             C  C A CTTI
GAM432 FCN2          TGCAGGTACGCGGGCCTGGGAA   6785 CT     _ T __ TTCC
                         GCAGGTAC CGG CC GGAA
                         |||||||| ||| || ||||
                         CGTCCATG GCC GG CCTT
                           __      C  C AC  CIII
GAM432 GYG          CTGCAGGTAACCATCAGAGAA    6773      _ GTC  ATTCC
                         CTGCAGGTA CCG  CGGA
                         ||||||||| |||  ||||
                         GACGTCCAT GGT  GTCT
                             T  A__   CTTII
GAM432 GYG          CTGCAGGTAACCATCAGAGAA    6773 T     _ G C AI
                         GCAGGTA CCG TC GG
                         ||||||| ||| || ||
                         CGTCCAT GGT AG CT
                           _    T _ T CT
GAM432 HTR6          CTGCAGGTAAGGGGCCTGGA    6772      CC_  C ATTC
                         CTGCAGGTA  GGTC GGA
                         |||||||||  |||| |||
                         GACGTCCAT  CCGG CCT
                           TCC  A  IIIC
GAM432 HTR6          CTGCAGGTAAGGGGCCTGGA    6772      CC_  C II
                         CTGCAGGTA  GGTC GG
                         |||||||||  |||| ||
                         GACGTCCAT  CCGG CC
                           TCC  A TI
GAM432 IRS2          GCAGGTACCTGCACTGGAAT    6781      G CC_  II
                         GCAGGTACC GT  GGAA
                         ||||||||| ||  ||||
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                    CGTCCATGG CG  CCTT
                     A TGA    AI
GAM432 IRS2        GCAGGTACCTGCACTGGAAT    6781 CTGC    G CC_
                     AGGTACC GT  GGAATTC
                     |||||||| || |||||||
                     TCCATGG CG  CCTTAGG
                     ____      A TGA
GAM432 LAMR1       CTGCAGGTA---GCACGGAA   6776       ACC TC  TT
                     CTGCAGGT GG CGGAA
                     |||||||| || |||||
                     GACGTCCA TC GCCTT
                       ___ GT   II
GAM432 LAMR1       CTGCAGGTA---GCACGGAA   6776 _     ACC TC
                     TGCAGGT GG CGGA
                     ||||||| || ||||
                     ACGTCCA TC GCCT
                     G   ___ GT
GAM432 MARK3       CTGC-GGAA--GGATCGGAATTCC  6778   A TACC TC
                     CTGC GG  GG CGGAATTCC
                     |||| || || |||||||||
                     GACG CC  CC GCCTTAAGG
                      _ TT__ TA
GAM432 MARK3       CTGC-GGAA--GGATCGGAATTCC  6778 _ A TACC TC
                     TGC GG  GG CGGAATTC
                     ||| || || ||||||||
                     ACG CC  CC GCCTTAAG
                     G _ TT__ TA
GAM432 MARK3       CTGCTGGCCGCCGCTGCGGAATTCC 6770   A A_ GTC       II
                     CTGC GGT CCG  CGGAATTCC
                     |||| ||| ||| ||||||||
                     GACG CCG GGC  GCCTTAAGG
                       A GC GAC        II
GAM432 MARK3       CTGCTGGCCGCCGCTGCGGAATTCC 6770 T A A_ GTC       I
                     GC GGT CCG  CGGAATTC
                     || ||| ||| |||||||
                     CG CCG GGC  GCCTTAAG
                     _ A GC GAC         I
GAM432 MYBPH       GCAGGTACCAGGGGCGG--TTCC   6782 _     _ TC AATTCI
                     CAGGTACC GG CGG
                     |||||||| || |||
                     GTCCATGG CC GCC
                     C    T CC  AAGIII
GAM432 MYBPH       GCAGGTACCAGGGGCGG--TTCC   6782 CTGC    _ TC AA
                     AGGTACC GG CGG TTCC
                     ||||||| || ||| ||||
                     TCCATGG CC GCC AAGG
                     ____      T CC __
GAM432 NRIP1       GCAGGTACC--ACAGGAAT    6784       GTCC I
                     GCAGGTACCG GGAA
                     |||||||||  ||||
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                          CGTCCATGGT  CCTT
                            GT__    A
GAM432  NRIP1           GCAGGTACC--ACAGGAAT      6784 CTGC     GTCC    T
                          AGGTACCG  GGAAT
                          |||||||| |||||
                          TCCATGGT  CCTTA
                          ____       GT__    C
GAM432  PHKG2           AGGTACCGGGCTGGTCTTC     6768      TCC AATTII
                          AGGTACCGG  GG
                          ||||||||| ||
                          TCCATGGCC  CC
                            CGA AGAAGI
GAM432  PHKG2           AGGTACCGGGCTGGTCTTC      6768 CTGCAGGT   TCC AA
                          ACCGG  GG TTC
                          ||||| || |||
                          TGGCC  CC AAG
                          _____    CGA AG
GAM432  POLR2E           CTGCAGGGAAAGGCAGCCGGAATTC 6771     TACC __      CII
                          CTGCAGG  GGT CCGGAATTC
                          ||||||| ||| |||||||||
                          GACGTCC  CCG GGCCTTAAG
                            CTTT TC       III
GAM432  POLR2E           CTGCAGGGAAAGGCAGCCGGAATTC 6771 TG   TACC __       I
                          CAGG  GGT CCGGAATT
                          ||||  ||| |||||||||
                          GTCC  CCG GGCCTTAA
                          __   CTTT TC      I
GAM432  RPL18           CTGCTCGGCCAGGTCCGGAA      6777   A_  ACC      TTC
                          CTGC GGT GGTCCGGAA
                          |||| ||| |||||||||
                          GACG CCG CCAGGCCTT
                            AG GT_      III
GAM432  RPL18           CTGCTCGGCCAGGTCCGGAA       6777   A_  ACC      I
                          TGC GGT GGTCCGGA
                          ||| ||| ||||||||
                          ACG CCG CCAGGCCT
                            AG GT_     I
GAM432  RTN2           CTCCAGCGGCGGGTCCGGAA      6775 T___  A ACC      I
                          GC GGT  GGTCCGGA
                          || ||| ||||||||
                          CG CCG  CCAGGCCT
                          AGGT _  C__      I
GAM432  RTN2           CTCCAGCGGCGGGTCCGGAA      6775 CT___  A ACC      TTC
                          GC GGT  GGTCCGGAA
                          || ||| |||||||||
                          CG CCG  CCAGGCCTT
                          GAGGT _  C__      III
GAM432  SLC6A3           CTGCATGCGT-CCGGTCCGG      6769    G A_       AATTC
                          CTGCA GT CCGGTCCGG
                          ||||| || |||||||||
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                        GACGT CG  GGCCAGGCC
                         A  CA          IIICC
GAM432  SLC6A3          CTGCATGCGT-CCGGTCCGG     6769    G A_      II
                        CTGCA GT  CCGGTCCG
                        IIIII II IIIIIIIII
                        GACGT CG  GGCCAGGC
                         A  CA        CI
GAM432  TDRD1          TGCAG-TCCCCCTGCCGGAATTC   6786    GTA G_T      I
                        GCAG  CC  G CCGGAATT
                        IIII  II I IIIIIIIII
                        CGTC  GG  C GGCCTTAA
                         AGG GA_        I
GAM432  TDRD1          TGCAG-TCCCCCTGCCGGAATTC   6786 CT   GTA G_T      C
                        GCAG  CC  G CCGGAATTC
                        IIII  II I IIIIIIIIII
                        CGTC  GG  C GGCCTTAAG
                       __  AGG GA _      T
GAM432  UNG           GCTGGGCCCGGTCCGGGAATT    6783 CA TA      AATI
                         GG  CCGGTCCGG
                         II IIIIIIIIII
                         CC  GGCCAGGCC
                        A_ CG       CTTA
GAM432  UNG           GCTGGGCCCGGTCCGGGAATT    6783 CTGCA TA      _  CC
                         GG  CCGGTCCGG AATT
                         II IIIIIIIIII IIII
                         CC  GGCCAGGCC TTAA
                        A____  CG      C  CC
GAM432  ZYX           CTGC--GTCCCGGTCCGGA      6774    AG A      ATT
                        CTGC GT CCGGTCCGGA
                        IIII II IIIIIIIIII
                        GACG CA GGCCAGGCCT
                         __ G        III
GAM432  ZYX           CTGC--GTCCCGGTCCGGA      6774    AG A      I
                        CTGC GT CCGGTCCGG
                        IIII II IIIIIIIII
                        GACG CA GGCCAGGCC
                         __ G      T
GAM433  ADRA1A         TGTCAGTAGGTTGAGCCTGAAA   6799  G  _ CA      CCA
                        TG CAGT GGT AGCCTGAAA
                        II IIII III IIIIIIIII
                        AC GTCA CCA TCGGACTTT
                         A  T AC      III
GAM433  ADRA1A         TGTCAGTAGGTTGAGCCTGAAA   6799 GG  _ CA      I
                         CAGT GGT AGCCTGAA
                         IIII III IIIIIIII
                         GTCA CCA TCGGACTT
                         A_ T AC    I
GAM433  ALEX3          TGGGACTGGGCTCAAGCCTG     6800   CAG  __       AAACC
                        TGG  TGG TCAAGCCTG
                        III  III IIIIIIIII
```

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                              ACC  ACC  AGTTCGGAC
                              CTG  CG      IIIAC
GAM433 ALEX3          TGGGACTGGGCTCAAGCCTG    6800  CAG  __      III
                              TGG  TGG  TCAAGCCT
                              III  III  IIIIIIII
                              ACC  ACC  AGTTCGGA
                              CTG  CG      CII
GAM433 AQP6           GGCCTTGG---AGCCTGAAA    6798  AG  TCA    I
                              GGC  TGG  AGCCTGA
                              III  III  IIIIIII
                              CCG  ACC  TCGGACT
                               GA  ___      T
GAM433 AQP6           GGCCTTGG---AGCCTGAAA    6798 TG  AG  TCA      C
                               GC  TGG  AGCCTGAAA
                               II  III  IIIIIIIII
                               CG  ACC  TCGGACTTT
                               __  GA  ___       C
GAM433 ATP2C1        TGACAGTGGTCACATCCTG     6801         AG_  AAACC
                              TGGCAGTGGTCA  CCTG
                              IIIIIIIIIIII  IIII
                              ACTGTCACCAGT  GGAC
                                   GTA  IIIAC
GAM433 ATP2C1        TGACAGTGGTCACATCCTG     6801         AG_  II
                              TGGCAGTGGTCA  CCT
                              IIIIIIIIIIII  III
                              ACTGTCACCAGT  GGA
                                   GTA  CI
GAM433 FZD4          TGACAGTGGTCATGTACTGAA    6802        AGC_  ACCA
                              TGGCAGTGGTCA  CTGAA
                              IIIIIIIIIIII  IIIII
                              ACTGTCACCAGT  GACTT
                                   ACAT  IIIA
GAM433 FZD4          TGACAGTGGTCATGTACTGAA    6802 G      AGC_  I
                               GCAGTGGTCA  CTGA
                               IIIIIIIIII  IIII
                               TGTCACCAGT  GACT
                               _        ACAT  I
GAM433 GOT2          CAGTGGGTGAAGCCTGAACCCA   6791 A  TC_    A  I
                               GTGG  AAGCCTGAA CC
                               IIII  IIIIIIIII II
                               CACC  TTCGGACTT GG
                               _  CAC      G I
GAM433 GOT2          CAGTGGGTGAAGCCTGAACCCA   6791 TGGCAGT  C      A
                               GGT AAGCCTGAA CCA
                               III IIIIIIIII III
                               CCA TTCGGACTT GGT
                               AC_____  C      G
GAM433 NBS1          GCAATGACAAAGCCTGAAAACA   6793    TC      CCI
                              CAGTGG AAGCCTGAAA
                              IIIIII IIIIIIIIII
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                    GTTACT TTCGGACTTT
                      GT       TGI
GAM433 NBS1         GCAATGACAAAGCCTGAAAACA   6793 TGGC   TC      CCA
                      AGTGG AAGCCTGAAA
                      ||||| ||||||||||
                      TTACT TTCGGACTTT
                      ____    GT       TGT
GAM433 OGG1         GCAGTGGTCA---CAGAACCCA   6795       ___    AAAI
                      GCAGTGGTCA AGCCTG
                      |||||||||| ||||||
                      CGTCACCAGT TTGGGT
                         GTC   IIIA
GAM433 OGG1         GCAGTGGTCA---CAGAACCCA   6795 TGGC    AGCCT A
                      AGTGGTCA   GAA CC
                      |||||||| |||  ||
                      TCACCAGT   CTT GG
                      ____      GT___  G
GAM433 PNOC        TGGCAGTGG-CAAGTC-AAAACC   6805     T   CC     A
                     TGGCAGTGG CAAG TGAAACC
                     ||||||||| |||| |||||||
                     ACCGTCACC GTTC GTTTGG
                        _  A_    I
GAM433 PNOC        TGGCAGTGG-CAAGTC-AAAACC   6805 _   T   CC    I
                      GGCAGTGG CAAG TGAAAC
                      |||||||| |||| ||||||
                      CCGTCACC GTTC GTTTG
                      A   _   A_   I
GAM433 RECK        TGGCAGTGGTCTACCAGGAA   6803      AA T_ ACC
                     TGGCAGTGGTC GCC GAA
                     ||||||||||| ||| |||
                     ACCGTCACCAG TGG CTT
                       A_  TC III
GAM433 RECK        TGGCAGTGGTCTACCAGGAA   6803      AA TGAI
                      GGCAGTGGTC GCC
                      |||||||||| |||
                      CCGTCACCAG TGG
                       A_  TCCT
GAM433 RGS9        GCGGTGGCTCAAGCCTGTAA   6792 A  _    AAII
                      GC GTGG TCAAGCCTG
                      || |||| |||||||||
                      CG CACC AGTTCGGAC
                       C  G     ATTI
GAM433 RGS9        GCGGTGGCTCAAGCCTGTAA   6792 TGGCA  _    AAACC
                       GTGG TCAAGCCTG
                       |||| |||||||||
                       CACC AGTTCGGAC
                      C____ G    ATTAG
GAM433 RNH         AGTGGTCAAGGCAGAGAACA   6790      _CT_ ACCI
                      GTGGTCAAG C  GAA
                      |||||||| | |||
```

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                              CACCAGTTC G  CTT
                                C TCT   GIII
GAM433  RNH              AGTGGTCAAGGCAGAGAACA      6790 T____     T TCA   GAAACC
                              GGCAG GG  AGCCT
                              IIIII II  IIIII
                              CCGTC CT  TCGGG
                              CAGTT   T TG_   IIIACC
GAM433  SERPINB9           GCGGTGGCTCAAGCCTGTAA     6792 A  _       AAII
                              GC GTGG TCAAGCCTG
                              II IIII IIIIIIIII
                              CG CACC AGTTCGGAC
                               C  G     ATTI
GAM433  SERPINB9           GCGGTGGCTCAAGCCTGTAA      6792 TGGCA  _      AAACC
                              GTGG TCAAGCCTG
                              IIII IIIIIIIII
                              CACC AGTTCGGAC
                               C____  G      ATTAG
GAM433  SHOX             GGCAGTGGTTCATGCTTGTAA     6796 G   _ A C AAI
                              CAGTGGT CA GC TG
                              IIIIIII II II II
                              GTCACCA GT CG AC
                                _     A A A ATI
GAM433  SHOX             GGCAGTGGTTCATGCTTGTAA     6796 TG   _ A C AAACCA
                              GCAGTGGT CA GC TG
                              IIIIIIII II II II
                              CGTCACCA GT CG AC
                               __     A A A ATTAII
GAM433  SLC14A2          GGC-GTGCTGAAGCCTGAA      6797  A GTC     I
                              GGC GTG  AAGCCTGA
                              III III  IIIIIIIII
                              CCG CAC  TTCGGACT
                               _ GAC      T
GAM433  SLC14A2          GGC-GTGCTGAAGCCTGAA      6797 TG A GTC     AC
                              GC GTG  AAGCCTGAA
                              II III  IIIIIIIII
                              CG CAC  TTCGGACTT
                               __ _ GAC      AI
GAM433  SLC26A4          GCAGGGGTC----CTGAAACCA    6794 _ T CAAG
                              CAG GGT  CCTGAAACC
                              III III  IIIIIIIIII
                              GTC CCA  GGACTTTGG
                               C  C  ____
GAM433  ZNF264          TGGCAGAG---AAGCCTGAAA    6804     T TCA     C
                              TGGCAG GG  AGCCTGAAA
                              IIIIII II  IIIIIIIII
                              ACCGTC CT  TCGGACTTT
                                T ___     I
GAM433  ZNF264          TGGCAGAG---AAGCCTGAAA    6804 _   T TCA
                              GGCAG GG  AGCCTGAA
                              IIIII II  IIIIIIII
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                          CCGTC CT  TCGGACTT
                          A    T ___
GAM434 CARD12        AAAGCTTCCCACCTTTCTAT    6809 AAAC       C__   I
                          CTTCCCACC  CTGT
                          ||||||||| ||||
                          GAAGGGTGG  GATA
                          TC__       AAA  I
GAM434 CARD12        AAAGCTTCCCACCTTTCTAT    6809 TGCAAAC     C__   T
                          CTTCCCACC  CTGTA
                          ||||||||| |||||
                          GAAGGGTGG  GATAT
                          C_____       AAA   T
GAM434 ENO2         GCAAGACCT-CCCACCCCAGT    6815  AC      TGI
                          CAA CTTCCCACCCC
                          ||| ||||||||||||
                          GTT GGAGGGTGGGG
                           CT       TCI
GAM434 ENO2         GCAAGACCT-CCCACCCCAGT    6815 TG  AC     T AT
                          CAA CTTCCCACCCC GT
                          ||| |||||||||||| ||
                          GTT GGAGGGTGGGG CA
                          __  CT       T GI
GAM434 FTSJ2        CCTTCCCACAGTCTGTTTT     6813       CC_  ATII
                          CCTTCCCAC  CTGT
                          ||||||||| ||||
                          GGAAGGGTG  GACA
                           TCA   AAAI
GAM434 LEP        CAAACATTCCCCACCCCTG      6810    C_      II
                          CAAAC TTCCCACCCCT
                          ||||| |||||||||||
                          GTTTG AGGGGTGGGGA
                          TA     CI
GAM434 LEP        CAAACATTCCCCACCCCTG      6810 TGCAAACC     TAT
                          TTCCCACCCCTG
                          ||||||||||||
                          AGGGGTGGGGAC
                          TTGTA___       CCI
GAM434 NUMA1       CAAA---TCCCACCCCAGT     6812 CAAACCT     TG
                          TCCCACCCC
                          |||||||||
                          AGGGTGGGG
                          GTTT___     TC
GAM434 NUMA1       CAAA---TCCCACCCCAGT     6812 TGCAAACCT    T
                          TCCCACCCC GT
                          ||||||||| ||
                          AGGGTGGGG CA
                          TT_____       T
GAM434 SPG4       CAAACCTTCAAACCTTCTCTATT  6811 A   CC  C_ G  I
                          AACCTTC ACC  CT TAT
                          ||||||| ||| || |||
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                              TTGGAAG  TGG  GA ATA
                          _       TT   AA  G   I
GAM434 SPG4      CAAACCTTCAAACCTTCTCTATT  6811 TGCA     CC  C_  G   I
                         AACCTTC  ACC  CT TATT
                         IIIIIII  III  II IIII
                         TTGGAAG  TGG  GA ATAA
                           ____        TT  AA  G   A
GAM434 TCF20     TGAAAACATGGACCATCCCTGTATT 6816  C   CTTC_  C      II
                         TG AAAC    CCA CCCTGTATT
                         II IIII    III IIIIIIIII
                         AC TTTG    GGT GGGACATAA
                          T   TACCT  A       II
GAM434 TCF20     TGAAAACATGGACCATCCCTGTATT 6816 GC   CTTC_  C      I
                          AAAC    CCA CCCTGTAT
                          IIII    III IIIIIIII
                          TTTG    GGT GGGACATA
                           T_  TACCT  A       I
GAM434 TSLP     AAACTCTTCCCACCACGAGTGTA  6808  _       CCTGTIIIT
                         AAAC CTTCCCACC
                         IIII IIIIIIIII
                         TTTG GAAGGGTGG
                           A       TGCTCACAT
GAM434 TSLP     AAACTCTTCCCACCACGAGTGTA  6808 TGCAAAC     CC___  TTI
                           CTTCCCACC   TGTA
                           IIIIIIIII   IIII
                           GAAGGGTGG   ACAT
                         GA_____       TGCTC  TCT
GAM434 ZNF148     GCAACAGCT-CCCACCCCTG     6814  ACC        II
                          GCAA  TTCCCACCCCT
                          IIII  IIIIIIIIIII
                          CGTT  GAGGGTGGGGA
                           GTC        CI
GAM434 ZNF148     GCAACAGCT-CCCACCCCTG     6814 TG  ACC        AT
                           CAA  TTCCCACCCCTGT
                           III  IIIIIIIIIIIII
                           GTT  GAGGGTGGGGACG
                           __  GTC         II
GAM435 BRCA1      ATGAATATGCCTGGTAGAAGACT  6821     G_  A  T  TCI
                          TGAATATGC  GG  TA  AAG
                          IIIIIIIII  II II III
                          ACTTATACG  CC  AT  TTC
                            GA  _  C   TGI
GAM435 BRCA1      ATGAATATGCCTGGTAGAAGACT  6821 TA     G_  A  T  T I
                          TGAATATGC  GG  TA  AAG  CT
                          IIIIIIIII  II II III  II
                          ACTTATACG  CC  AT  TTC  GA
                            __       GA  _  C  T  A
GAM435 DMC1      TGAATATGCAGTTTGATAT     6824        GATAIII
                          TGAATATGCGG
                          IIIIIIIIIII
```

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                        ACTTATACGTC
                        AAACTAT
GAM435 DMC1          TGAATATGCAGTTTGATAT    6824 TATG        ___       AAGTC
                        AATATGCGG  GATAT
                        |||||||||  |||||
                        TTATACGTC  CTATA
                            ____       AAA    ATIII
GAM435 NLGN1         ATGTAAA-GAGGGATATAA    6820 ATGAATATGC        I
                        GGGATATA
                        ||||||||
                        CCCTATAT
                        TACATTTCT_       T
GAM435 NLGN1         ATGTAAA-GAGGGATATAA    6820 TATGAATATGC       GT
                        GGGATATAA
                        |||||||||
                        CCCTATATT
                        ACATTTCT___       GI
GAM435 TGM4        TGAATCTGCCCTCATATAAGTC   6825 TATGAATA  GGG_      T
                        TGC  ATATAAGTC
                        |||  |||||||||
                        ACG  TATATTCAG
                        TTAG____  GGAG       T
GAM435 TP53        TATAAAAATG--GGATATAA     6823    TATGC      GT
                        TATGAA   GGGATATAA
                        ||||||   |||||||||
                        ATATTT   CCCTATATT
                            TTA__      II
GAM435 TP53        TATAAAAATG--GGATATAA     6823 ATGAATATGC        I
                        GGGATATA
                        ||||||||
                        CCCTATAT
                        ATATTTTA_      I
GAM435 TPM1        ATGCGGGATCCAT-AGTCT      6822        ATA_  II
                        ATGCGGGAT  AGTC
                        |||||||||  ||||
                        TACGCCCTA  TCAG
                         GGTA   AI
GAM435 ZNF16       ATGAATATGCAGCCTCCATAA-TCT 6819        GA__    GTCI
                        GAATATGCGG  TATAA
                        ||||||||||  |||||
                        CTTATACGTC  GTATT
                         GGAG   AIII
GAM435 ZNF16       ATGAATATGCAGCCTCCATAA-TCT 6819 TA        GA__    G I
                        TGAATATGCGG  TATAA TCT
                        |||||||||||  ||||| |||
                        ACTTATACGTC  GTATT AGA
                         __       GGAG    _  A
GAM436 ALDH3A2       TAA-AAT-TGATGCCAATTT    6852 TA    A C       CT
                        AGAAT TG TGCCAATTT
                        ||||| || |||||||||
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                              TTTTA AC ACGGTTAAA
                              A_     _T     II
GAM436 ARSD          AAGCAGATGCTGCCATGCTTCTGT  6830 TA AAT       A_     I
                              AG  ATGCTGCCA TTTCTGT
                              II  IIIIIIIII IIIIIII
                              TC  TACGACGGT GAAGACA
                              __  GTC     AC    C
GAM436 ATP10C        GAATGAGGTGC-AATTTCTGT    6842 TAAGAATATGC  C
                              TGC AATTTCTG
                              III IIIIIIII
                              ACG TTAAAGAC
                        ACTCC_____  _
GAM436 ATRX           TAAGAATAT--TGCACACAATTCTGT 6848      _ T _  T  I
                              TAAGAATAT GC GC CAATT CTGT
                              IIIIIIIII II II IIIII IIII
                              ATTCTTATA CG TG GTTAA GACA
                              A _ T  _  I
GAM436 BCL11B         AAGAATATGCTG-CAATTTCT    6832 TA       C     G
                              AGAATATGCTGC AATTTCT
                              IIIIIIIIIIII IIIIIII
                              TCTTATACGACG TTAAAGA
                              __      _     A
GAM436 CCNT2          TAAGAATATGGTGTCA--TTCTG  6854      C C AT   T
                              TAAGAATATG TG CA  TTCTG
                              IIIIIIIIII II II  IIIII
                              ATTCTTATAC AC GT  AAGAC
                              C  A __   I
GAM436 CKTSF1B1       AAGATTACTGCTGCCAACTT    6828 TA ATA_      CTG
                              AGA  TGCTGCCAATTT
                              III  IIIIIIIIIIII
                              TCT  ACGACGGTTGAA
                              __ AATG      TII
GAM436 DAZL           ATAGTGCTTTCAATTTCTG     6840 TAAGAATAT  GC
                              GCT  CAATTTCTG
                              III  IIIIIIIII
                              CGA  GTTAAAGAC
                              _____ AA
GAM436 DCX            TAA-AATATGCTGTAACATTTC  6850 TA       CCA_  TGT
                              AGAATATGCTG  ATTTC
                              IIIIIIIIIII  IIIII
                              TTTTATACGAC  TAAAG
                              A_       ATTG  III
GAM436 FGF5           TAAGAATATTTCTGACAAT     6846     G_ C  TTCTG
                              TAAGAATAT CTG CAAT
                              IIIIIIIII III IIII
                              ATTCTTATA GAC GTTA
                              AA  T  IIITG
GAM436 FHL1           ATATGCTGCTTTATTTCTGT    6841 TAAGAATA   GCCA
                              TGCT  ATTTCTG
                              IIII  IIIIIII
```

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                         ACGA   TAAAGAC
                    G_____   AA__
GAM436  GAD1        AAGAATATG-T-CCATTTTC   6831 TA      CTG  A
                    AGAATATG  CCA TTTCT
                    |||||||  ||| |||||
                    TCTTATAC  GGT AAAGG
                    __       A__  A
GAM436  GALK2       AGAAAGTCCTGCCAATTCCT    6837 TAAGAATATG
                    CTGCCAATTTCTG
                    |||||||||||||
                    GACGGTTAAGGAT
                    TTTCAG____
GAM436  HOXB3       AGGAT-TG-TGTCAATTTCTG    6838 TAAGAATA  C  C
                    TG TG CAATTTCTG
                    || || |||||||||
                    AC AC GTTAAAGAC
                    CTA_____  _  A
GAM436  IPP         TAGGATATCTGCTGCCAAT     6845 TAAGAATA_      TTCTG
                    TGCTGCCAAT
                    ||||||||||
                    ACGACGGTTA
                    ATCCTATAG      IIITG
GAM436  KITLG       TAA-AACATTCTGTTCCAATTTCTG 6847 TA     G  __      TI
                    AGAATAT CTG  CCAATTTCTG
                    ||||||| ||| |||||||||||
                    TTTTGTA GAC  GGTTAAAGAC
                    A_     A  AA      II
GAM436  LEF1        AATAGGGCTGCCAATTGCT     6836 TAAGAATAT      T  G
                    GCTGCCAATT CT
                    |||||||||| ||
                    CGACGGTTAA GA
                    CC_____       C T
GAM436  OGT         TAGGAATATGCTGGCTTGAATTT  6849 TAA      CCAATTTCTGTI
                    GAATATGCTG
                    ||||||||||
                    CTTATACGAC
                    ATC        CGAACTTAAAII
GAM436  PCDHA9      AAGCATTTTCT-CCAATTTCTGT  6835 TA AATATG  G
                    AG    CT CCAATTTCTGT
                    ||    || |||||||||||
                    TC    GA GGTTAAAGACA
                    __ GTAAAA  _
GAM436  PDE4D       AGAAAATTATGC-AATTTCTGT   6839 T  A   TGCC
                    AAGA TATGC   AATTTCTGT
                    |||| |||||   |||||||||
                    TTTT ATACG   TTAAAGACA
                    _  A  ____
GAM436  PPP4R1      TAAGGAAAATGCTCTGCCAATT   6844 TAA_ T   __      TCTGT
                    GAA ATGCT GCCAATT
                    ||| ||||| |||||||
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                      CTT TACGA  CGGTTAA
                      ATTC  T   GA     IIITG
GAM436  PRKY          TAAGAAAATACTGCCAATT   6851    T        TCTG
                      TAAGAA ATGCTGCCAATT
                      |||||| |||||||||||
                      ATTCTT TATGACGGTTAA
                         T        IIIT
GAM436  PTPRA         AAGCCTATG-TACCAATTTCT   6833 TA AA   C
                      AG  TATG TGCCAATTTCTG
                      ||  |||| |||||||||||
                      TC  ATAC ATGGTTAAAGAT
                      __  GG   _
GAM436  RAD18         AAGAATATGC-GCAATGTTTCT   6829 TA     T CAA_   T
                      AGAATATGC GC   TTTCTG
                      ||||||||| ||   ||||||
                      TCTTATACG CG   AAAGAT
                      __        _ TTAC   I
GAM436  SCA1          TAAGAATAT-TTAAAAATTTCT   6853     GCTGCC    GT
                      TAAGAATAT    AATTTCT
                      |||||||||    |||||||
                      ATTCTTATA    TTAAAGA
                          AATTT_     II
GAM436  SFRS1         TAAGGTCAATA--CTGCCAATTTC  6843   AAT_        TGT
                      TAAG    ATGCTGCCAATTTC
                      ||||    |||||||||||||
                      ATTC    TATGACGGTTAAAG
                          CAGT          III
GAM436  SHMT2         AAGAC-ATGGGCCCAATTTCTGT   6834 TA  A   CTG
                      AGA TATG  CCAATTTCTGT
                      ||| ||||  |||||||||||
                      TCT GTAC  GGTTAAAGACA
                      __  _   CCG
GAM436  TRAF5         TAAGAATATGAT-C--ATTTCTGT  6855       CTGCCA
                      TAAGAATATG    ATTTCTGT
                      ||||||||||    ||||||||
                      ATTCTTATAC    TAAAGACA
                           TAG___
GAM437  ALDH3A2       TAAGATGT---AGAATTCTATAAC  6868    ATA  G  _   G
                      TAAGATGT  AGAA TCT TAAC
                      ||||||||  |||| ||| ||||
                      ATTCTACA  TCTT AGA ATTG
                          ___   A   T   I
GAM437  C11orf8       AGA-GTATGAAAAGAAGTCTT   6864 TAAG  TAT       AAC
                      ATG  AAGAAGTCTT
                      |||  ||||||||||
                      TAC  TTCTTCAGAA
                      TCA_  TT_      AAI
GAM437  ENAM          AAGATGTATCCTAAGAAATCT   6858 TA    ___       AACG
                      AGATGTA  TAAGAAGTCTT
                      |||||||  |||||||||||
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                          TCTACAT ATTCTTTAGAG
                          __      AGG      IIIG
GAM437 F2R                TAAGATGGGTAGAGAAGTCTT    6867     TA _      AACG
                          TAAGATG TA AGAAGTCTT
                          ||||||| || |||||||||
                          ATTCTAC AT TCTTCAGAA
                              CC  C        IIIG
GAM437 FIGF               AAAATGCAGA-GAAGTCTT    6860 TA      TA      AA
                          AGATGTA AGAAGTCTT
                          ||||||| |||||||||
                          TTTACGT TCTTCAGAA
                          __       C_       CI
GAM437 MEN1               AATATGAACCTGAAGTCTTAA    6862 TAAG  T AA      CG
                          ATG AT  GAAGTCTTAA
                          ||| || ||||||||||
                          TAC TG  CTTCAGAATT
                          TA__ T GA        CI
GAM437 PLA2R1             TAAGCTTATGTATAAGACATTTTAA 6865 TAAG___    A  C   CGII
                          ATGTATAAGA GT TTAA
                          |||||||||| || ||||
                          TACATATTCT TA AATT
                          ATTCGAA        G  A  IIIG
GAM437 RFC4               AGATGGTCTC-GAAGTCTTA    6863 TAAGATGTATAA     AC
                          GAAGTCTTA
                          |||||||||
                          CTTCAGAAT
                          TACCAGAG____      CG
GAM437 SNRPA             AAG-TGTTGAGGTAAGTCTTAA    6859 TA A ATAAG_      CG
                          AG TGT    AAGTCTTAA
                          || |||     |||||||||
                          TC ACA    TTCAGAATT
                          __ _ ACTCCA        TI
GAM437 SPAP1             TAAGGTTTTATAGCAAGTCTTAA    6866   ATG_  AG     CGI
                          TAAG   TATA AAGTCTTAA
                          ||||   |||| |||||||||
                          ATTC   ATAT TTCAGAATT
                          CAAA  CG        III
GAM437 SUV39H2          AAGAT---TAAGAAGTCTT    6861 TA  GTA      A
                          AGAT   TAAGAAGTCTT
                          ||||   |||||||||||
                          TCTA   ATTCTTCAGAA
                          __   ___     A
GAM438 BCAT1            AGATGT--GCAGATGT-TCC    6875 AGAGATGTA      G
                          TGCAGATGT TCC
                          ||||||||| |||
                          ACGTCTACA AGG
                          TAC_____      _
GAM438 BCL11A           AGA-ATGTATGCAGCATG-GTC    6873  A      _ T CA
                          AGAG TGTATGCAG ATG GTC
                          |||| ||||||||| ||| |||
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                      TCTT ACATACGTC TAC CAG
                        _      G    _   II
GAM438  DDEF1          AGAGATGTAAGTGCTAGATG    6871        __  _    TGTCCA
                        AGAGATGTA TGC AGATG
                        ||||||||| ||| |||||
                        TCTCTACAT ACG TCTAC
                            TC   A    IIITAC
GAM438  DEFA6          AGAGCAGGA-GCAGATGTGT    6874   ATGTAT      CCA
                        AGAG    GCAGATGTGT
                        ||||    ||||||||||
                        TCTC    CGTCTACACA
                          GTCCT_       III
GAM438  ERBB4          ATAGCATGGGTGTTTCAACCATCTGCTT6880    A  ATG___  _ III
                        ATAGCATGG TGT    CATCT CTT
                        ||||||||| |||    ||||| |||
                        TATCGTACC ACA    GTAGA GAA
                          C  AAGTTG   C  III
GAM438  EXTL3          ATGTATGCAAGTGTGTGCAT    6883 AGAGATGT    A    C
                        ATGCAG TGTGT CA
                        |||||| ||||| ||
                        TACGTT ACACA GT
                        _____   C   C
GAM438  GPR48          AGATGTATGGAAAT-T-TCCAT    6877 AGAG    C   GTG
                        ATGTATG AGAT  TCCA
                        ||||||| ||||  ||||
                        TACATAC TTTA  AGGT
                        ____       C  A__
GAM438  KCNS3          AGCATGGATTTACATGCAT    6878        G__    III
                        AGCATGGAT TATGCA
                        ||||||||| ||||||
                        TCGTACCTA GTACGT
                          AAT    AII
GAM438  KCNS3          AGCATGGATTTACATGCAT    6878 ATAG    G__    CTCT
                        CATGGAT TATGCAT
                        ||||||| |||||||
                        GTACCTA GTACGTA
                        ____    AAT    ACII
GAM438  LDHB           GAGATGTATGGATAAATGT    6884 AG     C__    GTCCA
                        AGATGTATG AGATGT
                        ||||||||| ||||||
                        TCTACATAC TTTACA
                          __    CTA   AIIIT
GAM438  LNK            GATGT---CAGATGTGTCC    6885 AGAGATGTATG
                        CAGATGTGTC
                        ||||||||||
                        GTCTACACAG
                        CA_____
GAM438  PROS1          TGGATGTATGTTCAT-TCTT    6886       __  _ CTII
                        TGGATGTATG CAT CT
                        ||||||||| ||| ||
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                         ACCTACATAC GTA GA
                          AA  A AIII
GAM438 SLC16A7       ATAGCATGGATTCTTTCTATGCAT 6879        G_____        CTCTTI
                      ATAGCATGGAT    TATGCAT
                      IIIIIIIIII    IIIIIII
                      TATCGTACCTA    ATACGTA
                        AGAAAG      IIITTC
GAM438 SLC16A7       ATAGCATGGATTCTTTCTATGCAT 6879        G_____        IIIA
                      ATAGCATGGAT    TATGCA
                      IIIIIIIIII    IIIIII
                      TATCGTACCTA    ATACGT
                        AGAAAG      AIII
GAM438 TGFBR2        ATCGCATGGATGGGGACATCTGTT 6882 A        TAT     CI
                       GCATGGATG  GCATCT
                       IIIIIIIII  IIIIII
                       CGTACCTAC  TGTAGA
                       G     CCC     CI
GAM438 TGFBR2        ATCGCATGGATGGGGACATCTGTT 6882 ATA       TAT     CTTI
                        GCATGGATG  GCATCT
                        IIIIIIIII  IIIIII
                        CGTACCTAC  TGTAGA
                       TAG       CCC    CAAI
GAM438 TRIM9         ATAGTA--GTTGTATGCATCT    6881   CA  A       CT
                        ATAG TGG TGTATGCATCT
                        IIII III IIIIIIIIIII
                        TATC ATC ACATACGTAGA
                         __   A     II
GAM438 TRIM9         ATAGTA--GTTGTATGCATCT    6881 _ CA  A       I
                        TAG TGG TGTATGCATC
                        III III IIIIIIIIII
                        ATC ATC ACATACGTAG
                        T   __  A     I
GAM438 TRPM2         AGCTGCGTG-AGATGTGTCC     6876 AGAGA TA C       A
                        TG TG AGATGTGTCC
                        II II IIIIIIIIII
                        AC AC TCTACACAGG
                      G____ GC _     G
GAM438 ZNF36        AGAGATGTATTTGGAGTTGTTGTTGCCAT6872       GCA TG CCATIIIA
                      AGAGATGTAT GA TGT
                      IIIIIIIIII II III
                      TCTCTACATA CT ACA
                        AAC CA A_____
GAM439 CACNA1C        AATTCCCT---TGTTCTTG    6892 TAGAATTA AAA
                       TCT TGTTTCTT
                       III IIIIIIII
                       AGG ACAAAGAA
                       _____ GA_
GAM439 DDX1         AGAATTC-CTAAGACTAATGTTTCTTGA6893 TA   A  _____      III
                      GAATT TCTAA  ATGTTTCTTGA
                      IIIII IIIII  IIIIIIIIIII
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                              CTTAA GGATT    TACAAAGAACT
                              __   _  CTGAT       GII
GAM439  DLX4        AAATA-CTCAATGTTTCTTG   6891 ATTAT  A      I
                          CT AATGTTTCTT
                          || ||||||||||
                          GA TTACAAGAA
                    TTTAT  G        I
GAM439  DLX4        AAATA-CTCAATGTTTCTTG   6891 TAGAATTAT  A
                          CT AATGTTTCTTG
                          || |||||||||||
                          GA TTACAAAGAAC
                   AT_____ G
GAM439  ECM2         TAGAATTATAGAAAAGTTTC   6901      CT   T   TTG
                        TAGAATTAT AAA GTTTC
                        ||||||||| ||| |||||
                        ATCTTAATA TTT CAAAG
                          TC  T    III
GAM439  EPHA3         TATAAAAATATAAATGTTTC   6902 __  T TC      TTG
                        TAGAA TA TAAATGTTTC
                        ||||| || ||||||||||
                        ATTTT AT ATTTACAAAG
                     AT  T __        III
GAM439  ERBB2IP      GAATTTATCTCCCTGATGTTTCTT  6896 AAT   AA___      I
                        TATCT   ATGTTTCT
                        |||||   ||||||||
                        ATAGA   TACAAAGA
                     ___    GGGAC     I
GAM439  ERBB2IP      GAATTTATCTCCCTGATGTTTCTT  6896 TAGAA   AA___       I
                        TTATCT   ATGTTTCTTGA
                        ||||||   |||||||||||
                        AATAGA   TACAAAGAATT
                     TA___    GGGAC     I
GAM439  FLRT2       ATT-TCTAAATGTCTTTCT     6894 ATTA      CII
                        TCTAAATGTTT
                        |||||||||||
                        AGATTTACAGA
                   TAA_       AAG
GAM439  FOXO1A       TAGAACCATTTAAATGTTT     6900     C     CTTG
                        TAGAATTAT TAAATGTTT
                        ||||||||| |||||||||
                        ATCTTGGTA ATTTACAAA
                          A      IIIA
GAM439  FOXO1A       TAGAACCATTTAAATGTTT     6900     C     II
                        TAGAATTAT TAAATGTT
                        ||||||||| ||||||||
                        ATCTTGGTA ATTTACAA
                          A    AI
GAM439  GRM1        GAATAATCTAAATGCTTTGTT    6897 AATT       CTI
                        ATCTAAATGTTT
                        ||||||||||||
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                          TAGATTTACGAA
                  TAT_          ACA
GAM439  GRM1      GAATAATCTAAATGCTTTGTT   6897 TAGAATT        CTTGA
                      ATCTAAATGTTT
                      ||||||||||||
                      TAGATTTACGAA
                  TAT____         ACAAG
GAM439  IFIT1     GAATTAT---AATGTTTCT    6898      CTA
                  GAATTAT AATGTTTC
                  ||||||| ||||||||
                  CTTAATA TTACAAAG

                      ___
GAM439  MTCP1     CTAAACTTCTGTTTCTTGA       6895    ____       ||||T
                  CTAAA TGTTTCTTG
                  ||||| |||||||||
                  GATTT ACAAAGAAC
                      GAAG        T|||
GAM439  RAD21     AATTATCTACAATGTCTTTT      6889      _    CT||
                  AATTATCTA AATGTTT
                  ||||||||| |||||||
                  TTAATAGAT TTACAGA
                      G      AAA|
GAM439  SCN3A     GAATTATCTCATTTATTCTT    6899 TAGA      AAATGT
                      ATTATCT    TTCTTG
                      |||||||    ||||||
                      TAATAGA    AAGAAT
                      ____          GTAAAT
GAM439  TFDP2     AATTATCTAAATGTCACTT       6890           T ||
                  AATTATCTAAATGTT CT
                  ||||||||||||||| ||
                  TTAATAGATTACAG GA
                      T  A|
GAM439  TFDP2     AATTATCTAAATGTCACTT       6890 TAGAAT        T
                      TATCTAAATGTT CTTG
                      ||||||||||| ||||
                      ATAGATTTACAG GAAT
                      _____          T
GAM440  BAALC     GAAAGCTATGCAAAATTGCAATGTC 6909 TGAAAG  TG  C      ||
                      GTG AA TTGCAATGTC
                      ||| || ||||||||||
                      TAC TT AACGTTACAG
                  TTTCGA  GT  T       A|
GAM440  CALCRL    GAAAGA-GTGAAAGCTTTGCAATGT 6910 TGA   T  C___      C|
                      AAGG GTGAA  TTGCAATGT
                      |||| |||||  |||||||||
                      TTTC CACTT  AACGTTACA
                      ___   T   TCGA       C|
GAM440  DCX       TGAAAGGTGTCAGACCTGAAA    6912       GA_   CAATGTC
                      TGAAAGGTGT ACTTG
                      |||||||||| |||||
```

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                         ACTTTCCACA  TGGAC
                         GTC    TTTIIIC
GAM440  DRD2         TGCAGGGTGTGAACTGTCCATCTC  6915  AAA        TGCA G  I
                         TG  GGTGTGAACT   AT TC
                         ||  |||||||||   || ||
                         AC  CCACACTTGA   TA AG
                         GTC        CAGG  G  I
GAM440  ITK          TGAAAGGTGGTGCACCTTG       6911      _ AA_   CAATGT
                         TGAAAGGTG TG  CTTG
                         ||||||||| ||  ||||
                         ACTTTCCAC AC  GAAC
                          C GTG    IIICTG
GAM440  MTF1         TGAAAGGTGAGGA-TTTCAA       6914      T_ ACTTGCAATGT
                         TGAAAGGTG GA
                         ||||||||| ||
                         ACTTTCCAC CT
                          TC  AAAGTTIIICT
GAM440  NDRG3         AAGGA-TGGACTTGCAATG        6908 TGAAA   T A
                          GGTG GA CTTGCAATG
                          |||| || |||||||||
                          CTAC CT GAACGTTAC
                          _____  _ _
GAM440  OCRL         TGAAAGG-GAGA-CTAATGCAATGTC 6913      TGT ACT_       I
                         TGAAAGG  GA  TGCAATGTC
                         |||||||  ||  |||||||||
                         ACTTTCC  CT  ACGTTACAG
                          CT_ GATT       I
GAM440  RORB         AAAAGTCTTGGACCTTGCAATGT   6905 TGAAAGG  T A      CI
                         TG GA CTTGCAATGT
                         || || |||||||||
                         AC CT GAACGTTACA
                         TTCAGA_ _ G      AT
GAM440  SRD5A2       AAACATGAGAGTTTGCAATGTC    6906 TGAAAG  T AC
                         GTG GA  TTGCAATGTC
                         ||| ||  |||||||||
                         TAC CT  AACGTTACAG
                         TG____  T CA
GAM440  ZNF215      AAGGTGTGACGTGAC-TGCAA      6907 TGAAA GT   AC    T
                         G GTGA  TTGCAA GT
                         | |||| ||||||| ||
                         C CACT  GACGTT CA
                         CACA_ TG    __    _
GAM441  PCDHGA8     AGAATGAT-CAGATTGTAGCATC   6918 TGAG    C AT_  G
                         AATGATC AGA   TAG ATC
                         ||||||| |||   ||| |||
                         TTACTAG TCT   ATC TAG
                         ____    _ AAC  G
GAM441  TXNRD1      TGAGAATGATGAAGACATCAGG     6919      CC  _   ATC
                         TGAGAATGAT AGA ATTAGG
                         |||||||||| ||| ||||||
```

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                              ACTCTTACTA TCT TAGTCC
                                 CT  G       III
GAM442  ACCN2          TGGACGTGGCCCTCTACAAGGGCC  6932   C   G   A       I
                       TGG CGTGG CCTC ACAAGGGCC
                       III IIIII IIII IIIIIIIII
                       ACC GCACC GGAG TGTTCCCGG
                            T   G   A       I
GAM442  APXL           GGCCGTGGG-ATC-GCAAGGG  6926 TG     CC AA    C
                       GCCGTGGG TC CAAGGG
                       IIIIIIII II IIIIII
                       CGGCACCC AG GTTCCC
                       __       T_ C_   T
GAM442  CACNG8         GGCCGTGGGCCACCACCGGGGC  6928 TG     TCA AA   C
                       GCCGTGGGCC AC GGGC
                       IIIIIIIIII II IIII
                       CGGCACCCGG TG CCCG
                       __         TGG GC   T
GAM442  HMOX1          TGGCCGTG----TCAACAAGG  6929      GGCC      G
                       TGGCCGTG TCAACAAGG
                       IIIIIIII IIIIIIIII
                       ACCGGCAC AGTTGTTCC
                       ____          I
GAM442  ING1           CCTTGCACCTCAACAAAGGC   6922 TGGCCG G
                       TG GCCTCAACAAGGGC
                       II IIIIIIIIIIIIII
                       AC TGGAGTTGTTTCCG
                       _____   G
GAM442  LHX3           TGGGC-TGGGCCTCAGCAAGG   6931 T_ CG    A   GC
                       GGC TGGGCCTCA CAAGG
                       III IIIIIIIII IIIII
                       CCG ACCCGGAGT GTTCC
                       AC  __    C  II
GAM442  PACSIN1        GGCCGTGGG----GACAAGG   6925 TG    CCTCA
                       GCCGTGGG ACAAGG
                       IIIIIIII IIIIII
                       CGGCACCC TGTTCC
                       __       C____
GAM442  PACSIN1        GGCCGTGGGCAT-GGCAAGGG   6927 TG    CTCAA    C
                       GCCGTGGGC CAAGGG
                       IIIIIIIII IIIIII
                       CGGCACCCG GTTCCC
                       __        TACC_   C
GAM442  PDE4A          TGGCCGTGGGAATTATTAAGG   6930      CCTCAAC GCC
                       TGGCCGTGGG    AAGG
                       IIIIIIIIII    IIII
                       ACCGGCACCC    TTCC
                          TTAATAA   III
GAM442  PLAU           CCATGGGCCTC-ACAAATGCC   6923 TGGCCG    A   G
                       TGGGCCTCA CAAG GC
                       IIIIIIIII IIII II
```

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                         ACCCGGAGT GTTT CG
                         _____        _   A
GAM442 STAT1          CCTTGTGCCCCAACAAGGGCC    6924 TGGCCGTGG
                         GCCTCAACAAGGGCC
                         |||||||||||||
                         CGGGGTTGTTCCCGG
                      ACA_____
GAM443 CAPN10         TAAAGTTACATCCTAAAAGTG    6944      _      CTCT
                         TAAGGTTGCA CCTAAAAGTG
                         |||||||||| |||||||||
                         ATTTCAATGT GGATTTTCAC
                            A      |||T
GAM443 CAPN10         TAAAGTTACATCCTAAAAGTG    6944 A     _      I
                          AGGTTGCA CCTAAAAGT
                          ||||||||| |||||||||
                          TTCAATGT GGATTTTCA
                          _     A      I
GAM443 FANCF         AGGTTGCACTGAGCAGTGATC    6940      CTAAA  CTI
                         GGTTGCAC   AGTG
                         ||||||||   ||||
                         CCAACGTG   TCAC
                          ACTCG    TAI
GAM443 FANCF         AGGTTGCACTGAGCAGTGATC    6940 TAAG    CTAAA  C T
                          GTTGCAC   AGTG TC
                          |||||||   |||| ||
                          CAACGTG   TCAC AG
                         ____      ACTCG   T T
GAM443 GJB5          AGGTTGCACCTATGAGAGATGCT   6939 GGT     AA ___ I
                          TGCACCTA AG  TGC
                          |||||||| || |||
                          ACGTGGAT TC  ACG
                          ___      AC TCT  I
GAM443 GJB5          AGGTTGCACCTATGAGAGATGCT   6939 TAAG     AA ___ CTI
                          GTTGCACCTA AG  TGCT
                          |||||||||| || ||||
                          CAACGTGGAT TC  ACGA
                          ____      AC TCT  TCI
GAM443 IL1R1         AGGAGGCACCT-AAAGAACTCT    6941 _ TT    A T  I
                          GG GCACCTAAA G GCTC
                          || ||||||||| | ||||
                          CC CGTGGATTT C TGAG
                          T TC   _T  I
GAM443 IL1R1         AGGAGGCACCT-AAAGAACTCT    6941 TAAGGTT    A T
                          GCACCTAAA G GCTCT
                          ||||||||| | |||||
                          CGTGGATTT C TGAGA
                         CTC____      _T
GAM443 MPL          AAGGTTGCACAGCTAGTAAATGTG   6936     ___ AAAGTIIIC
                          AAGGTTGCAC CTA
                          |||||||||| |||
```

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                          TTCCAACGTG GAT
                          TC  CATTTACAC
GAM443 MPL        AAGGTTGCACAGCTAGTAAATGTG  6936 TA      __  A_    CTCTI
                      AGGTTGCAC CTA AAGTG
                      IIIIIIIII III IIIII
                      TCCAACGTG GAT TTTAC
                  __        TC  CA   ACTII
GAM443 OPRM1       AGGTTGGATGACCTAAAAGT     6938    C___       III
                      AGGTTG ACCTAAAAG
                      IIIIII IIIIIIIII
                      TCCAAC TGGATTTTC
                        CTAC    AII
GAM443 OPRM1       AGGTTGGATGACCTAAAAGT     6938 TAA T C      CTC
                      GG TG ACCTAAAAGTG
                      II II IIIIIIIIIII
                      CC AC TGGATTTTCAT
                  CAA T _        CII
GAM443 P2RY6      GGTTGCA--TTAAAGTGCTC     6942     CCTA   I
                      GGTTGCA  AAAGTGC
                      IIIIIII  IIIIIII
                      CCAACGT  TTTCACG
                        AA__      A
GAM443 PACE4      AAGGTTGCAGGGTACAAAGT     6935      CCTAAAAGIII
                      AAGGTTGCA
                      IIIIIIIII
                      TTCCAACGT
                        CCCATGTTTCA
GAM443 PACE4      AAGGTTGCAGGGTACAAAGT     6935 TA     CCTA__  GCTC
                      AGGTTGCA  AAAGT
                      IIIIIIII  IIIII
                      TCCAACGT  TTTCA
                  __        CCCATG  AIII
GAM443 PPP4R1     GTTGCACCTCAGAGCTGATC     6943     AAA T II
                      GTTGCACCT AG GCT
                      IIIIIIIII II III
                      CAACGTGGA TC CGA
                        G__ T CT
GAM443 WASF3      AAGGTGCCATCTAAA-GTGCTCT  6937_ T AC_   A   I
                      AGGT GC  CTAAA GTGCTC
                      IIII II  IIIII IIIIII
                      TCCA CG  GATTT CACGAG
                      T  _ GTA   _     I
GAM443 WASF3      AAGGTGCCATCTAAA-GTGCTCT  6937 TA  T AC_   A
                      AGGT GC  CTAAA GTGCTCT
                      IIII II  IIIII IIIIIII
                      TCCA CG  GATTT CACGAGA
                      __  _ GTA    _
GAM443 WEE1       TGCAATGCCTACAAAGTGCTC    6945  ___   _   IIIG
                      TGCA  CCTA AAAGTGCT
                      IIII  IIII IIIIIIIII
```

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                         ACGT  GGAT TTTCACGA
                          TAC  G      GIII
GAM444 ADRA2B        TCCCCCTCAGCAGCAGGCCCCACT  6952 TT  G  _        A    I
                         CCC CT GGCAGCAGGC CCGCT
                         |II II IIIIIIIIII IIIII
                         GGG GA TCGTCGTCCG GGTGA
                          __  G  G       G   C
GAM444 CHRM1         TTGCGGCTGGATAGCAGGCAC  6955 TTCCC   C_      CGCT
                          GCTGG AGCAGGCAC
                          IIIII IIIIIIIII
                          CGACC TCGTCCGTG
                          AACGC  TA   IIIT
GAM444 EPM2A         CCTGCAGGCAGCAGGAACTGC   6948 TTCCC T    C C T
                          GC GGCAGCAGG AC GC
                          II IIIIIIIII II II
                          CG CCGTCGTCC TG CG
                          A___ T    T A T
GAM444 FUT7          TCCCGTCTGCCGCAGCAGGCACC  6951 TT  _ __        GCTI
                          CCCG CTG GCAGCAGGCACC
                          IIII III IIIIIIIIIII
                          GGGC GAC CGTCGTCCGTGG
                          __  A  GG      GIII
GAM444 GYPC          TTCCTCCCTGG--GCAGGCACC  6953 _  _ G  CA    GC
                          TTC CC CTGG GCAGGCACC
                          III II IIII IIIIIIIII
                          AGG GG GACC CGTCCGTGG
                          A  A _  __     II
GAM444 HOXC11        TTTCCGCTGGCAGACATGC   6956 TTC      _ G ACCGC
                          CCGCTGGCAG CA GC
                          IIIIIIIIII II II
                          GGCGACCGTC GT CG
                          AAA      T A IIITC
GAM444 MYCL2         TTCCCAGACTGGAGGCAGGCACC  6954    __   CA      GCTI
                          TTCCC GCTGG GCAGGCACC
                          IIIII IIIII IIIIIIIII
                          AAGGG TGACC CGTCCGTGG
                           TC   TC      IIIT
GAM444 PIN1L         CCACTGGCCAGCAGGCAGCG   6949 TTCCCG  _      C C
                          CTGGC AGCAGGCA CG
                          IIIII IIIIIIIII II
                          GACCG TCGTCCGT GC
                          _____       G   C C
GAM444 TCF8          TCCCGGCCCAGG--GCAGGCACCGC  6950 TT  __TG CA      I
                          CCCG C G GCAGGCACCGCT
                          IIII I I IIIIIIIIIIII
                          GGGC G C CGTCCGTGGCGG
                          __  CG GT C_       I
GAM445 ATP8A2        TCTCCTCA--CTCAGGGTT    6980    GC    CCG
                          TCTCCTCG CTCAGGGTT
                          IIIIIIII IIIIIIIII
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                        AGAGGAGT GAGTCCCAA
                            __          III
GAM445   BLNK           CCTCTGGTCTCAAGGGTTCCG     6959 TCTCCTC  C   _     _ A
                        GG CTCA GGGTTCCG C
                        || |||| ||||||||| |
                        CC GAGT CCCAAGGC G
                        GA_____ A   T      C G
GAM445   BYSL           CTCATCCTCAGGG-TCCACA      6971 TCTCCTCGG       T
                          CCTCAGGGT CCGC
                          ||||||||| ||||
                          GGAGTCCCA GGTG
                        A_____      _
GAM445   CACNB1         TCTCCCCTGGGGCCTCAGGGT     6979      ___       TCCGCA
                        TCTCCTC GGCCTCAGGGT
                        ||||||| |||||||||||
                        AGAGGGG CCGGAGTCCCA
                          ACC        IIIACG
GAM445   CHRNB2         TCCTGGGCCTCAGGGAGCCG      6974 TCTC  C      TT  _
                        CT GGCCTCAGGG CCG C
                        || ||||||||| ||| |
                        GA CCGGAGTCCC GGC G
                        ____  C      TC  C
GAM445   COL4A2         TCCTCGGCCT---GGATCCGC     6975 TCTC     CA   T
                        CTCGGCCT GGGT CCG
                        |||||||| |||| |||
                        GAGCCGGA CCTA GGC

                         ____     __  _
GAM445   CPM            CTCCTAA-CCTCAGGGTGATCCGC  6967 TC   C        __   AI
                        TCCT GGCCTCAGGGT  TCCGC
                        |||| |||||||||||  |||||
                        AGGA TTGGAGTCCCA  AGGCG
                        __  _       CT   GI
GAM445   DDX38          TCCGCAGCCTCAGGGCTCC       6972 TCTCCT          GC
                         CGGCCTCAGGGTTCC
                         |||||||||||||||
                         GTCGGAGTCCCGAGG
                        GC____          GC
GAM445   EBP            CTCCTCGGC--CAGTGTTC       6969 TC      TCAGG  CG
                        TCCTCGGCC    GTTC
                        |||||||||    ||||
                        AGGAGCCGG    CAAG
                            __     TCA__  CI
GAM445   EPHB3          CTGCACGGTCCTCAGGGTCCC     6964 TCTCCT _       GCA
                        CGG CCTCAGGGTTCC
                        ||| |||||||||||
                        GCC GGAGTCCCAGGG
                        ACGT__ A       GII
GAM445   JAG2           CCTCGGCCTCCGGGTCCGGCA     6962 TCTCCT     A   C
                        CGGCCTC GGGTTC GCA
                        ||||||| ||||| |||
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                        GCCGGAG CCCAGG CGT
                        _____      G     C
GAM445  LZTS1           CCTCCGCCTCAGGGCCTTCC    6960 TCTCCTCG      __  GC
                        GCCTCAGGGT TCC
                        |||||||||| |||
                        CGGAGTCCCG AGG
                        GG_____          GA  GG
GAM445  NUCB1           CTCCT-GGTATCAGGGTTC     6968 TC  C CC      CG
                        TCCT GG  TCAGGGTTC
                        |||| || |||||||||
                        AGGA CC  AGTCCCAAG
                        __   _ AT       TI
GAM445  OVOL1           TCGGCCACAGAGGGTTCCG     6977 TCTCCT  CCTC       _
                        CGG   AGGGTTCCG C
                        |||   ||||||||| |
                        GTC   TCCCAAGGC G
                        GT____  ____       C
GAM445  PCSK2           CTCCTTCAGGCCTCA-GGTTCC  6963 TC   __     G  GCA
                        TCCT C GGCCTCAGG TTCC
                        |||| | ||||||||| ||||
                        AGGA G CCGGAGTCC AAGG
                        __   A T      _ AII
GAM445  RENBP           CCTCCTCTTCAGGGTTCCGC    6961 TCT   GGCC
                        CCTC   TCAGGGTTCCGC
                        ||||   ||||||||||||
                        GGAG   AGTCCCAAGGCG
                        ___   A___
GAM445  REPS2           CTCCTCGGCCTCA-GCTGCCGC  6970 TC        GGTT  A
                        TCCTCGGCCTCAG   CCGC
                        |||||||||||||   ||||
                        AGGAGCCGGAGTC   GGCG
                        __          GAC_  G
GAM445  SLC5A5          TCCCCTCTCACTCTGGGTTCCGC 6981      GGC  A      AI
                        TCTCCTC  CTC GGGTTCCGC
                        |||||||  ||| |||||||||
                        AGGGGAG  GAG CCCAAGGCG
                         AGT  A      II
GAM445  TBX6            CTCCT-GGCCTCAGGTGATCTGC 6966 TC   C     GT_ C A
                        TCCT GGCCTCAGG  TC GC
                        |||| |||||||||  || ||
                        AGGA CCGGAGTCC  AG CG
                        __   _    ACT A G
GAM445  WNT5B           TCGGCCTCAGCCCTCCCCA     6978 TCTC    _ AG_ T GC
                        CTCGGCC TC  GGT CC
                        ||||||| ||  ||| ||
                        GAGTCGG AG  TCA GG
                        ____       G GGG  C II
GAM445  XRCC3           TCCTC--CCGC-GGGTTCCGCA  6976 T    CG CTCA
                        CTCCT GC   GGGTTCCGC
                        ||||| ||   |||||||||
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                          GAGGG CG   CCCAAGGCG
                           _   __  ____
GAM445  YWHAZ        TCGTAGTCCCCAGGGTTCC     6973 TCTCCTC _        C
                         GG CCTCAGGGTTCCG
                         || |||||||||||
                         TC GGGGTCCCAAGGT
                        CA_____  A       C
GAM445  ZNF264       CTCCT-GGCCTCAGGTGATCC   6965 TC  C     GT_  C
                       TCCT GGCCTCAGG  TCCG
                       |||| |||||||||  ||||
                       AGGA CCGGAGTCC  AGGT
                       __  _      ACT  I
GAM446  APC         ATCAAACCTATTTACAAAATTTTC 6988 TA     TC___  T  C  TII
                       TCAAACCT   CAA ATT TTC
                       ||||||||   ||| ||| |||
                       AGTTTGGA   GTT TAA AAG
                       __     TAAAT  T  A  TII
GAM446  B3GNT3      ATCAAACC-TCAAACCTTC      6990 A_____      CAATATTI
                       TCAAACCTTC
                       ||||||||||
                       AGTTTGGAAG
                      TAGTTTGG       IIITTATA
GAM446  B3GNT3      ATCAAACC-TCAAACCTTC      6990 TA_____       AATATTCTT
                       TCAAACCTTCC
                       |||||||||||
                       AGTTTGGAAGG
                      AGTTTGG       IIITCTTCT
GAM446  BAZ2A       TCAA---TTCAAATATTCTTC    7006 TATCAAACC  C
                       TTC AATATTCTT
                       ||| |||||||||
                       AAG TTATAAGAA
                      TT_____  T
GAM446  CAMLG      TATAAATACCTTCCAAT-TTC     6997 TATCAA      ATI
                       ACCTTCCAAT
                       ||||||||||
                       TGGAAGGTTA
                      ATTTA_      AAG
GAM446  CAMLG      TATAAATACCTTCCAAT-TTC     6997 TATCAA_     A  TTC
                       ACCTTCCAAT TTC
                       |||||||||| |||
                       TGGAAGGTTA AAG
                      ATATTTA       _  III
GAM446  CNR1       ATCTAACAATACAATATTCTTCT   6993  A  CTTC       I
                       TC AAC   CAATATTCTTC
                       || |||   |||||||||||
                       AG TTG   GTTATAAGAAG
                        A  TTAT          I
GAM446  CNR1       ATCTAACAATACAATATTCTTCT   6993 TA A  CTTC       I
                       TC AAC   CAATATTCTTCT
                       || |||   ||||||||||||
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                                AG TTG   GTTATAAGAAGA
                              __  A  TTAT          T
GAM446 CUL3          TATCAAACCTGTGCTCCAA      6998         ____      TATTCTTC
                        TATCAAACCT   TCCAA
                        ||||||||||   |||||
                        ATAGTTTGGA   AGGTT
                            CACG    IIITCTTC
GAM446 CUL3          TATCAAACCTGTGCTCCAA      6998         ____      IIIT
                        TATCAAACCT   TCCA
                        ||||||||||   ||||
                        ATAGTTTGGA   AGGT
                            CACG    TIII
GAM446 CUL3          TATCAAACCTT-TAAAATT      7000        CCAATATI
                        TATCAAACCTT
                        |||||||||||
                        ATAGTTTGGAA
                            ATTTTAAI
GAM446 CUL3          TATCAAACCTT-TAAAATT      7000        CCAATATTCTT
                        TATCAAACCTT
                        |||||||||||
                        ATAGTTTGGAA
                            ATTTTAAIIIT
GAM446 CYBB         CAATCAATCCAATATTCTTCT     6995 AAACCT            I
                          TCCAATATTCTTC
                          |||||||||||||
                          AGGTTATAAGAAG
                        TTAGTT              I
GAM446 CYBB         CAATCAATCCAATATTCTTCT     6995 TA   ACCT
                          TCAA   TCCAATATTCTTCT
                          ||||   |||||||||||||
                          AGTT   AGGTTATAAGAAGA
                            __   ____
GAM446 DMP1        TATGCAACCTTCCAACTCCAATTCTTCT6999 ATCA        ____        I
                          AACCTTCCAAT   ATTCTTC
                          |||||||||||   |||||||
                          TTGGAAGGTTG   TAAGAAG
                          ____         AGGT    I
GAM446 DMP1        TATGCAACCTTCCAACTCCAATTCTTCT6999 TATCA        ____        III
                          AACCTTCCAAT   ATTCTTCT
                          |||||||||||   ||||||||
                          TTGGAAGGTTG   TAAGAAGA
                        ATACG         AGGT      III
GAM446 DMRT2       ATTAAAATTTT-AATATTCTTC      6992 TATCAAACCTTCC
                            AATATTCTTCT
                            |||||||||||
                            TTATAAGAAGG
                        AATTTTAAAA___
GAM446 EGLN1        ATCAATGCTCATTCCAATAT      6989 TA_____  AACC        CTTC
                          TCA   TTCCAATATT
                          |||   ||||||||||
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                          AGT    AAGGTTATAG
                          AGTTACG  ____         IIIT
GAM446  EHF        TATAAAGACCCCACCATTATTCTTCT 6996 ATCAAA   T  A        I
                          CCT CCA TATTCTTC
                          III III IIIIIIII
                          GGG GGT ATAAGAAG
                          TTTCTG  T  A      I
GAM446  EHF        TATAAAGACCCCACCATTATTCTTCT 6996 TATCAAA__   T  A       II
                          CCT CCA TATTCTTCT
                          III III IIIIIIIII
                          GGG GGT ATAAGAAGA
                          ATATTCTG  T  A       II
GAM446  FZD7         TCAAACCTTCC--TCTTCGTTC   7003 _        AATA  TTI
                          CAAACCTTCC    TTC
                          IIIIIIIIII   III
                          GTTTGGAAGG   AAG
                          A         AG__  CAA
GAM446  FZD7         TCAAACCTTCC--TCTTCGTTC   7003 TATC      AATAT
                          AAACCTTCC    TCTTC
                          IIIIIIIII    IIIII
                          TTTGGAAGG    AGAAG
                          ____        _____
GAM446  GOLGA4         AAACCTTCCGCTTATCTTCTTCT  6984 AAC    AATAT   I
                          CTTCC    TCTTC
                          IIIII    IIIII
                          GAAGG    AGAAG
                          ___    CGAAT    A
GAM446  GOLGA4         AAACCTTCCGCTTATCTTCTTCT  6984 TATCAAAC    AATAT   I
                          CTTCC    TCTTCT
                          IIIII    IIIIII
                          GAAGG    AGAAGA
                          _____    CGAAT    A
GAM446  IL17         TCAAACCTTCC----TTCTT     7005        AATATTC
                          TCAAACCTTCC
                          IIIIIIIIIII
                          AGTTTGGAAGG
                          AAGAAII
GAM446  IL17         TCAAACCTTCC----TTCTT     7005 TATC    AATA
                          AAACCTTCC    TTCT
                          IIIIIIIII    IIII
                          TTTGGAAGG    AAGA
                          ____    ____
GAM446  LAMA4         TAT-AAACCTAA-AATATTCTTCT 7001 ATC    TCC       I
                          AAACCT  AATATTCTTC
                          IIIIII  IIIIIIIIII
                          TTTGGA  TTATAAGAAG
                          ATA    TT_      I
GAM446  LAMA4         TAT-AAACCTAA-AATATTCTTCT 7001 TATC    TCC
                          AAACCT  AATATTCTTCT
                          IIIIII  IIIIIIIIIII
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                              TTTGGA    TTATAAGAAGA
                              ATA_       TT_
GAM446  LLT1          TATCAG---TTCCAATATGCTTCT  7002    AACC       T
                          TATCA    TTCCAATAT CTTCT
                          IIIII    IIIIIIIII IIIII
                          ATAGT    AAGGTTATA GAAGA
                              C___       C
GAM446  LLT1          TATCAG---TTCCAATATGCTTCT  7002 _  AACC       T
                           ATCA   TTCCAATAT CTTC
                           IIII   IIIIIIIII IIII
                           TAGT   AAGGTTATA GAAG
                           A C___      C
GAM446  MASP1           CAAACCTTCCCAACTTTCT       6994        _ A  II
                          CAAACCTTCC AAT TTC
                          IIIIIIIIII III III
                          GTTTGGAAGG TTG AAG
                              G   A  AI
GAM446  MASP1           CAAACCTTCCCAACTTTCT       6994 TATCAA    _  A
                             ACCTTCC AAT TTCTTC
                             IIIIIII III IIIIII
                             TGGAAGG TTG AAGAGG
                              _____     G   A
GAM446  MKI67        TCACACCTTCCAAAGTGCCTCT    7007 CAA      TATT   I
                          ACCTTCCAA   CTTC
                          IIIIIIIII   IIII
                          TGGAAGGTT   GGAG
                          GTG      TCAC   I
GAM446  MKI67        TCACACCTTCCAAAGTGCCTCT    7007 TATCAA      TATT
                          ACCTTCCAA   CTTCT
                          IIIIIIIII   IIIII
                          TGGAAGGTT   GGAGA
                          TG____       TCAC
GAM446  NFIL3         AATCCATC-AATATTCTTC       6986 AAA  TTC       I
                          CC  CAATATTCTT
                          II  IIIIIIIIII
                          GG  GTTATAAGAA
                          TTA  TA_       G
GAM446  NFIL3         AATCCATC-AATATTCTTC       6986 TATCAAACCTTC
                             CAATATTCTT
                             IIIIIIIIII
                             GTTATAAGAA
                          GTA_____
GAM446  NOX4          ATCATCACATCAAATATTCTTC  6991 _   AACCT C       T
                          TATCA    TC AATATTCTTC
                          IIIII    II IIIIIIIIII
                          GTAGT    AG TTATAAGAAG
                          A   GT___ T        T
GAM446  PTGFR          ACCTTTTGCCAATATTCTT     6987    ___        III
                          ACCTT  CCAATATTCT
                          IIIII  IIIIIIIIII
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                        TGGAA  GGTTATAAGA
                          AAC        AII
GAM446 PTGFR         ACCTTTTGCCAATATTCTT     6987 TATCAAACCTT        C
                            CCAATATTCTT
                            IIIIIIIIII
                            GGTTATAAGAA
                       AC_____         A
GAM446 SHANK2        AAATCTTCCAATAATTTC     6985 AAAC       TTCTTII
                            CTTCCAATA
                            IIIIIIIII
                            GAAGGTTAT
                     TTTA        TAAAAGI
GAM446 SHANK2        AAATCTTCCAATAATTTC     6985 TATCAAAC       TTC
                           CTTCCAATA  TTC
                           IIIIIIIII  III
                           GAAGGTTAT  AAG
                    _____         TAA
GAM446 SPG4          TCAAACCTTCAAACCTTCT     7004       C   A  II
                          TCAAACCTTC AAT TTC
                          IIIIIIIIII III III
                          AGTTTGGAAG TTG AAG
                             T   G  AI
GAM446 SPG4          TCAAACCTTCAAACCTTCT     7004 TATC      C   A    C
                          AAACCTTC AAT TTCTT
                          IIIIIIII III IIIII
                          TTTGGAAG TTG AAGAG
                       ____      T   G   A
GAM447 ADAR          TGTG-AGAGCCTGTGTTCCCAGT   7026 _  G     GT    I
                         GTG AGAGCCTG  TTCTCAG
                         III IIIIIIII  IIIIIII
                         CAC TCTCGGAC  AAGGGTC
                           A _    AC    I
GAM447 ADAR          TGTG-AGAGCCTGTGTTCCCAGT   7026 GTGTG      GT
                          GAGAGCCTG  TTCTCAGT
                          IIIIIIIII  IIIIIII
                          CTCTCGGAC  AAGGGTCA
                        CA___        AC
GAM447 BLTR2         TGTG-AGAGCCTGCCTTGCCAG   7023 _  G     G  C  I
                          GTG AGAGCCTG TTT TCA
                          III IIIIIIII III III
                          CAC TCTCGGAC GAA GGT
                           A _        G  C  I
GAM447 BLTR2         TGTG-AGAGCCTGCCTTGCCAG   7023 GTGTG      G  C  T
                          GAGAGCCTG TTT TCAG
                          IIIIIIIII III IIII
                          CTCTCGGAC GAA GGTC
                        CA___       G  C  C
GAM447 CSF1R         AGAGCCTGGTTTTCTCAGT     7010          _    II
                          AGAGCCTGGTTT CTCAG
                          IIIIIIIIIIII IIIII
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                    TCTCGGACCAAA GAGTC
                        A    AI
GAM447 EGLN2         TGCAGGGCTTGGTTTCTCTGT    7018 G A C       AGI
                      G AG GC TGGTTTCTC
                      | II II IIIIIIIII
                      C TC CG ACCAAAGAG
                       G  C  A      ACI
GAM447 EGLN2         TGCAGGGCTTGGTTTCTCTGT    7018 GTGTGG A C      AGT
                          AG GC TGGTTTCTC
                          II II IIIIIIIII
                          TC CG ACCAAAGAG
                    _____  C  A      ACA
GAM447 FLII       TGTGGAGAGAGTTGGATTTCCCAG  7020 GT    CC_ _      TI
                    GTGGAGAG  TGG TTTCTCAG
                    IIIIIIII  III IIIIIIII
                    CACCTCTC  ACC AAAGGGTC
                     __    TCA  T      TI
GAM447 FLII       TGTGGAGAGAGTTGGATTTCCCAG  7020 GT    CC_ _      I
                     GGAGAG  TGG TTTCTCA
                     IIIIII  III IIIIIII
                     CCTCTC  ACC AAAGGGT
                     __   TCA  T     I
GAM447 GNL1       GAGAGCCTGTTGACTCTGT     7011        GTTT AGII
                    GAGAGCCTG  CTC
                    IIIIIIIII  III
                    CTCTCGGAC  GAG
                      AACT  ACAI
GAM447 HNRPF       GGAGAGCAGGACTGGTTTCT    7012      ____      IIIA
                    GGAGAGC  CTGGTTTC
                    IIIIIII  IIIIIIIII
                    CCTCTCG  GACCAAAG
                      TCCT      AIII
GAM447 HNRPF       GGAGAGCAGGACTGGTTTCT    7012 GT TG A  GC      CAG
                     G  G GA CTGGTTTCT
                     |  | II IIIIIIIII
                     C  C CT GACCAAAGA
                     T_ GT _  __      CAA
GAM447 IMMP2L      TGTGGCG--CC-GGTTTCTCA   7022 _  AGA  T
                    GTGG  GCC GGTTTCTC
                    IIII  III IIIIIIIII
                    CACC  CGG CCAAAGAG
                     A  G__  _
GAM447 IMMP2L      TGTGGCG--CC-GGTTTCTCA   7022 GT  AGA  T
                    GTGG  GCC GGTTTCTCA
                    IIII  III IIIIIIIII
                    CACC  CGG CCAAAGAGT
                     __  G__  _
GAM447 MATN2       TGTGGCAAACCAGGTTTCTCAGT  7027    AG  T       I
                    GTGG  AGCC GGTTTCTCAG
                    IIII  IIII IIIIIIIIII
```

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                        CACC  TTGG CCAAAGAGTC
                        GT    T          I
GAM447 MATN2      TGTGGCAAACCAGGTTTCTCAGT   7027 GT   AG   T        I
                        GTGG  AGCC GGTTTCTCAGT
                        ||||  |||| ||||||||||
                        CACC  TTGG CCAAAGAGTCA
                        __    GT   T        T
GAM447 NPR2L      GTGGAGAGCCTGCCTTGCTCAG    7014 GTGT      G  _
                        GGAGAGCCTG TTT CTCAGT
                        |||||||||| ||| ||||||
                        CCTCTCGGAC GAA GAGTCG
                        ___        G   C
GAM447 NPR2L      GTGGAGAGCCTGCCTTGCTCAG    7014 T        G  _  I
                        GGAGAGCCTG TTT CTCA
                        |||||||||| ||| ||||
                        CCTCTCGGAC GAA GAGT
                        _          G   C   I
GAM447 OAS3       TGTGGAGAGTCAGGCTGTCTAAG    7021     CCT  _  CAI
                        TGGAGAG  GGTT TCT
                        |||||||  |||| |||
                        ACCTCTC  CCGA AGA
                        AGT      C    TII
GAM447 OAS3       TGTGGAGAGTCAGGCTGTCTAAG    7021 GT      CCT  _  C TI
                        GTGGAGAG  GGTT TCT AG
                        ||||||||  |||| ||| ||
                        CACCTCTC  CCGA AGA TC
                        __        AGT  C   T TI
GAM447 PAX4       TGTGGAGAG---GGTCACTCAG    7024 _      CCT  T
                        GTGGAGAG  GGTT CTCA
                        ||||||||  |||| ||||
                        CACCTCTC  CCAG GAGT
                        A         ___  T
GAM447 PAX4       TGTGGAGAG---GGTCACTCAG    7024 GT      CCT  T
                        GTGGAGAG  GGTT CTCAG
                        ||||||||  |||| |||||
                        CACCTCTC  CCAG GAGTC
                        __        ___  T
GAM447 PXN        TGGAGAGGCT--TTTCTCAGT     7019 _    C GG      I
                        GGAGAG CT TTTCTCAG
                        |||||| || |||||||||
                        CCTCTC GA AAAGAGTC
                        A      C  __   I
GAM447 PXN        TGGAGAGGCT--TTTCTCAGT     7019 GTGT  A CTGG
                        GGAG GC   TTTCTCAG
                        |||| ||   |||||||||
                        TCTC CG   AAAGAGTC
                        ____      _ A___
GAM447 RDS        TGGAGTGCACTA-TTTCTCAGT    7017 A _  G      I
                        GGAG GC CTG TTTCTCAG
                        |||| || ||| ||||||||
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                              CCTC CG GAT AAAGAGTC
                                A  T  _        I
GAM447 RDS          TGGAGTGCACTA-TTTCTCAGT   7017 GTGTGGAGA _ G
                              GC CTG TTTCTCAGT
                              || ||| |||||||||
                              CG GAT AAAGAGTCA
                            TCA_____ T _
GAM447 S100A1      GTGTGGAGA-CCTGTCTTCAACAGT 7016      G   G  T_  I
                            GTGTGGAGA CCTG TTTC CAGT
                            ||||||||| |||| |||| ||||
                            CACACCTCT GGAC GAAG GTCA
                                _  A  TT  I
GAM447 S100A1      GTGTGGAGA-CCTGTCTTCAACAGT 7016      G   G  T_  I
                            TGTGGAGA CCTG TTTC CAG
                            |||||||| |||| |||| |||
                            ACACCTCT GGAC GAAG GTC
                                _  A  TT  I
GAM447 SGCA        TGTTTAGAGCCTGGGTTC-CAG  7025_ GG     T  CAI
                            GT AGAGCCTGG TTCT
                            || ||||||||| ||||
                            CA TCTCGGACC AAGG
                              A AA     C  TII
GAM447 SGCA        TGTTTAGAGCCTGGGTTC-CAG   7025 GT GG     T  T  T
                            GT AGAGCCTGG TTC CAG
                            || ||||||||| ||| |||
                            CA TCTCGGACC AAG GTC
                             __ AA     C _ C
GAM447 SHMT1       GGAAAGCCTGGTTGATTCTCA   7013          ___  III
                            GGAGAGCCTGGTT  TCTC
                            |||||||||||||  ||||
                            CCTTTCGGACCAA  AGAG
                              CTA    TII
GAM447 TACC1       GTGGGGAGAGCCT-TTTTC     7015  T    GG  TCA
                            GTG GGAGAGCCT TTTC
                            ||| ||||||||| ||||
                            CAC CCTCTCGGA AAAG
                             C     A_  III
GAM447 TACC1       GTGGGGAGAGCCT-TTTTC     7015  T    GG  I
                            GTG GGAGAGCCT TTT
                            ||| ||||||||| |||
                            CAC CCTCTCGGA AAG
                             C     AA  I
GAM448 ADAR        TGTG-AGAGCCTGTGTTCCCAGT  7026 _ G     GT   I
                            GTG AGAGCCTG TTCTCAG
                            ||| |||||||| |||||||
                            CAC TCTCGGAC AAGGGTC
                             A _   AC  I
GAM448 ADAR        TGTG-AGAGCCTGTGTTCCCAGT  7026 GTGTG     GT
                             GAGAGCCTG TTCTCAGT
                             ||||||||| |||||||
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                         CTCTCGGAC AAGGGTCA
                       CA___        AC
GAM448 BLTR2           TGTG-AGAGCCTGCCTTGCCAG   7023 _ G      G  C  I
                          GTG AGAGCCTG TTT TCA
                          ||| ||||||||| ||| |||
                          CAC TCTCGGAC GAA GGT
                          A _        G C  I
GAM448 BLTR2           TGTG-AGAGCCTGCCTTGCCAG   7023 GTGTG     G  C  T
                          GAGAGCCTG TTT TCAG
                          ||||||||| ||| ||||
                          CTCTCGGAC GAA GGTC
                       CA___        G  C   C
GAM448 CSF1R           AGAGCCTGGTTTTCTCAGT      7010          _   II
                          AGAGCCTGGTTT CTCAG
                          ||||||||||||| |||||
                          TCTCGGACCAAA GAGTC
                                A   AI
GAM448 EGLN2           TGCAGGGCTTGGTTTCTCTGT    7018 G A C      AGI
                          G AG GC TGGTTTCTC
                          | || || |||||||||
                          C TC CG ACCAAAGAG
                          G  C  A     ACI
GAM448 EGLN2           TGCAGGGCTTGGTTTCTCTGT    7018 GTGTGG A C     AGT
                          AG GC TGGTTTCTC
                          || || |||||||||
                          TC CG ACCAAAGAG
                       _____    C  A     ACA
GAM448 FLII            TGTGGAGAGAGTTGGATTTCCCAG 7020 GT     CC_ _     TI
                          GTGGAGAG  TGG TTTCTCAG
                          ||||||||  ||| |||||||||
                          CACCTCTC  ACC AAAGGGTC
                          __      TCA  T     TI
GAM448 FLII            TGTGGAGAGAGTTGGATTTCCCAG 7020 GT     CC_ _     I
                          GGAGAG  TGG TTTCTCA
                          ||||||  ||| ||||||||
                          CCTCTC  ACC AAAGGGT
                          __     TCA  T     I
GAM448 GNL1            GAGAGCCTGTTGACTCTGT      7011       GTTT  AGII
                          GAGAGCCTG   CTC
                          |||||||||   |||
                          CTCTCGGAC   GAG
                          AACT  ACAI
GAM448 HNRPF           GGAGAGCAGGACTGGTTTCT     7012        ____      IIIA
                          GGAGAGC  CTGGTTTC
                          |||||||  ||||||||
                          CCTCTCG  GACCAAAG
                            TCCT     AIII
GAM448 HNRPF           GGAGAGCAGGACTGGTTTCT     7012 GT TG A GC       CAG
                          G  G GA CTGGTTTCT
                          |  | || |||||||||
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                         C  C  CT  GACCAAAGA
                         T_ GT _ __        CAA
GAM448 IMMP2L            TGTGGCG--CC-GGTTTCTCA    7022 _   AGA  T
                           GTGG  GCC GGTTTCTC
                           |||  ||| |||||||||
                           CACC  CGG CCAAAGAG
                           A   G__  _
GAM448 IMMP2L            TGTGGCG--CC-GGTTTCTCA    7022 GT   AGA  T
                           GTGG  GCC GGTTTCTCA
                           ||||  ||| |||||||||
                           CACC  CGG CCAAAGAGT
                           __   G__  _
GAM448 MATN2             TGTGGCAAACCAGGTTTCTCAGT   7027    AG  T       I
                           GTGG  AGCC GGTTTCTCAG
                           ||||  |||| |||||||||
                           CACC  TTGG CCAAAGAGTC
                            GT    T         I
GAM448 MATN2             TGTGGCAAACCAGGTTTCTCAGT   7027 GT  AG  T       I
                           GTGG  AGCC GGTTTCTCAGT
                           ||||  |||| ||||||||||
                           CACC  TTGG CCAAAGAGTCA
                           __    GT   T        T
GAM448 NPR2L            GTGGAGAGCCTGCCTTGCTCAG    7014 GTGT      G  _
                            GGAGAGCCTG TTT CTCAGT
                            |||||||||| ||| ||||||
                            CCTCTCGGAC GAA GAGTCG
                           ____          G  C
GAM448 NPR2L            GTGGAGAGCCTGCCTTGCTCAG    7014 T        G  _  I
                            GGAGAGCCTG TTT CTCA
                            |||||||||| ||| ||||
                            CCTCTCGGAC GAA GAGT
                            _          G  C  I
GAM448 OAS3            TGTGGAGAGTCAGGCTGTCTAAG    7021     CCT  _  CAI
                           TGGAGAG  GGTT TCT
                           |||||||  |||| |||
                           ACCTCTC  CCGA AGA
                            AGT    C   TII
GAM448 OAS3            TGTGGAGAGTCAGGCTGTCTAAG    7021 GT      CCT  _  C  TI
                           GTGGAGAG  GGTT TCT AG
                           ||||||||  |||| ||| ||
                           CACCTCTC  CCGA AGA  TC
                           __       AGT  C  T  TI
GAM448 PAX4           TGTGGAGAG---GGTCACTCAG    7024 _     CCT  T
                           GTGGAGAG  GGTT CTCA
                           ||||||||  |||| ||||
                           CACCTCTC  CCAG GAGT
                           A    ___   T
GAM448 PAX4           TGTGGAGAG---GGTCACTCAG    7024 GT    CCT  T
                           GTGGAGAG  GGTT CTCAG
                           ||||||||  |||| |||||
```

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                              CACCTCTC  CCAG GAGTC
                              __     ___     T
GAM448 PXN          TGGAGAGGCT--TTTCTCAGT    7019 _    C GG       I
                       GGAGAG CT TTTCTCAG
                       |||||| || |||||||||
                       CCTCTC GA AAAGAGTC
                            A    C  __      I
GAM448 PXN          TGGAGAGGCT--TTTCTCAGT    7019 GTGT  A CTGG
                         GGAG GC  TTTCTCAG
                         |||| ||  ||||||||
                         TCTC CG  AAAGAGTC
                       ___    _ A___
GAM448 RDS          TGGAGTGCACTA-TTTCTCAGT    7017   A _ G       I
                       GGAG GC CTG TTTCTCAG
                       |||| || ||| |||||||||
                       CCTC CG GAT AAAGAGTC
                          A T   _       I
GAM448 RDS          TGGAGTGCACTA-TTTCTCAGT    7017 GTGTGGAGA _ G
                          GC CTG TTTCTCAGT
                          || ||| |||||||||
                          CG GAT AAAGAGTCA
                       TCA_____ T  _
GAM448 S100A1       GTGTGGAGA-CCTGTCTTCAACAGT 7016      G   G  T_ I
                       GTGTGGAGA CCTG TTTC  CAGT
                       ||||||||| |||| ||||  ||||
                       CACACCTCT GGAC GAAG  GTCA
                         _  A  TT I
GAM448 S100A1       GTGTGGAGA-CCTGTCTTCAACAGT 7016      G   G  T_ I
                       TGTGGAGA CCTG TTTC  CAG
                       |||||||| |||| ||||  |||
                       ACACCTCT GGAC GAAG  GTC
                         _  A  TT I
GAM448 SGCA         TGTTTAGAGCCTGGGTTC-CAG    7025 _ GG      T  CAI
                       GT AGAGCCTGG TTCT
                       || ||||||||| ||||
                       CA TCTCGGACC AAGG
                       A AA      C  TII
GAM448 SGCA         TGTTTAGAGCCTGGGTTC-CAG    7025 GT GG      T  T T
                       GT AGAGCCTGG TTC CAG
                       || ||||||||| ||| |||
                       CA TCTCGGACC AAG GTC
                       __ AA      C _ C
GAM448 SHMT1        GGAAAGCCTGGTTGATTCTCA     7013            ___  III
                       GGAGAGCCTGGTT  TCTC
                       |||||||||||||  ||||
                       CCTTTCGGACCAA  AGAG
                             CTA   TII
GAM448 TACC1        GTGGGGAGAGCCT-TTTC        7015 T      GG  TCA
                       GTG GGAGAGCCT TTTC
                       ||| |||||||| ||||
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                          CAC CCTCTCGGA  AAAG
                           C       A_    III
GAM448  TACC1             GTGGGGAGAGCCT-TTTTC    7015   T      GG   I
                          GTG GGAGAGCCT  TTT
                          III IIIIIIIII  III
                          CAC CCTCTCGGA  AAG
                           C       AA  I
GAM449  AXL               ACCATGGTCCTAGAGAG-GCA    7063      _  _ T  CTGG
                          ACCATGGTC TAGA AG GCA
                          IIIIIIIII IIII II III
                          TGGTACCAG ATCT TC CGT
                               G   C  _  IIIT
GAM449  CNGA1               TCTAGAAGTGGACGTCACTGGT   7073 ACCA  TCTAGAA  G
                           TGG    GT CACTGGT
                           III     II IIIIIII
                           ACC     CA GTGACCA
                           C___   TG_____  _
GAM449  CRY2              TGGCTCCAGGAGTGCACTG    7074 ACCATGG   A      G
                          TCTAG AGTGCACTG
                          IIIII IIIIIIIII
                          AGGTC TCACGTGAC
                          _____     C   G
GAM449  CUL3             ATGGTCTAGAACATGTACTG    7065 ACCATG    _  C  G
                          GTCTAGAA GTG ACTG
                          IIIIIIII III IIII
                          CAGATCTT TAC TGAC
                          _____     G  A  A
GAM449  CYP3A43           CCATC-TCTT-AAGTGCACT    7070 ACCATG  AG_      G
                          GTCT AAGTGCACT
                          IIII IIIIIIIII
                          TAGA TTCACGTGA
                          G_____   GAA      A
GAM449  MS4A1            ACCAAGG-CTGGA-GTGCACTGGT  7064    T T A A
                          ACCA GG CT GA GTGCACTGGT
                          IIII II II II IIIIIIIIII
                          TGGT CC GA CT CACGTGACCA
                           T  _  C  _
GAM449  NAGA             CCATGGTCTAG--GCTCAGTGGT   7071 AC      AA G  C
                          CATGGTCTAG  GT CA TGGT
                          IIIIIIIIII  II II IIII
                          GTACCAGATC  CG GT ACCA
                           __       __ A  C
GAM449  PCLO             CCAAGGTTCTAGAAGTTGACTG   7069 AC T _    GC  GT
                          CA GGT CTAGAAGT ACTG
                          II III IIIIIIII IIII
                          GT CCA GATCTTCA TGAC
                          __ T  A    AC  AI
GAM449  PRELP            CCAGGAGTTTGGGTGTGCACTGGT  7068 ACCATGGTCTAGAA         I
                          GTGCACTGGT
                          IIIIIIIIII
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                          CACGTGACCA
                          GTCCTCAAACCCA_        A
GAM449  RFX2          CCATGGTCTGGTGGGGCCCTGGT  7072 AC      AGAAGT  A    I
                          CATGGTCT    GC CTGGT
                          |||||||    || |||||
                          GTACCAGA    CG GACCA
                              __    CCACCC G   C
GAM449  SYK           CATGCT-TAGAAACTGCACTGGT  7066 ACCATG TC     _
                          G TAGAAG TGCACTGGT
                          | |||||| |||||||||
                          C ATCTTT ACGTGACCA
                          A_____GA   G
GAM449  TEGT          CCACTGTGTCAAACTGTGCACTGGT 7067 ACCA _  T AA       II
                          TG GTC AG GTGCACTGGT
                          || ||| || |||||||||
                          AC CAG TT CACGTGACCA
                          GTG_ A  T GA      AI
GAM450  ADCY2         TGACAATGACTCAATGCTTTTAA  7080  TT__      CTTGAATTGI
                          TGAC   ACTCAATGC
                          ||||   |||||||||
                          ACTG   TGAGTTACG
                          TTAC       AAAATTIIIG
GAM450  BCL6          TGTCTTCAC-CAATGCCTTG    7083 TGAC_  T      AATT
                          TTAC CAATGCCTTG
                          |||| ||||||||||
                          AGTG GTTACGGAAC
                          ACAGA  _       IIIG
GAM450  C10orf2       TGAC---CTCACTGCCTTGAAT   7087  TTA  A      T
                          TGAC  CTCA TGCCTTGAAT
                          ||||  |||| ||||||||||
                          ACTG  GAGT ACGGAACTTA
                          ___  G    I
GAM450  CLCA3         TGGCTTCATGGATGGCTTGAATTG 7089  A  ACTCA  C      I
                          TG CTT   ATG CTTGAATTG
                          || |||   ||| |||||||||
                          AC GAA   TAC GAACTTAAC
                          C  GTACC  C      I
GAM450  HAS3          CTTACT-AGTTTCTTGAATTG    7077 TGACTTACTCAATGC
                              CTTGAATT
                              ||||||||
                              GAACTTAA
                          TGATCAAA_____
GAM450  NET1          TAGTCAACACTGACTTGAATTG   7079 TGACTTACT  A C
                          CA TG CTTGAATTG
                          || || |||||||||
                          GT AC GAACTTAAC
                          TT_____ G T
GAM450  P2RY1         TGACTTACTCAAT-CTTTG      7081  _       GCCTTGAATT
                          TGACTT ACTCAAT
                          |||||| |||||||
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                        ACTGAA TGAGTTA
                         A     GAAACIIIGT
GAM450 PRKY            TGGCTTTATCAATGCCTATGAA    7086  A  AC      _   TTG
                        TG CTT  TCAATGCCT TGAA
                        II III  IIIIIIIII IIII
                        AC GAA  AGTTACGGA ACTT
                         C  AT      T   III
GAM450 RAB11A         TGACTGACTACAGCAATGCCTT    7084 ____    T T_       GAATTG
                        TGACT AC  CAATGCCTT
                        IIIII II  IIIIIIIII
                        ACTGA TG  GTTACGGAA
                        ACTG  _ TC      IIIGTT
GAM450 SCN1A         TGAATGTTCTCAATGCCGAGACATTG 7082 TGACTTA_     TT _  II
                           CTCAATGCC GA ATTG
                           IIIIIIIII II IIII
                           GAGTTACGG CT TAAC
                        ACTTACAA     CT G  II
GAM450 SGCG           TGACTTACT---TGCATTAAACTG  7088      CAA  C
                        TGACTTACT TGC TTGAATTG
                        IIIIIIIII III IIIIIIII
                        ACTGAATGA ACG AATTTGAC
                              ___  T
GAM450 SMG1          TTAAACAAT-CCTTGAATT     7090 TGACTTACT  G
                          CAAT CCTTGAAT
                          IIII IIIIIIII
                          GTTA GGAACTTA
                        T_____  _
GAM450 TAF1         TGACTTACTGAGCTCCCTT     7085      CAATG  GAATT
                        TGACTTACT    CCTT
                        IIIIIIIII    IIII
                        ACTGAATGA    GGGA
                        CTCGA  AIIIG
GAM450 ZNF26        GACTTACTCCTAAAGGCTT      7078 TG    AAT___  CTTGAATT
                        ACTTACTC    GC
                        IIIIIIII    II
                        TGAATGAG    CG
                        __    GATTTC  AAAIIIGT
GAM451 CLASP1      GGCCCGTGGCATCGCCGCA      7095 TG     CT__   CTGA
                        GCCCGTGGC  CCGCA
                        IIIIIIIII  IIIII
                        CGGGCACCG  GGCGT
                        __     TAGC   CIII
GAM451 DUSP4       CCCGGCTCCTCCGCACTGA      7093 TGGCCC  GG
                        GT CCTCCGCACTGA
                        II IIIIIIIIIIII
                        CG GGAGGCGTGACT
                        C_____ A_
GAM451 MEN1        TGGGCGGCGGCCTCCGCGCT     7096 T_ CC      A GA
                        GGC GTGGCCTCCGC CT
                        III IIIIIIIIIII II
```

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                          CCG  CGCCGGAGGCG GA
                          AC  C_        C II
GAM451 RAD52              TGGTGCGTGGCCT-CGCTCT    7097  CC      C A GA
                          TGG  CGTGGCCTC GC CT
                          III  IIIIIIIII II II
                          ACC  GCACCGGAG CG GA
                            AC      _ A II
GAM451 RFP               GGCGCCGAG--CTCCGCACTGA    7094 TG _ T  C
                          GC CCG GGC TCCGCACTGA
                          II III III IIIIIIIIII
                          CG GGC TCG AGGCGTGACT
                          __  C _ _
GAM451 TNFRSF4            TGGACC-TGTTCTCCGCACTG    7098  C G GC       A
                          TGG CC TG CTCCGCACTG
                          III II II IIIIIIIIII
                          ACC GG AC GAGGCGTGAC
                            T _ AA      I
GAM452 ATP2C1            TAGCAGCAG-C--ATCTGCAAGA    7110 CTTA    ACTA   _
                          GCAGCAG   ATCTG AAG
                          IIIIIII   IIIII III
                          CGTCGTC   TAGAC TTC
                          ____      G___   G
GAM452 ATP7A            TTAGCAGCAGTTCAGCAATCT    7113 CT      AC___    GAAGA
                          TAGCAGCAG   TAATCT
                          IIIIIIIII   IIIIII
                          ATCGTCGTC   GTTAGA
                          __          AAGTC   GIIIA
GAM452 COL9A3           TAGC--CAGTCATTAATCTGAAG   7108 CTTAG _ GAC      A
                          CAG CA  TAATCTGAAG
                          III II  IIIIIIIIII
                          GTC GT  ATTAGACTTC
                          CG___  A A__      C
GAM452 CREBL2          TTAGCCAGCAAACAGTAATCTGAA  7112 CT  _   __      GAI
                          TAGC AGCAGAC TAATCTGAA
                          IIII IIIIIII IIIIIIIII
                          ATCG TCGTTTG ATTAGACTT
                          __   G   TC      AII
GAM452 DAD1           TAGCAGTAAGTGTCAAATCTGAAGA 7107 CTTA  C_ ACT__       II
                          GCAG AG   AATCTGAAGA
                          IIII II   IIIIIIIIII
                          CGTC TC   TTAGACTTCT
                          ____    AT ACAGT      TT
GAM452 FACL2           AGCAGCAGAC--AGCTGCAGA     7103 CTTAGC    TAAT A
                          AGCAGAC   CTG AG
                          IIIIIII   III II
                          TCGTCTG   GAC TC
                          _____       TC__ G
GAM452 HOXA7           CTTAGCAGCAAAATTTCT    7104         CTAA  GAAG
                          CTTAGCAGCAGA  TCT
                          IIIIIIIIIII  III
```

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                            GAATCGTCGTTT   AGA
                              TAAA   IIIA
GAM452 MADH7        TTAGCAGCAAAGTAGTTTGAAG   7114 CT       C ATC   A
                      TAGCAGCAGA TA  TGAAG
                      |||||||||| ||  |||||
                      ATCGTCGTTT AT  ACTTC
                        __      C  CAA   A
GAM452 MPHOSPH9       TAGCAGCAGCAAAATCAGA   7111 CTTA     ACT  T AG
                      GCAGCAG  AATC GA
                      |||||||  |||| ||
                      CGTCGTC  TTAG CT
                        ____      GTT  T AA
GAM452 NPR2        AGCAGCAGAAGACT-ATCTGA    7101 CTT   C  A   AG
                      AGCAG AGACTA TCTGA
                      ||||| |||||| |||||
                      TCGTC TCTGAT AGACT
                        ___     T  _  GA
GAM452 RAF1        CTTAGCAGCAG-CTTCTCTGAA   7105       A AA   GA
                      CTTAGCAGCAG CT  TCTGAA
                      ||||||||||| ||  ||||||
                      GAATCGTCGTC GA  AGACTT
                         _  AG    II
GAM452 SGCA        AGCAGCAGATATTTATTCTGAA   7102 CTTAGC   C___ A   GA
                      AGCAGA   TA TCTGAA
                      ||||||   || ||||||
                      TCGTCT   AT AGACTT
                      _____       ATAA A   AC
GAM452 USH2A      TAGCAGCAG--GAATGCTGGAAG   7109 CTTA     ACT  _ _ A
                      GCAGCAG   AAT CTG AAG
                      |||||||   ||| ||| |||
                      CGTCGTC   TTA GAC TTC
                        ____     C__  C C C
GAM452 ZNF10      CTTACCAG-AGA---ATCTGAAGA  7106   G  C  CTA
                      CTTA CAG AGA  ATCTGAAG
                      |||| ||| |||  ||||||||
                      GAAT GTC TCT  TAGACTTC
                        G  _  ___
GAM453 FCER1A      ACCAGTTTCACTCAG--TTTA    3104 TA     CA   GATTTAT
                      CCAGTTTC TCAG
                      |||||||| ||||
                      GGTCAAAG AGTC
                        __       TG   AAATTII
GAM453 IFRD1      ACCAGTTTCAAT-AGTATT      3103 TA     C C GATTTA
                      CCAGTTTC AT AG
                      |||||||| || ||
                      GGTCAAAG TA TC
                        __      T _ ATAACI
GAM453 LIFR        TAGCAGTTAAAATCAGGATTCAT  3116 TAC   TCC      CI
                      CAGTT ATCAGGATTTAT
                      ||||| |||||||||||
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                        GTCAA   TAGTCCTAAGTA
                        ATC    TTT        II
GAM453 PSMA2            TAACAGTTT--ATTAGGATTTAT  3115 TAC    CC C      C
                        CAGTTT  AT AGGATTTAT
                        IIIIII II IIIIIIIII
                        GTCAAA  TA TCCTAAATA
                        ATT      __ A        I
GAM453 PSME3           CCAGTTTCCCCATCACGAT       3108 TACCAG TT    G  TTAT
                           T  CCATCA GAT
                           I  IIIIIII III
                           A  GGTAGT CTA
                        TCAA__GG   G  TCII
GAM453 RCN1           TACCACTTTCACTTAATCAGGATTT  3113   G  C____       ATCII
                        TACCA TTTC   ATCAGGATTT
                        IIIII IIII    IIIIIIIIII
                        ATGGT AAAG    TAGTCCTAAA
                          G  TGAAT        IIICT
GAM453 SCA1           CCAGTTTCCACTGTCCGGCTTGAT  3109 TACC      CA___   ATTTATCI
                        AGTTTCCAT   GG
                        IIIIIIIII    II
                        TCAAAGGTG   CC
                        ____         ACAGG  GAACTAAA
GAM453 SPON1          AGTCTCCAAAATCAGGATTT      3105 TA  TTTCC       AT
                          CCAG   ATCAGGATTT
                          IIII    IIIIIIIIII
                          GGTT   TAGTCCTAAA
                        A_  T____         AT
GAM453 SRGAP2         TACCAGTTTTGATCAGTTGGATT   3114       CC   GATTTATCI
                        TACCAGTTT ATCAG
                        IIIIIIIII IIIII
                        ATGGTCAAA TAGTC
                          AC    AACCTAAII
GAM453 TCEB1L        CCAGTTTCCAACTCATGAT         3110 TACC     __  G  TTAT
                        AGTTTCCA TCA GAT
                        IIIIIIII III III
                        TCAAAGGT AGT CTA
                        ____        TG  A  TTII
GAM453 WNT8B        CCAGTTTCC-TCAGTTTTT          3111 TACC    A  GA A
                        AGTTTCC TCAG TTT
                        IIIIIII IIII III
                        TCAAAGG AGTC AAA
                        ____       _  AA  G
GAM453 ZNF124        TTTACATTTACAGGATTTAT         3117 TACCAGTTTCCAT
                          CAGGATTTAT
                          IIIIIIIIII
                          GTCCTAAATA
                        AAAT_____
GAM454 AF3P21        TGGCAAGGG-CTGCGGCGCCA         7144        GTCCTT  GA
                        TGGCAAGGGT   CGCCA
                        IIIIIIIII    IIIII
```

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                        ACCGTTCCCG    GCGGT
                        ACGCC_    II
GAM454  AF3P21       TGGCAAGGG-CTGCGGCGCCA   7144 _        GTCCTT   I
                        GGCAAGGGT    CGCC
                        |||||||||    ||||
                        CCGTTCCCG    GCGG
                        A    ACGCC_    I
GAM454  AMY2B        CATGGGTTCCACATCGCCAGAT   7132 AA    G   T__        I
                        GGGT TCC  TCGCCAGA
                        |||| ||| |||||||||
                        CCCA AGG  AGCGGTCT
                        A_    _   TGT       I
GAM454  AMY2B        CATGGGTTCCACATCGCCAGAT   7132 TGGCAA    G   T__
                        GGGT TCC  TCGCCAGAT
                        |||| ||| |||||||||
                        CCCA AGG  AGCGGTCTA
                        _____    _   TGT
GAM454  CDK6        CAAGGGTGTTCTCCGCAGGAT    7133       C    C AI
                        AAGGGTGT CTTCGC AG
                        |||||||| |||||| ||
                        TTCCCACA GAGGCG TC
                        A    _   CT
GAM454  CDK6        CAAGGGTGTTCTCCGCAGGAT    7133 TGGCAA    C    CA
                        GGGTGT CTTCGC GAT
                        |||||| |||||| |||
                        CCCACA GAGGCG CTA
                        _____    A   TC
GAM454  COPA        GGCAGGGGGTCTCCTTCGCC    7136   A_  G      II
                        GGCA GGGT TCCTTCGC
                        |||| |||| |||||||||
                        CCGT CCCA AGGAAGCG
                        CC   G    GI
GAM454  COPA        GGCAGGGGGTCTCCTTCGCC    7136 TG A_  G      AGA
                        GCA GGGT TCCTTCGCC
                        ||| |||| |||||||||
                        CGT CCCA AGGAAGCGG
                        __   CC   G    AII
GAM454  DUSP5       GGCCAGGGTGTCCACGGCCAG    7137 A      TTC    I
                        GC AGGGTGTCC  GCCA
                        || ||||||||| ||||
                        CG TCCCACAGG  CGGT
                        G    TGC    I
GAM454  DUSP5       GGCCAGGGTGTCCACGGCCAG    7137 TG A      TTC    AT
                        GC AGGGTGTCC  GCCAG
                        || ||||||||| |||||
                        CG TCCCACAGG  CGGTC
                        __  G    TGC    CI
GAM454  GAA         TGGCC-GGG-GTCCTTCGC    7142    AA  T       CAG
                        TGGC GGG GTCCTTCGC
                        |||| ||| |||||||||
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                       ACCG  CCC CAGGAAGCG
                          G_  _       III
GAM454 GAA             TGGCC-GGG-GTCCTTCGC    7142   AA  T    I
                       TGGC  GGG GTCCTTCG
                       IIII III IIIIIIII
                       ACCG  CCC CAGGAAGC
                          G_  _       G
GAM454 IL15            TGGCAAGGGGTTTCCAGCAGCCA  7140        TG_  TT _  GATI
                       TGGCAAGGG  TCC  C GCCA
                       IIIIIIIII  III I IIII
                       ACCGTTCCC  AGG G CGGT
                            CAA  TC T   IIIT
GAM454 IL15            TGGCAAGGGGTTTCCAGCAGCCA  7140 GG    TG_  TT _  I
                          CAAGGG  TCC  C GCC
                          IIIIII  III I III
                          GTTCCC  AGG G CGG
                        __     CAA  TC T  I
GAM454 KCNK4           GTGTCCTTCTCCCCCAGAT     7139       G___       III
                       GTGTCCTTC  CCAGA
                       IIIIIIIII  IIIII
                       CACAGGAAG  GGTCT
                            AGGG    AII
GAM454 KLHL1           AAGCGTACCCCTCGCCAGAT     7129 TGGCAAGG  GT
                          GT CCTTCGCCAGA
                          II IIIIIIIIIII
                          CA GGGAGCGGTCT
                       _____     TG
GAM454 KLHL1           AAGCGTACCCCTCGCCAGAT     7129  G GT        I
                          AG GT CCTTCGCCAGA
                          II II IIIIIIIIIII
                          TC CA GGGAGCGGTCT
                           G  TG        I
GAM454 MADH7           AGGGTGTCCT--GCC-GAT      7131       TC  AGA
                       AGGGTGTCCT GCC
                       IIIIIIIIII III
                       TCCCACAGGA CGG
                             __  CTA
GAM454 OPHN1           TGGCAAGGGTTTATGTCCT      7141        ____    IIIA
                       TGGCAAGGGT  GTCC
                       IIIIIIIIII  IIII
                       ACCGTTCCCA  CAGG
                        AATA    AIII
GAM454 OPHN1           TGGCAAGGGTTTATGTCCT      7141        ____  T____  GCCA
                       TGGCAAGGGT  GTCC  TC  GA
                       IIIIIIIIII  IIII  II  II
                       ACCGTTCCCA  CAGG  AG  CT
                        AATA   AIIIT ACCG
GAM454 PRKY            TGGCAAGGGTATACTCCACC     7143        C     AGA
                       TGGCAAGGGTGT CTTCGCC
                       IIIIIIIIIII IIIIIII
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                        ACCGTTCCCATA GAGGTGG
                            T    III
GAM454  PRKY            TGGCAAGGGTATACTCCACC    7143        C    I
                        GGCAAGGGTGT CTTCGC
                        |||||||||||| ||||||
                        CCGTTCCCATA GAGGTG
                            T    I
GAM454  SORCS2          GCAAAGGTGTCCTT-G-CAGA   7134        C  CAI
                        GCAAGGGTGTCCTT GC
                        ||||||||||||| ||
                        CGTTCCACAGGAA CG
                            _   TCT
GAM454  SORCS2          GCAAAGGTGTCCTT-G-CAGA   7134 TGGC       C  C
                        AAGGGTGTCCTT GC AGA
                        ||||||||||| || |||
                        TTTCCACAGGAA CG TCT
                        ____       _ _
GAM454  TBL2          AGGGTGTCCCCGTTGGCCAG      7130        C___  III
                        AGGGTGTCCTT   GCCA
                        ||||||||||    ||||
                        TCCCACAGGGG   CGGT
                          CAAC    CII
GAM454  TDE1           GGTGTCCTTGGCACTCAGA      7138        __  _  III
                        GGTGTCCTT CGC CAG
                        ||||||||| ||| |||
                        CCACAGGAA GTG GTC
                          CC   A  TII
GAM454  VCL           GGCAGGAAGTGTCCTTCAGACAG   7135 GC A       CCI
                        A GGGTGTCCTTCG
                        | ||||||||||||
                        C TTCACAGGAAGT
                        __ C       CTG
GAM454  VCL           GGCAGGAAGTGTCCTTCAGACAG   7135 TG  A_     C_  ATI
                        GCA GGGTGTCCTTCG CAG
                        ||| |||||||||||| |||
                        CGT TTCACAGGAAGT GTC
                        __  CC       CT CII
GAM455  AKAP2          CATGAGTCAGAGAAAACATGA    7149   __       III
                        CATGGG AGAGAAAACATG
                        |||||| |||||||||||||
                        GTACTC TCTCTTTGTAC
                          AG        TII
GAM455  AKAP2          CATGAGTCAGAGAAAACATGA    7149 TCTCATGGG        I
                        AGAGAAAACATGA
                        |||||||||||||
                        TCTCTTTGTACT
                        CTCAG____         T
GAM455  ALB          TTTTCTTTCTCTT-ATTCT        7186 TGTT       A   G
                        TTCTTTCTCTTA TTCT
                        |||||||||||| ||||
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                        AAGAAAGAGAAT AAGA
                        ____        _  G
GAM455  APPL            TCTCATGGGAGAAGAGTAAAC   7156        _ __   ATGAI
                        TCTCATGGGAGA GA  AAAC
                        |||||||||||| || ||||
                        AGAGTACCCTCT CT  TTTG
                               T  CA   IIIAG
GAM455  APPL            TCTCATGGGAGAAGAGTAAAC   7156       _  AAAIII
                        TCTCATGGGAGA GA
                        |||||||||||| ||
                        AGAGTACCCTCT CT
                            T  CATTTG
GAM455  APTX            TGATCTCTTTCTCTTCCTGTGTGTT 7169 T      TAA    TII
                        TG TTTCTTTCTCT  TTCTGT
                        || |||||||||||  ||||||
                        AC AGAGAAAGAGA  AGGACA
                            T       ___  CAC
GAM455  B3GALT2          TGTTTTCTTCTC-CTTAATACTATT 7165      CT    T   I
                        TGTTTTCTTT CTTAAT CTGTT
                        |||||||||| |||||| |||||
                        ACAAAGAAG GAATTA GATAA
                             AG    T   I
GAM455  B3GAT1          TTTTCTTTCCCTTTTTTGTGTT   7188 TGTT       AA C
                        TTCTTTCTCTT TT TGTT
                        |||||||||| || ||||
                        AAGAAAGGGAA AA ACAA
                        ____            AA C
GAM455  BAP1            CTCCTAGGAGAGAAAGCAT      7150  A       ACAII
                        CTC TGGGAGAGAAA
                        ||| ||||||||||
                        GAG ATCCTCTCTTT
                             G       CGTAI
GAM455  BAP1            CTCCTAGGAGAGAAAGCAT      7150 TC A       A  A
                        TC TGGGAGAGAAA CATG
                        || ||||||||||| ||||
                        AG ATCCTCTCTTT GTAT
                        __  G     C  I
GAM455  BCRP2           TCATGGGAGCCAAGGAAGCA     7152      AG AACIII
                        TCATGGGAG AA
                        |||||||| ||
                        AGTACCCTC TT
                           GG  CCTTCG
GAM455  BCRP2           TCATGGGAGCCAAGGAAGCA     7152 TCTC    AG AACATGA
                        ATGGGAG AA
                        ||||||| ||
                        TACCCTC TT
                        ____       GG  CCTTCGT
GAM455  CACNA1C         TGTTTTCTTCTTGTCTCCATTCT  7163      C__  A  GTTI
                        TGTTTTCTTT  TCTT ATTCT
                        ||||||||||  |||| |||||
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                          ACAAAAGAAG  AGAG TAAGA
                             AAC   G    IIIT
GAM455 CASP8      TCTCCATGGGAGAGGATACA    7155  _      AAA  TGA
                  TCTC ATGGGAGAG  ACA
                  IIII IIIIIIIII  III
                  AGAG TACCCTCTC  TGT
                     G      CTA  III
GAM455 CASP8      TCTCCATGGGAGAGGATACA    7155  _        AAAACII
                  TCTC ATGGGAGAG
                  IIII IIIIIIIII
                  AGAG TACCCTCTC
                     G    CTATGTI
GAM455 CD1C       TTTCTTTCTCTCAGAAAAGCTGTT 7174 TGTTTT       ATT___  I
                     CTTTCTCTTA   CTGTT
                     IIIIIIIIIII    IIIII
                     GAAAGAGAGT   GACAA
                     _____    CTTTTC   A
GAM455 CDH7       TTTTCTTTCTTTT--TCCTGT   7187 TGTT     C AA
                  TTCTTTCT TT TTCTGT
                  IIIIIIIII II  IIIIII
                  AAGAAAGA AA AGGACA
                     ____     A __
GAM455 COL13A1     TTTTCTTTCTTTTTTAATAATCTGT 7177 TGTT    C__   __  TII
                   TTCTTTCT TTAAT TCTGT
                   IIIIIIIII IIIII IIIII
                   AAGAAAGA AATTA AGACA
                     ____     AAA   TT   TTI
GAM455 COL4A3     TTTTTTTTCTCTTAGCATCTCTGT 7183 TGTTTTC    A___   TI
                  TTTCTCTTA  TTCTGT
                  IIIIIIIIII  IIIIII
                  AAAGAGAAT  GAGACA
                  AAA____      CGTA   TC
GAM455 CRH       TGTCTTCCTTTCTCTT--TACTGTT 7162   _     AATT  I
                 TGTTTC TTTCTCTT  CTGTT
                 IIIIIII IIIIIIII   IIIII
                 ACAGAAG AAAGAGAA   GACAA
                     G    AT__  I
GAM455 DDEF2     TTTTCTTTCTCTTAGTTGCTTTT  7184 TGTT       ATTCTGTTI
                 TTCTTTCTCTTA
                 IIIIIIIIIIII
                 AAGAAAGAGAAT
                     ____     CAACGAAAA
GAM455 EGLN3     TCTTGGCA-AGAAAACATGA   7154 CA_ GA        I
                 TGG GAGAAAACATG
                 III IIIIIIIIIII
                 ACC TTCTTTGTAC
                 AGA G_       I
GAM455 EGLN3     TCTTGGCA-AGAAAACATGA   7154 TCTCA  GA
                 TGG GAGAAAACATGA
                 III IIIIIIIIIIII
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                          ACC  TTCTTTTGTACT
                        A____    G_
GAM455 ENTPD5       TTTTCTTTCCTTCTGAATT     7178 TGTT      CTTAA    T
                      TTCTTTCT    TTCTG
                      ||||||||    |||||
                      AAGAAAGG    AAGAC
                    ____        _____     T
GAM455 GPR44        TCTGATGG-AGAGAAAACAT    7158  C  G      GA
                      TCT ATGG AGAGAAAACAT
                      ||| |||| |||||||||||
                      AGA TACC TCTCTTTTGTA
                        C   _        ||
GAM455 GPR44        TCTGATGG-AGAGAAAACAT    7158 CTCATG        I
                        GGAGAGAAAACA
                        ||||||||||||
                        CCTCTCTTTGT
                      AGACTA          I
GAM455 ITSN1        TCTCATGGGAAATGATAAC      7157         _ A  ATGA
                      TCTCATGGGAGA GA AAC
                      |||||||||||| || |||
                      AGAGTACCCTTT CT TTG
                        A  A   IIIA
GAM455 ITSN1        TCTCATGGGAAATGATAAC      7157         _ AAAII
                      TCTCATGGGAGA GA
                      |||||||||||| ||
                      AGAGTACCCTTT CT
                        A  ATTGI
GAM455 KLHL1        TGTTTTCTTGTTTCCTACTATTCTGTT7164        TC_   __       III
                      TGTTTTCTT  TCTTA ATTCTGTT
                      |||||||||  ||||| ||||||||
                      ACAAAAGAA  AGGAT TAAGACAA
                        CAA   GA        III
GAM455 KLHL1        TGTTTTCTTT-T-GAAATTCT    7170        CTCTT    GT
                      TGTTTTCTTT    AATTCT
                      ||||||||||    ||||||
                      ACAAAGAAA     TTAAGA
                        ACT__    II
GAM455 MEF2C        TTTTCTTTCTCTT--TCCTGTT   7190 TGTT        AA
                      TTCTTTCTCTT TTCTGT
                      ||||||||||| ||||||
                      AAGAAAGAGAA AGGACA
                    ____        __
GAM455 MEIS1        TCATTGCAGAAAAAACATGA    7153  GGG       I
                      CAT AGAGAAAACATG
                      ||| ||||||||||||
                      GTA TCTTTTTTGTAC
                      ACG        I
GAM455 MEIS1        TCATTGCAGAAAAAACATGA    7153 TCTCATGGG
                        AGAGAAAACATGA
                        |||||||||||||
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                              TCTTTTTTGTACT
                           TAACG____
GAM455  OAS3             CATGTTAGGAGAGAAAACA      7148 CA___           III
                           TGGGAGAGAAAAC
                           |||||||||||||
                           ATCCTCTCTTTTG
                         GTACA          TII
GAM455  OAS3             CATGTTAGGAGAGAAAACA      7148 TCTCA           TGA
                           TGGGAGAGAAAACA
                           ||||||||||||||
                           ATCCTCTCTTTTGT
                         CA___           CCC
GAM455  PABPC3             TGTTTCCTTGCTCAGTTATCAATTCTGTT7167      T  _____        III
                           TGTTTTCTT CTC    TTAATTCTGTT  A
                           |||||||| |||   |||||||||| |
                           ACAAAGGAA GAG   AGTTAAGACAA  T
                              C  TCAAT        III
GAM455  PAX4             CTCATAGG---GAAAACATGA    7151 _      AGA
                           TCATGGG  GAAAACATG
                           |||||||  |||||||||
                           AGTATCC  CTTTTGTAC
                         G      ___
GAM455  PAX4             CTCATAGG---GAAAACATGA    7151 TC     AGA
                           TCATGGG  GAAAACATG
                           |||||||  |||||||||
                           AGTATCC  CTTTTGTAC

                         __      ___
GAM455  PGD             ATTGGAGAAAGAAAACATG      7147 A_ _          III
                           TGG GAGAGAAAACAT
                           ||| ||||||||||||
                           ACC CTTTCTTTTGTA
                         TA  T        CII
GAM455  PGD             ATTGGAGAAAGAAAACATG      7147 TCTCAT           A
                           GGGAGAGAAAACATG
                           |||||||||||||||
                           CTCTTTCTTTTGTAC
                         _____          G
GAM455  PKHD1            TTTTGTTTTTCGTTTTTAATTCTGTT 7181 _    CTTTCTC       II
                           TGTTTT    TTAATTCTGTT
                           ||||||    |||||||||||
                           ACAAAA    AATTAAGACAA
                         A   AGCAAA_        CC
GAM455  PPP1R12B          TTTTCTTTCTGCTTAAATGCTG   7179 TGTT     _   TT_  TT
                           TTCTTTCT CTTAA  CTG
                           |||||||| |||||  |||
                           AAGAAAGA GAATT  GAC
                         ____          C   TAC  TT
GAM455  PRSS7            TTTTCTTTCTTTTTTAAATTCTG   7182 TGTT       CTT___       I
                           TTCTTTCT   AATTCTGTT
                           ||||||||   |||||||||
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                        AAGAAAGA    TTAAGACGA
                  ____        AAAAAT      I
GAM455  PUM2       TTCTTTCTCTTGCTCCTGT    7173 TGTTTTCT    AA
                        TTCTCTT TTCTG
                        |||||||  |||||
                        AAGAGAA AGGAC
                  _____        CG
GAM455  RP1        TCTCATGGGA---AAAA-ATGA   7160          AACATG
                        TCTCATGGGAGAGAA
                        ||||||||||||||
                        AGAGTACCCTTTTTT
                              ACTIII
GAM455  RP1        TCTCATGGGA---AAAA-ATGA   7160           AACI
                        TCTCATGGGAGAGAA
                        ||||||||||||||
                        AGAGTACCCTTTTTT
                              ACTI
GAM455  SCA7        TCGTTCGTCTTAATTCTGTT    7161 TGTTTCTTTC
                        TCTTAATTCTGT
                        ||||||||||||
                        AGAATTAAGACA
                  GC_____
GAM455  SLC17A5      TTTTCTTTCT-TT-ATTCTTTT   7189 TGTT     CTTA   GT
                        TTCTTTCT  ATTCT
                        ||||||||   |||||
                        AAGAAAGA   TAAGA
                  ____        AA__    AA
GAM455  TAF7       TTGTCGTTTC-CTTAATTCT    7176 TGTTT _  T     GT
                        TC TTTC CTTAATTCT
                        || |||| |||||||||
                        AG AAAG GAATTAAGA
                  C____  C  _     AG
GAM455  TDO2       TGTATTCTTTCTCATCTTAATGCT  7166   T      TTAATTC  I
                        TGT TTCTTTCTC    TGTT
                        ||| |||||||||     ||||
                        ACA AAGAAAGAG    ACGA
                  T      TAGAATT  I
GAM455  TMEM1       TGTGTATTTTCTCTGCTAATTCTGT  7168 ____       CTC     TII
                        TGTTTTCTTT TTAATTCTGT
                        |||||||||| ||||||||||
                        ATAAAAGAGA GATTAAGACA
                  ACAC       C__       III
GAM455  TRIM9      TTTCTTTCT-TT-CTTTTGTT    7175 TGT      C AA  GT
                        TTTCTTTCT TT TTCT
                        ||||||||| || ||||
                        AAAGAAAGA AA AAGA
                  G__      A CA  II
GAM455  TRIM9      TGTTTTCTTTCT-TTCTTTCT    7171         C AA   GT
                        TGTTTTCTTTCT TT TTCT
                        |||||||||||| || ||||
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                                      ACAAAAGAAAGA AA  AAGA
                                         _  GA    II
GAM455  TRIM9         TGCTTTCTTTCT-TTCTTTC-GTT  7172          CTTAA   GTT
                          TGTTTTCTTTCT    TTCT
                          IIIIIIIIIII    IIII
                          ACGAAAGAAAGA    AAGA
                                          _____   AAG
GAM455  TRIM9            TTTTCTTTCT-TTCTTTCT      7185 TG        CTTAA   G
                            TTTTCTTTCT    TTCT
                            IIIIIIIIII    IIII
                            GAAAGAAAGA    AAGA
                          AA          _____      A
GAM455  UTX           TTTTCTATCTTCTTAATTC        7180 TGTT  T  _      TGT
                          TTCT TCT CTTAATTC
                          IIII III IIIIIIII
                          AAGA AGA GAATTAAG
                          _____   T   A      TAI
GAM455  ZNF277          TCTCATAGGAGA-AAAACATGA   7159            A   I
                           TCTCATGGGAGAGAAA CATGA
                           IIIIIIIIIIIIIIII IIIII
                           AGAGTATCCTCTTTTT GTACT
                                       _    I
GAM455  ZNF277          TCTCATAGGAGA-AAAACATGA   7159 _          A   I
                            CTCATGGGAGAGAAA CATG
                            IIIIIIIIIIIIIII IIII
                            GAGTATCCTCTTTTT GTAC
                          A         _    I
GAM456  ACK1         CGCCGGAACTTTCCGGCCC      7195   C   _    II
                          CGCT GAACTT CCGGCC
                          IIII IIIIII IIIIII
                          GCGG CTTGAA GGCCGG
                               C    A   GI
GAM456  ACK1         CGCCGGAACTTTCCGGCCC      7195 TGGACGCTC    _
                          GAACTT CCGGCCCT
                          IIIIII IIIIIIII
                          CTTGAA GGCCGGGG
                          C_____     A
GAM456  ASB1         GACCCGCGACCACTTCCGGC     7197 GA__  TCGA     III
                          CGC   ACTTCCGG
                          III   IIIIIIII
                          GCG   TGAAGGCC
                          CTGG  CTGG     GII
GAM456  ASB1         GACCCGCGACCACTTCCGGC     7197 TGGA   TCGA      CCT
                          CGC   ACTTCCGGC
                          III   IIIIIIIII
                          GCG   TGAAGGCCG
                          GG__  CTGG      CGI
GAM456  COPA        TGGAAACACGAACTTCCGGTCTCTT 7200   C  T       CC  II
                          TGGA GC CGAACTTCCGG  CTT
                          IIII II IIIIIIIIIII  III
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                          ACCT TG GCTTGAAGGCC GAG
                           T T       A_  AA
GAM456 COPA              TGGAAACACGAACTTCCGGTCTCTT 7200  C T      CCCTI
                          GA GC CGAACTTCCGG
                          || || |||||||||||
                          CT TG GCTTGAAGGCC
                           T T       AGAGI
GAM456 DDX1              TGGCGGCGCGCGCTTCCGGCCC  7204  AC T AA      TT
                          TGG GC CG CTTCCGGCCC
                          ||| || || ||||||||||
                          ACC CG GC GAAGGCCGGG
                           GC C GC        ||
GAM456 DDX1              TGGCGGCGCGCGCTTCCGGCCC  7204 ___ A  T AA      I
                          GG CGC CG CTTCCGGCC
                          || ||| || |||||||||
                          CC GCG GC GAAGGCCGG
                          CCG _ C __       I
GAM456 FUT6             GGA-GCTGAAAC--CCGGCCCTT 7198  C  C  CT      I
                          GGA GCT GAA TCCGGCCC
                          ||| ||| ||| ||||||||
                          CCT CGA CTT GGGCCGGG
                           _  _ T_      A
GAM456 FUT6             GGA-GCTGAAAC--CCGGCCCTT 7198 TGGAC  C  CT
                            GCT GAA  TCCGGCCCT
                            ||| ||| |||||||||
                            CGA CTT  GGGCCGGGA
                          CT___  _ T_
GAM456 GCN5L1            TGGACGCTC-ACCT--CGGC   7201       GA  C CC
                          TGGACGCTC ACTTC GGC
                          ||||||||| ||||| |||
                          ACCTGCGAG TGGAG CCG
                            __   _ ||
GAM456 GCN5L1            TGGACGCTC-ACCT--CGGC   7201 _     GA  C
                           GGACGCTC ACTTC GG
                           ||||||||| ||||| ||
                           CCTGCGAG TGGAG CC
                          A    __   _
GAM456 MAPK12           GGGCGCTCCCGCTCCCGGCCCTT 7199 GA   GAA      I
                           CGCTC  CTTCCGGCCCT
                           |||||  |||||||||||
                           GCGAG  GAGGGCCGGGA
                          CC   GGC       I
GAM456 MAPK12           GGGCGCTCCCGCTCCCGGCCCTT 7199 T A   GAA      I
                            GG CGCTC  CTTCCGGCCCTT
                            || ||||  ||||||||||||
                            CC GCGAG  GAGGGCCGGGAA
                           _ _  GGC        G
GAM456 MLLT2            ACGCTCGAAGACCGCCGGC    7193     __ T III
                          ACGCTCGA ACT CCGG
                          |||||||| ||| ||||
```

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                        TGCGAGCT TGG GGCC
                         TC  C  GII
GAM456 MLLT2         ACGCTCGAAGACCGCCGGC    7193 TGGACG   __ T  _ T
                        CTCGA ACT CCGGC CC
                        ||||| ||| ||||| ||
                        GAGCT TGG GGCCG GG
                        _____     TC  C   C I
GAM456 RRM2         CGCGCG--CTCCCGGCCCTT    7196 _ T AA       I
                        GC CG CTTCCGGCCCT
                        || || |||||||||||
                        CG GC GAGGGCCGGGA
                        G C __     I
GAM456 SOX11        TGGACGCTCCAAC--CCGGGCC    7203    G TT  C T
                        TGGACGCTC AAC CCGG CC
                        ||||||||| ||| |||| ||
                        ACCTGCGAG TTG GGCC GG
                        G __  C I
GAM456 SOX11        TGGACGCTCCAAC--CCGGGCC    7203    G TT  CI
                        TGGACGCTC AAC CCGG
                        ||||||||| ||| ||||
                        ACCTGCGAG TTG GGCC
                        G __  CG
GAM456 TBL1X        ACCCTGTAACGTCCGGCCCTT    7194 G CG T    I
                        C CT AAC TCCGGCCCT
                        | || ||| |||||||||
                        G GA TTG AGGCCGGGA
                        G CA C    I
GAM456 TBL1X        ACCCTGTAACGTCCGGCCCTT    7194 TGGACGCTCG T
                        AAC TCCGGCCCTT
                        ||| ||||||||||
                        TTG AGGCCGGGAA
                        GACA_____  C
GAM456 TOP3A        TGG-CG-TGGAACTTCCGCCC    7202  A CTC    G T
                        TGG CG  GAACTTCCG CCC
                        ||| || ||||||||| |||
                        ACC GC  CTTGAAGGC GGG
                        _ AC_    _ I
GAM456 TOP3A        TGG-CG-TGGAACTTCCGCCC    7202  A CTC    GI
                        TGG CG  GAACTTCCG
                        ||| || |||||||||
                        ACC GC  CTTGAAGGC
                        _ AC_    GG
GAM457 ADAMTS4      CAGGGTGAGGGCTATGAGGGGTC   7213 TC    CA  A___   CI
                        AGGGTGAGG GTTA  GGGTC
                        ||||||||| |||| |||||
                        TCCCACTCC CGAT  CCCAG
                        __     __  ACTC   TI
GAM457 ALEX2        TCCGGGTGAGGCTCTTCAG    7220 A     AGTTAAGGGTC
                        TC GGGTGAGGC
                        || |||||||||
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                                    AG CCCACTCCG
                               G          AGAAGTCIIIC
GAM457 CACNB1            TCAGGGTGAGG--GTGAAGG      7221          CA  T   GT
                        TCAGGGTGAGG GT AAGG
                        IIIIIIIIII II IIII
                        AGTCCCACTCC CA TTCC
                                 __  C   II
GAM457 CRHR1            TCAGGGTGAAGGCAG-CAAGG      7219       _    T   GTC
                        TCAGGGTGA GGCAGT AAGG
                        IIIIIIIII IIIIII IIII
                        AGTCCCACT CCGTCG TTCC
                                T     _   III
GAM457 FBXL11          AGGGAGAGCACAGTTAAGG        7209 TCAG  T  _       GTC
                        GG GAG GCAGTTAAGG
                        II III IIIIIIIIII
                        CC CTC TGTCAATTCC
                        ____   T  G      TGI
GAM457 GGT1            TCCGGGTCAGG--GTTAAGGGT      7224 A   G  CA       C
                        TC GGGT AGG GTTAAGGGT
                        II IIII III IIIIIIIII
                        AG CCCA TCC CAATTCCCA
                         G   G   __      I
GAM457 GGT2            TCCGGGTCAGG--GTTAAGGGT      7224 A   G  CA       C
                        TC GGGT AGG GTTAAGGGT
                        II IIII III IIIIIIIII
                        AG CCCA TCC CAATTCCCA
                         G   G   __      I
GAM457 ID1            CAGGCTGGATGCAGTTAAGGG        7211 TC  G AG_       CC
                        AGG TG  GCAGTTAAGGGT
                        III II  IIIIIIIIIIII
                        TCC AC  CGTCAATTCCCG
                        __   G  CTA          II
GAM457 MAP2K2          GGGTGAGGCAG--GAGGGT        7217 TCAGGG      TTA
                        TGAGGCAG AGGGT
                        IIIIIIII IIIII
                        ACTCCGTC TCCCA
                        _____       C__
GAM457 MAPK4           GGGTGAGGCAAATACAGGG        7216 TCAGGG      TTA_  TC
                        TGAGGCAG AGGG
                        IIIIIIII IIII
                        ACTCCGTT TCCC
                        _____       TATG   CA
GAM457 MASP1           TCAGGGTGAGGC--TCAGGGGT      7223          AGTTA  TC
                        TCAGGGTGAGGC AGGG
                        IIIIIIIIIIII IIII
                        AGTCCCACTCCG TCCC
                                AG___  CA
GAM457 MATN2          CAGGGTGAG--ATTTCCGGGTC       7214 TC       CAG AA
                        AGGGTGAGG TT GGGTC
                        IIIIIIIII II IIIII
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                        TCCCACTCT  AA  CCCAG
                         __      A__  GG
GAM457 MPO             TCAGGGTGAGGAAGAAAAAGG    7222       C TT   TCC
                        TCAGGGTGAGG AG  AAGGG
                        ||||||||||| || |||||
                        AGTCCCACTCC TC  TTTCC
                          T TT   III
GAM457 NIPSNAP1        CAGGGTGAGG--GAACAGGGTC    7215 TC       CAGTTA
                        AGGGTGAGG    AGGGTC
                        |||||||||    ||||||
                        TCCCACTCC    TCCCAG
                         __         CTTG__
GAM457 NRXN1          GTGACGAAGAAATAAGGGTCC     7218 TCAGGGT   C T
                         GAGG AG TAAGGGTCC
                         |||| || |||||||||
                         CTTC TT ATTCCCAGG
                         _____  _ T
GAM457 PML           AGGGTGAGGGCAGTGCAGG       7208 TCAG    _  TA   TC
                        GGTGAGG CAGT  AGGG
                        ||||||| |||| ||||
                        CCACTCC GTCA  TCCT
                         ____      C  CG   TI
GAM457 SLC21A2        AGGGTG--GCACTTAAGGGTC     7210 TCAG  GA   G
                        GGT  GGCA TTAAGGGTC
                        |||  |||| |||||||||
                        CCA  CCGT AATTCCCAG
                        ____  __     G
GAM457 TMP21          AGGGTAAAGAGAAAGTTAAGGGT   7207 TCA GT__  C       CCI
                        GG   GAGG AGTTAAGGGT
                        ||   |||| ||||||||||
                        CC   CTCT TCAATTCCCA
                        ___ ATTT  T      CAI
GAM457 XPNPEP2        CAGGGTGAGGGGAGCTAAG       7212 TC      C_     GGTC
                        AGGGTGAGG AGTTAAG
                        ||||||||| |||||||
                        TCCCACTCC TCGATTC
                         __       CC    GIII
GAM457 ZNF132        TCAGGGTGA---AG--AAGGGCCC   7225          CAGTT
                        TCAGGGTGAGG    AAGGGTC
                        ||||||||||||   |||||||
                        AGTCCCACTTC    TTCCCGG
                         _____
GAM458 ABCD4        GGGGT--CCTGCACAGGACC        7253    GG       CI
                        GGGGT CCTGCACAGG
                        ||||| ||||||||||
                        CCCCA GGACGTGTCC
                         __        TG
GAM458 ABL1        AGGGGGAG-CCACCACAGGCCC       7239 _   T  TG      I
                        GGGGG GGCC CACAGGCC
                        ||||| |||| ||||||||
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                              CCCCC TCGG  GTGTCCGG
                              T    _    TG         I
GAM458  ABL1          AGGGGGAG-CCACCACAGGCCC    7239 CAAG   T   TG
                              GGGG GGCC  CACAGGCCC
                              IIII IIII  IIIIIIIII
                              CCCC TCGG  GTGTCCGGG
                              ____     _    TG
GAM458  ADSS          CAAGGGGGTACCATG-ACTGCCCC  7245       G _ C  AG   I
                              CAAGGGGGTG CC TG AC  GCCC
                              IIIIIIIIII II II II  IIII
                              GTTCCCCAT GG AC TG  CGGG
                               _ T _ A_  G
GAM458  ASH1          AGGGGGTGGCC-GC-CAGGC      7235 _       T A    I
                              GGGGGTGGCC GC CAGG
                              IIIIIIIIII II IIII
                              CCCCCACCGG CG GTCC
                              T      _  _    I
GAM458  ASH1          AGGGGGTGGCC-GC-CAGGC      7235 CAAG      T A
                              GGGGTGGCC GC CAGGC
                              IIIIIIIII II IIIII
                              CCCCACCGG CG GTCCG

                              ____       _  _
GAM458  CACNA2D2       AGGGAGTGG---GCACAGGCC    7237 _       CCT
                              GGGGGTGG  GCACAGGC
                              IIIIIIII  IIIIIIII
                              CCCTCACC  CGTGTCCG
                              T        ___
GAM458  CACNA2D2       AGGGAGTGG---GCACAGGCC    7237 CAAG      CCT
                              GGGGTGG  GCACAGGC
                              IIIIIII  IIIIIIII
                              CCTCACC  CGTGTCCG

                              ____       ___
GAM458  CCR2          TGTTT-CTTGCTTGCATCAG      7261 TGTCTA     C  CCC
                              CTTGCTTGCA CAG
                              IIIIIIIIII III
                              GAACGAACGT GTC
                              ACAAA_      A  III
GAM458  CORO2B        AAGGCTGTACCCTGCACAG       7229    GG  G      II
                              AAGG GTG CCTGCACA
                              IIII III IIIIIIIII
                              TTCC CAT GGACGTGT
                               GA  G      CI
GAM458  CORO2B        AAGGCTGTACCCTGCACAG       7229 CA GG  G       CC
                              AGG GTG CCTGCACAGG
                              III III IIIIIIIIII
                              TCC CAT GGACGTGTCT
                              __  GA  G       II
GAM458  CYFIP2        GGGAGAGCATGCACAGGCCC      7254 T_ C       II
                              GGG GGC TGCACAGGCC
                              III III IIIIIIIIII
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                        CCC  TCG ACGTGTCCGG
                        TC  T        GI
GAM458  CYFIP2          GGGAGAGCATGCACAGGCCC    7254 CAAGGGGGT  C
                        GGC TGCACAGGCC
                        ||| |||||||||
                        TCG ACGTGTCCGG
                        _____      T
GAM458  EXTL1           TCCACTCTGCCGCTGCACCAGC   7259 TGTC  _  __      CCG
                        TACT TGCT TGCACCAGC
                        |||| |||| |||||||||
                        GTGA ACGG ACGTGGTCG
                        ____    G  CG      AGI
GAM458  GALK1           GGGACTGGCCTG--CAGGCCC    7250 _  G      CA   I
                        GGG TGGCCTGCA GGCC
                        ||| |||||||| ||||
                        CCT ACCGGACGT CCGG
                        C  G      __  I
GAM458  GALK1           GGGACTGGCCTG--CAGGCCC    7250 CAAGGGGG      CA
                        TGGCCTGCA GGCC
                        ||||||||| ||||
                        ACCGGACGT CCGG
                        TG_____      __
GAM458  GSPT1           GGGGGTGGCGGCGCTGC-CGGGCCC 7247 CAA G    _  ACA   I
                        GG GGTGGC CTGC  GGCCC
                        || |||||| |||| |||||
                        CC CCGCCG GACG  CCGGG
                        ___  A   C  GC_   G
GAM458  GSPT1           GGGGGTGGCGGCGCTGC-CGGGCCC 7247 GG     _  ACA   I
                        GGTGGC CTGC  GGCC
                        |||||| |||| ||||
                        CCGCCG GACG  CCGG
                        CA   C  GC_  I
GAM458  HDAC7A          AGGGCCTGGTGTGTCTGCACAGGGCC 7231 A  GG  GC      CI
                        GG GTG CTGCACAGG
                        || ||| |||||||||
                        CC CAC GACGTGTCC
                        A A_  A_      CG
GAM458  HDAC7A          AGGGCCTGGTGTGTCTGCACAGGGCC 7231 CAA__  GG  GC      _  CII
                        GG GTG CTGCACAGG CC
                        || ||| |||||||||| ||
                        CC CAC GACGTGTCC GG
                        CCGGA A_  A_      C ACI
GAM458  HOXC9           CAAGGCGCCGGCTGCACGGGCCC   7243 CA  G _      A   I
                        AGGG GT GGCCTGCAC GGCCC
                        |||| || |||||||||| |||||
                        TTCC CG CCGGACGTG CCGGG
                        G_  G G    C  I
GAM458  HOXC9           CAAGGCGCCGGCTGCACGGGCCC   7243 A  G _      A   I
                        AGGG GT GGCCTGCAC GGCC
                        |||| || ||||||||| ||||
```

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                              TTCC CG CCGGACGTG CCGG
                               _  G G        C  I
GAM458  IGHMBP2        CAAGGAGG-GGTTGGCACAGGCC  7242      T CCT      C
                         CAAGGGGG GG  GCACAGGCC
                         ||||||| ||  |||||||||
                         GTTCCTCC CC  CGTGTCCGG
                          _  AAC      I
GAM458  IGHMBP2        CAAGGAGG-GGTTGGCACAGGCC  7242 _    T CCT      I
                         AAGGGGG GG  GCACAGGC
                         ||||||| ||  ||||||||
                         TTCCTCC CC  CGTGTCCG
                        G   _ AAC      I
GAM458  IL19        GGATGGCCTG--CAGGCCC       7255         CA  I
                      GGGTGGCCTGCA GGCC
                      |||||||||||| ||||
                      CCTACCGGACGT CCGG
                           __  G
GAM458  IL6R     AGGGGGTGGCTTCCTGCCACAGCGCC 7232 CAAG      ___  _  _ CII
                      GGGGTGGC  CTGC ACAG GCC
                      ||||||||  |||| |||| |||
                      CCCCACCG  GACG TGTC CGG
                       ____       AAG  G  G  CGI
GAM458  IL6R     AGGGGGTGGCTTCCTGCCACAGCGCC 7232 GGG  GG  _  _ I
                      GGT  CCTGC ACAG GC
                      |||  ||||| |||| ||
                      CCG  GGACG TGTC CG
                     A__  AA   G   G I
GAM458  IVD      AGGGGGTGGGCTGCAGCAG       7234       C   CAII
                      AGGGGGTGG CTGCA
                      ||||||||| |||||
                      TCCCCCACC GACGT
                           C   CGTC
GAM458  IVD      AGGGGGTGGGCTGCAGCAG       7234 CAAG     C   CA
                      GGGGTGG CTGCA  GGCC
                      ||||||| ||||| ||||
                      CCCCACC GACGT  TCGG
                       ____      C   CG
GAM458  LAMC1       CTACTTGCTCTACCCCAGC       7246 TGTCTA    _  A   CC
                      CTTGCT TGC CCAGC
                      |||||| ||| |||||
                      GAACGA ATG GGTCG
                       _____     G  G  TA
GAM458  MAPK4       AGGGGGTGTG-TGCACAGGCC    7238 _    GCC      I
                      GGGGGTG TGCACAGGC
                      ||||||| ||||||||||
                      CCCCCAC ACGTGTCCG
                       T   AC_     I
GAM458  MAPK4       AGGGGGTGTG-TGCACAGGCC    7238 CAAG    GCC
                      GGGGTG TGCACAGGCC
                      |||||| ||||||||||
```

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                         CCCCAC  ACGTGTCCGG
                         ____       AC_
GAM458 MLC1              GGGGGTGGCCTGCAGACAGG    7249          __  III
                         GGGGGTGGCCTGC ACAG
                         |||||||||||| ||||
                         CCCCCACCGGACG TGTC
                                TC   CII
GAM458 MLC1              GGGGGTGGCCTGCAGACAGG    7249 CAAGGG      __   CC
                              GGTGGCCTGC ACAGG
                              |||||||||| |||||
                              CCACCGGACG TGTCC
                         _____        TC   CA
GAM458 NF2               GGAGTTGC-TGCACAGGCC     7252   G C       I
                              GGGGT GC TGCACAGGC
                              ||||| || |||||||||
                              CCTCA CG ACGTGTCCG
                                A  _      G
GAM458 NF2               GGAGTTGC-TGCACAGGCC     7252 CAAGGGGGTG C
                                    GC TGCACAGGC
                                    || |||||||||
                                    CG ACGTGTCCG
                         AA_____    _
GAM458 PLCG1            GGGGGCGGCGGCGGCACAGGCC    7248  _    CT      I
                              GG GGTGGC GCACAGGC
                              || |||||| ||||||||
                              CC CCGCCG CGTGTCCG
                               G   C_     I
GAM458 PLCG1            GGGGGCGGCGGCGGCACAGGCC    7248 CAA G    CT      C
                              GG GGTGGC GCACAGGCC
                              || |||||| |||||||||
                              CC CCGCCG CGTGTCCGG
                           ___ G   C_      T
GAM458 RASGRP2          AGCGGGTGG----CACAGGCC    7236 _ G     CTGC
                             G GGGTGGC   ACAGGC
                             | |||||||   ||||||
                             C CCCACCG   TGTCCG
                             T G      ____
GAM458 RASGRP2          AGCGGGTGG----CACAGGCC    7236 CAAGG    CTGC
                                 GGGTGGC   ACAGGC
                                 |||||||   ||||||
                                 CCCACCG   TGTCCG
                             G____      ____
GAM458 SAR1             TACTGACCTGCACCAGCACG     7258 TGTCTACTT        C
                              GCTTGCACCAGC C
                              |||||||||||| |
                              TGGACGTGGTCG G
                             C_____        T
GAM458 SCN4A            AAGGGGGTGGGCTG-GCAGTGCCC 7230       C  CA _  I
                             AGGGGGTGG CTG  CAG GCC
                             ||||||||| ||| ||| |||
```

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                        TCCCCCACC GAC  GTC CGG
                            C  C_  A  I
GAM458 SCN4A            AAGGGGGTGGGCTG-GCAGTGCCC  7230 CA      C  CA  _  I
                        AGGGGGTGG CTG  CAG GCCC
                        ||||||||| |||  ||| ||||
                        TCCCCCACC GAC  GTC CGGG
                           __    C  C_  A  A
GAM458 SFRS7           TAATTACTTTGCACCAGCC      7257 TGTCTACT   _      C
                        TGCTT GCACCAGCC
                        ||||| |||||||||
                        ATGAA CGTGGTCGG
                        _____    A   A
GAM458 SH2D1A         TGTCTACTTGCCTTAAACC        7260        GC_  AGCCC
                        TGTCTACTTGCTT ACC
                        ||||||||||| |||
                        ACAGATGAACGGA  TGG
                            ATT  IIIGC
GAM458 SOX9           GGGGTGGCCAGTTCACAGCTGCCC  7251 GGGT  TG__   __  I
                        GGCC  CACAG GCC
                        ||||  ||||| |||
                        CCGG  GTGTC CGG
                        ____   TCAA   GA  I
GAM458 SSRP1         GGTGGCCTGGGCAGAGCCC        7256      CA  _  II
                        GGTGGCCTG CAG GCC
                        ||||||||| ||| |||
                        CCACCGGAC GTC CGG
                            CC  T  GI
GAM458 SSRP1         GGTGGCCTGGGCAGAGCCC        7256 CAAGG  __    GCA   C
                        GGGT GGCCT CAGGC
                        |||| ||||| |||||
                        CCCG TCGGG GTCCG
                        GA___  TC  ___   A
GAM458 TBX6         AGGGGGTGG-GTGGGCAGGCCC    7240 _     CC CA   I
                        GGGGGTGG TG CAGGCC
                        |||||||| || ||||||
                        CCCCCACC AC GTCCGG
                        T    C_  CC   I
GAM458 TBX6         AGGGGGTGG-GTGGGCAGGCCC    7240 CAAG    CC CA
                        GGGGTGG TG CAGGCCC
                        ||||||| || |||||||
                        CCCCACC AC GTCCGGG
                        ____   C_ CC
GAM458 TEM6        AGGGGGTGGGGTGCACCCATGCCC  7233 CAAG    CC  AG__  I
                        GGGGTGG TGCAC  GCCC
                        ||||||| |||||  ||||
                        CCCCACC ACGTG  CGGG
                        ____      CC  GGTA  T
GAM458 TEM6        AGGGGGTGGGGTGCACCCATGCCC  7233 GG    CC   AG__  I
                        GGGTGG TGCAC  GCC
                        ||||||| |||||  |||
```

```
                          CCCACC  ACGTG   CGG
                          __      CC      GGTA   I
GAM458  TNFAIP1    AAGGGGCAGTAGCCTTCTGCACAGGGCC7228 CA      __      ___      _  CIII
                          AGGGG  GTGGCCT  GCACAGG CC
                          ||||| |||||||  ||||||| ||
                          TCCCC  CATCGGA  CGTGTCC GG
                          __     GT      AGA      C  AIII
GAM458  TNFAIP1    AAGGGGCAGTAGCCTTCTGCACAGGGCC7228 GGG       ___      CCI
                          GGTGGCCT  GCACAGG
                          |||||||| |||||||
                          TCATCGGA  CGTGTCC
                          G__      AGA      CII
GAM458  TRPM2      CAAGGGCCCAGC-TGCACAGGCCC  7244    GG  C        I
                          CAAGGG  TGGC TGCACAGGCCC
                          |||||| |||| |||||||||||
                          GTTCCC  GTCG ACGTGTCCGGG
                            GG   _        I
GAM458  TRPM2      CAAGGGCCCAGC-TGCACAGGCCC  7244 _    GG  C        I
                          AAGGG  TGGC TGCACAGGCC
                          ||||| |||| ||||||||||
                          TTCCC  GTCG ACGTGTCCGG
                          G   GG   _        I
GAM458  WNT5A      AGGGGGTGGGGGGC-GAGGCCC   7241 _      CCT AC   I
                          GGGGGTGG  GC AGGCC
                          |||||||| || |||||
                          CCCCCACC  CG TCCGG
                          T     CCC C_   I
GAM458  WNT5A      AGGGGGTGGGGGGC-GAGGCCC   7241 CAAG     CCT AC
                          GGGGTGG  GC AGGCCC
                          ||||||| || |||||
                          CCCCACC  CG TCCGGG
                          ____      CCC C_
GAM459  ABCG1      ATTTTTTAGGAAGAAACCGGA    7271 ATA       TAA__  III
                          TTTTAGGAA    CGG
                          ||||||||| |||
                          AAAATCCTT    GCC
                          TAA       CTTTG  TII
GAM459  COL15A1    AATAATATTTTAGGGAAAA    7269         AATAII
                          AATGATATTTTAGG
                          ||||||||||||||
                          TTATTATAAAATCC
                            CTTTTI
GAM459  COL15A1    AATAATATTTTAGGGAAAA    7269 GA       AATAACGG
                          ATGATATTTTAGG
                          |||||||||||||
                          TATTATAAAATCC
                          __        CTTTTTII
GAM459  GOCAP1     AATGATATTTTAGGAGATAA    7265        _  ATAIII
                          AATGATATTTT AGGA
                          |||||||||| ||||
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```
                          TTACTATAAAA TCCT
                          A    CTATTI
GAM459  GOCAP1         AATGATATTTTTAGGAGATAA    7265 GA      _   ATAACGGA
                          ATGATATTTT AGGA
                          |||||||||| ||||
                          TACTATAAAA TCCT
                          __      A   CTATTAII
GAM459  MGAT5         GAATGATATATATATGCTTAATGG  7272      TT_ GGAA  C AI
                          GAATGATAT  TA   TAA GG
                          |||||||| ||   ||| ||
                          CTTACTATA  AT   ATT CC
                          TAT  ACGA  A  II
GAM459  MME          AATG-TATTTTAGGGAAATA     7267    A      AATII
                          AATG TATTTTAGG
                          |||| |||||||||
                          TTAC ATAAAATCC
                          _        CTTTA
GAM459  MME          AATG-TATTTTAGGGAAATA     7267 GA  A      AATAACGG
                          ATG TATTTTAGG
                          ||| |||||||||
                          TAC ATAAAATCC
                          __  _    CTTTATAI
GAM459  MORC         AATGTT-TTTAAGGAATAAC     7270 GAATGATA   _      G
                          TTTTA GGAATAACG
                          ||||| |||||||||
                          AAAAT CCTTATTGT
                          TACA____    T      I
GAM459  POLK         AATTATATTTTAGGCAAAAAC    7268 AATG      AATAI
                          ATATTTTAGG
                          ||||||||||
                          TATAAAATCC
                          A___     GTTTT
GAM459  POLK         AATTATATTTTAGGCAAAAAC    7268 GAATG      AAT_ GGA
                          ATATTTTAGG  AAC
                          ||||||||||  |||
                          TATAAAATCC  TTG
                          TAA__     GTTT GII
GAM459  PTPN2        AAAGATATTTTTAGGAAAAAC    7266 AT   _   TAAI
                          GATATTTT AGGAA
                          |||||||| |||||
                          CTATAAAA TCCTT
                          T_     A    TTTI
GAM459  PTPN2        AAAGATATTTTTAGGAAAAAC    7266 GAAT     _ T GGA
                          GATATTTT AGGAA AAC
                          |||||||| ||||| |||
                          CTATAAAA TCCTT TTG
                          TT__     A  T AII
GAM459  XBP1         AATAAGTATTTTAGGGAAAAC    7264 GA  _     AAT  GGA
                          ATGA TATTTTAGG  AAC
                          |||| |||||||||  |||
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                              TATT ATAAAATCC  TTG
                              __   C       CTT  AII
GAM460 ARF3          AGCAGGTT-ATGGGCAGCT    7281 TA  AGCTTG       A
                          AGG    ATGGGCAGCT
                          III    IIIIIIIIII
                          TCC    TACCCGTCGA
                          G_ AA____        C
GAM460 ARHH         AAAGAGCCCTCAGTGGGCAGCT  7276 TA   GA__     AGA
                       AGGAGCTT  TGGGCAGCT
                       IIIIIIII  IIIIIIIII
                       TTCTCGGG  ACCCGTCGA
                       __      AGTC      CII
GAM460 FIGF      TAAGCAG-TTGACATCAGGCAGCTAGA7287   G  C   ___       II
                   TAAG AG TTGAT   GGGCAGCTAGA
                   IIII II IIIII   IIIIIIIIIII
                   ATTC TC AACTG   TCCGTCGATCT
                       G _   TAG          II
GAM460 FRK        AGGAGCT----GGGCAGCT     7282 TAAG    TGAT
                      GAGCT   GGGCAGCT
                      IIIII   IIIIIIIII
                      CTCGA   CCCGTCGA

                     ____    ____
GAM460 KPNA3       AAGGAGTATCAGTGGGCAGCT   7277 TA   C_ GA     AGA
                      AGGAG  TT TGGGCAGCT
                      IIIII  II IIIIIIIII
                      TCCTC  AG ACCCGTCGA
                      __    AT TC      CII
GAM460 LPL       AAGGGGATGGCAGGGCAGCTAGA   7279 TAA  GCTTGAT      I
                       GGA    GGGCAGCTAGA
                       III    IIIIIIIIIII
                       CCT    CCCGTCGATCT
                      TCC ACCGT__        T
GAM460 NOS2A       TAAAGGGCTTGATGGGGAGC   7288 T_  A     C TAG
                     AAGG GCTTGATGGG AGC
                     IIII IIIIIIIIII III
                     TTCC CGAACTACCC TCG
                     AT  _       C III
GAM460 PFKFB4      AGGTCCATGCTGGGCAGCT    7284 TAAGGAGCT A    AG
                        TG TGGGCAGCT
                        II IIIIIIIII
                        AC ACCCGTCGA
                     CAGGT____ G     CC
GAM460 PRM1     GGAACTCTG-TGGGCAGCTGAGA   7286 TAAGGA  GA     _
                     GCTT TGGGCAGCT AGA
                     IIII IIIIIIIII III
                     TGAG ACCCGTCGA TCT
                     _____    AC       C
GAM460 SLC12A7     TAGGAAGCCCCATGGGCAGCT  7289 TA _ G     AGA
                     AGGA GCTT ATGGGCAGCT
                     IIII IIII IIIIIIIIII
```

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                            TCCT CGGG TACCCGTCGA
                            A_    T  G       III
GAM460  SMCX            AAGCAGGCTTGATGGTCAGAAAGA  7275 TAA  A     G  CT  I
                            GG GCTTGATGG CAG  AGA
                            II IIIIIIIII III  III
                            TC CGAACTACC GTC  TCT
                            TCG  _        A  TT  C
GAM460  SYNGR1          AGGCACCTGCTGGGCAGCT    7283 TAAGGA   A      AG
                              GCTTG TGGGCAGCT
                              IIIII IIIIIIIII
                              TGGAC ACCCGTCGA
                            CG____   G    CC
GAM460  TACR1           AAGGCTTTTTATGGGCAGC    7278 TA  AGCTTG      TAG
                              AGG    ATGGGCAGC
                              III    IIIIIIIII
                              TCC    TACCCGTCG
                            __  GAAAAA     TII
GAM460  WRN             AGGTGCG-GCTGGGCAGCTAGA  7285 TAAGGA  TTGA
                              GC  TGGGCAGCTAGA
                              II  IIIIIIIIIIII
                              CG  ACCCGTCGATCT
                            CA____  CCG_
GAM460  ZNF74           AGGAG---GAGTGGGCAGCT    7280 TA  CTTGA     A
                              AGGAG   TGGGCAGCT
                              IIIII   IIIIIIIII
                              TCCTC   ACCCGTCGA
                            C_   _____      C
GAM461  ABCD1           GGCA---GGGGCCGGGGACG    5808 TG  TCC      TC
                              GCA  GGGGCCGGGG GC
                              III  IIIIIIIIII II
                              CGT  CCCCGGCCCC TG
                            __   ___      __
GAM461  AES         GCATACCTGGGACCCGGGGTCGGGG  5804 _____  C      C   TCGCGGII
                              TGG ATCCGGGG CGGGG
                              III IIIIIIII IIIII
                              ACC TGGGCCCC GCCCC
                            TATGG  C     A   CTIIIGGC
GAM461  FLNA           GGCGGCCTGGGCCGGGGTTGAGG  5811 T_  ATCCG      CGC  I
                              GGC  GGGCCGGGGT GG
                              III  IIIIIIIIII II
                              CCG  CCCGGCCCCA CC
                            CG  GA___      ACT  C
GAM461  GALNT2         GGGATGCCGGGGCCGAGGCCG    5805 T  C  _       CGG
                              GG AT CCGGGGCCGGGGTCG
                              II II IIIIIIIIIIIIII
                              CC TA GGCCCCGGCTCCGGC
                            _ _  C      CII
GAM461  INSM1          TCGGGGGCCGGGGTGGAGG     5812 TGGCAT   CC_  T
                              CCGGGG  GGGG CGCG
                              IIIIII  IIII III
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                            GGCCCC  TCCC GCGC
                         CC____        ACC      _
GAM461 NGB               GGCTGCCGGG--CGGGGTCGC   5810 TG AT   GC      G
                         GC CCGGG CGGGGTCGC
                         ||  ||||| |||||||||
                         CG GGCCC GCCCCAGCG
                         __ AC   __     G
GAM461 PTPRS             GGCATCCGGGGCCAGTGGTGTCGG  5806 TG        _  CG  I
                         GCATCCGGGGCCGG GGT CGG
                         ||||||||||||| ||| |||
                         CGTAGGCCCCGGTC CCA GCC
                         __         A CA C
GAM461 RPS6KA2           GGC-TCCGAGGCCGGGGTC     5807 TG A        GC
                         GC TCCGGGGCCGGGGTC
                         || |||||||||||||||
                         CG AGGCTCCGGCCCCAG
                         __ _       AI
GAM461 RUNX3             ATCCCGGGCCGGGGTGGGGG    5802 TGGCATCCG     CGC
                         GGGCCGGGGT G
                         |||||||||| |
                         CCCGGCCCCA C
                         G_____      CCC
GAM461 SGT               GGCA--CAGGGCCGGGGTGGC   5809 TG  TC       C G
                         GCA CGGGGCCGGGGT GC
                         ||| ||||||||||| ||
                         CGT GTCCGGCCCCA CG
                         __ __       C G
GAM461 TRAF1             CATTCGGGGCCGGAGTGGC     5803 TGGCATC       C G
                         CGGGGCCGGGGT GC
                         |||||||||||| ||
                         GCCCCGGCCTCA CG
                         A_____      C A
GAM462 HSF2BP            AGCGAGGAGTGGCCTTGGCGAGGTCCC7303 GCTT      ___ _   I
                         GGAGTGGCC  GC AGGTCC
                         ||||||||| || ||||||
                         CCTCACCGG  CG TCCAGG
                         ____      AAC C   I
GAM462 HSF2BP            AGCGAGGAGTGGCCTTGGCGAGGTCCC7303 TA  TT     ___ _      III
                         GC GGAGTGGCC  GC AGGTCCC
                         || ||||||||| || |||||||
                         CG CCTCACCGG  CG TCCAGGG
                         __ CT      AAC C    AII
GAM462 IL12RB2           GCTGGGCGGTGGCCGCAGG     7305 T A_       II
                         GCT GG GTGGCCGCAG
                         ||| || |||||||||||
                         CGA CC CACCGGCGTC
                         C GC      CI
GAM462 IL12RB2           GCTGGGCGGTGGCCGCAGG     7305 TAGCTT A_       TCC
                         GG GTGGCCGCAGG
                         || |||||||||||
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                         CC  CACCGGCGTCC
                     AC____  GC       CGI
GAM462  JUND             GGAGTGGCCGCGGCCTCCC    7307        A  CII
                         GGAGTGGCCGC GGTC
                         IIIIIIIIII IIII
                         CCTCACCGGCG CCGG
                              _  AGG
GAM462  MAP3K11          TAGCTTGGAGGGACCCGAGCTTCC  7308       T  GC G_  CI
                         TAGCTTGGAG GGCC AG TCC
                         IIIIIIIIII IIII II III
                         ATCGAACCTC CTGG TC AGG
                               C  GC GA  II
GAM462  MAP3K11          TAGCTTGGAGGGACCCGAGCTTCC  7308       T  GCA  CCI
                         AGCTTGGAG GGCC  GGT
                         IIIIIIIII IIII  III
                         TCGAACCTC CTGG  TCG
                               C  GC_  AAG
GAM462  MDM2           GCTTGGAGT---CGGGGGTCCC    7306 _     GGC CA
                         CTTGGAGT CG GGTCC
                         IIIIIIII II IIIII
                         GAACCTCA  GC CCAGG
                              C    ___  CC
GAM462  MDM2           GCTTGGAGT---CGGGGGTCCC    7306 TAGC    GGC CA
                          TTGGAGT CG GGTCC
                          IIIIIII II IIIII
                          AACCTCA  GC CCAGG
                          ____     ___  CC
GAM462  USP6        CTGGGGGTGGC---AGGTCCC    7304    A_   CGC
                          TTGG GTGGC AGGTCC
                          IIII IIIII  IIIIII
                          GACC CACCG  TCCAGG
                              CC   ___
GAM462  USP6        CTGGGGGTGGC---AGGTCCC     7304 TAGCTT A   CGC
                          GG GTGGC  AGGTC
                          II IIIII  IIIII
                          CC CACCG  TCCAG
                          C_____  _  ___
GAM463  CIT          GAAAGCAG-T----TCACAGATG   7322 TGAAAGC    GA
                          AGGTAG  TCACAGA
                          IIIIII  IIIIIII
                          TTCGTC  AGTGTCT
                          T_____     A_
GAM463  DDT          AAGCAGCCAGT-TCACAGATG    7317 TGAAAG  G  GA
                          CAG TAG  TCACAGAT
                          III III  IIIIIIII
                          GTC GTC  AGTGTCTA
                          _____   G  A_
GAM463  LZTS1        AAGCAGGTAGGGACTCCCAG      7315 TGAAAG     A__ A AT
                          CAGGTAGG  TC CAG
                          IIIIIIII  II III
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                          GTCCATCC  AG GTC
                 _____       CTG  G  GG
GAM463 MSL3L1        GAAAGCAGGCAGCATGACAG    7321 TG       G  C   AT
                     AAAGCAGGTAG AT ACAG
                     |||||||||| || ||||
                     TTTCGTCCGTC TA TGTC
                 __        G  C   GI
GAM463 MTR         AAGCAGGTAAGTGTCAGCCAGATG  7314 TGAAAG    A_ __    I
                     CAGGTAGG  TCA CAGATG
                     |||||||| ||| ||||||
                     GTCCATTC AGT GTCTAC
                 _____      AC  CG    G
GAM463 POLH         AAGTAGCTGGGATCACAGGTG    7318 TGAA  AGGTA    ATG
                     AGC   GGATCACAG
                     |||   |||||||||
                     TCG   CCTAGTGTC
                 A___  AC___     CAC
GAM463 PRPS1         AATGCAGGTAGGAGGTCCCAG    7311 TGAAA     __ A ATG
                     GCAGGTAGGA  TC CAG
                     |||||||||| || |||
                     CGTCCATCCT AG GTC
                 A____        CC G  GTI
GAM463 S100A4        GACAGCAGTCAGGATCACA     7320 TGAA  G      GAT
                     AGCAG TAGGATCACA
                     ||||| ||||||||||
                     TCGTC GTCCTAGTGT
                 TG__   A     GII
GAM463 STAT1         AGCAGGAGGGAATCACAGATG    7319 TGAAAGCA  TA  _
                     GG  GGA TCACAGATG
                     || ||| |||||||||
                     CC  CCT AGTGTCTAC
                 _____  TC  T
GAM463 TAX1BP1       AAAGCAGGTAAGATTAACAGA    7312 TGAA       C_   TG
                     AGCAGGTAGGAT ACAGA
                     |||||||||||| |||||
                     TCGTCCATTCTA TGTCT
                 ____        AT   CT
GAM463 USP14        AAGTAGCTGGGATCACAGGTG    7318 TGAA  AGGTA    ATG
                     AGC   GGATCACAG
                     |||   |||||||||
                     TCG   CCTAGTGTC
                 A___  AC___     CAC
GAM463 WDR4         AAGCAG--AGGACAAATCACAGATG  7316 TGAA  C  TA      I
                     AG AGG  GGATCACAGATG
                     || ||| |||||||||||
                     TC TCC  TTTAGTGTCTAC
                 G___ _  TG      G
GAM463 XRCC2        AAAGT-GCTAGGATCACAG     7313 TGAAA AGG      A
                     GC  TAGGATCACAG
                     || |||||||||||
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                                  CG  ATCCTAGTGTC
                         TCA__  ___          C
GAM464 AVP               CATAGAGCAGGGCATGGGGACTC  7326       A_____        IIIG
                            CATAGAG    ATGGGGACT
                            |||||||    |||||||||
                            GTATCTC    TACCCCTGA
                               GTCCG       GIII
GAM464 AVP               CATAGAGCAGGGCATGGGGACTC  7326 TCCCAGCA  AGA       I
                                TAG  ATGGGGACTC
                                |||  ||||||||||
                                GTC  TACCCCTGAG
                         C_____    CCG        T
GAM464 CTNNA1              CCATCACTAAGAGAATGGGCATCTC  7328 A  AT       GACTI
                             GC  AGAGAATGGG
                             ||  ||||||||||
                             TG  TCTCTTACCC
                          G  AT          GTAGI
GAM464 CTNNA1             CCATCACTAAGAGAATGGGCATCTC  7328 TCCCAG   __      GA_  II
                             CAT  AGAGAATGGG  CTC
                             |||  ||||||||||  |||
                             GTG  TCTCTTACCC  GAG
                          TA____   AT       GTA  CC
GAM464 EPHX1             TCCCAGCAT-GGGCA-GGGGAC   7337       AGAGAAT    T
                            TCCCAGCAT    GGGGAC
                            |||||||||    ||||||
                            AGGGTCGTA    CCCCTG
                              CCCGT__     I
GAM464 EPHX1            TCCCAGCAT-GGGCA-GGGGAC   7337 _       AGAGAAT   I
                           CCCAGCAT    GGGGA
                           ||||||||    |||||
                           GGGTCGTA    CCCCT
                         A        CCCGT__   I
GAM464 FGR             TCCCTGC-TACAGAATGGGG     7335    A  A  G     ACT
                          TCCC GC TA AGAATGGGG
                          |||| || || |||||||||
                          AGGG CG AT TCTTACCCC
                            A  _  G        III
GAM464 FGR             TCCCTGC-TACAGAATGGGG     7335 _  A  A  G     I
                          CCC GC TA AGAATGGG
                          ||| || || ||||||||
                          GGG CG AT TCTTACCC
                            A  A  _  G        I
GAM464 FXR2             CCAACAGGTGGAGAATGGGG     7327    TA__       III
                           CCAGCA  GAGAATGGG
                           ||||||  |||||||||
                           GGTTGT  CTCTTACCC
                             CCAC       CII
GAM464 FXR2             CCAACAGGTGGAGAATGGGG     7327 TCC  CATA       ACT
                           CAG  GAGAATGGGG
                           |||  ||||||||||
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                    GTC   CTCTTACCCC
                    TT_  CAC_      CAI
GAM464  HNF3G       CCCATGCCAGAGAGAATGGTGAC  7330 ___  CAT      G I
                        CCAG  AGAGAATGG GA
                        |||| ||||||||| ||
                        GGTC  TCTCTTACC CT
                    TAC      ___        A  I
GAM464  HNF3G       CCCATGCCAGAGAGAATGGTGAC  7330 TC _ AT_      G  TCI
                        CCA GC  AGAGAATGG GAC
                        ||| || ||||||||| |||
                        GGT CG  TCTCTTACC CTG
                    __ A GTC       A CII
GAM464  IER5        TCCCCGGAGAACGAATGGGGAACTC  7336   AGCATAGA      _ II
                        TCCC    GAATGGGGA CTC
                        ||||    ||||||||| |||
                        AGGG    CTTACCCCT GAG
                        GCCTCTTG      T II
GAM464  IER5        TCCCCGGAGAACGAATGGGGAACTC  7336   AGCATAGA     CTI
                        CCC    GAATGGGGA
                        |||    |||||||||
                        GGG    CTTACCCCT
                        CCTCTTG_      TGA
GAM464  PRKCABP     CCCAGCTCGGTAGGGGAATGGGGA  7331 CCAGCA  A_      I
                        TAG  GAATGGGG
                        |||  ||||||||
                        ATC  CTTACCCC
                    GAGCC_ CC      I
GAM464  PRKCABP     CCCAGCTCGGTAGGGGAATGGGGA  7331 TC   A___  A_      CTCI
                        CCAGC  TAG  GAATGGGGA
                        |||||  ||| |||||||||
                        GGTCG  ATC  CTTACCCCT
                    __  AGCC  CC      TIII
GAM464  PTPN7       CCCTGAACAGAGAATGGAGGCCTC  7332 ___ C       ACTI
                        G ATAGAGAATGGGG
                        | |||||||||||||
                        C TGTCTCTTACCTC
                    GA T        CIII
GAM464  PTPN7       CCCTGAACAGAGAATGGAGGCCTC  7332 TC  AGC       A_  I
                        CC  ATAGAGAATGGGG CTC
                        ||  ||||||||||||| |||
                        GG  TGTCTCTTACCTC GAG
                    __ ACT        CG  G
GAM464  RECQL       CCTGCATGGAAAAGAATGGGGA  7329 A  ___        III
                        CC GCAT  AGAGAATGGGG
                        || |||| |||||||||||
                        GG CGTA  TTTCTTACCCC
                        A  CCT        TII
GAM464  RECQL       CCTGCATGGAAAAGAATGGGGA  7329 TCCCA  ___        CTC
                        GCAT  AGAGAATGGGGA
                        |||| |||||||||||
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                                    CGTA  TTTCTTACCCCT
                              A____      CCT        CTI
GAM464 SURF5          TCCCAGCATGGCCAATGGG     7333        AGAG    GACT
                              TCCCAGCAT  AATGGG
                              ||||||||| ||||||
                              AGGGTCGTA  TTACCC
                                    CCGG    IIIC
GAM464 SURF5          TCCCAGCATGGCCAATGGG     7333        AGAG    II
                              TCCCAGCAT  AATGG
                              ||||||||| |||||
                              AGGGTCGTA  TTACC
                                    CCGG   CI
GAM464 TIMM23         CAGCACACAGAATGGGGAATC    7325     G      CTI
                              AGCATA AGAATGGGGA
                              |||||| ||||||||||
                              TCGTGT TCTTACCCCT
                                    G      TAI
GAM464 TIMM23         CAGCACACAGAATGGGGAATC    7325 TCCCAG  G      CTC
                              CATA AGAATGGGGA
                              |||| ||||||||||
                              GTGT TCTTACCCCT
                              _____    G      TAG
GAM464 TRIM9         TCCCATTACTGAGAATGGG      7334   GC A      GACT
                              TCCCA AT GAGAATGGG
                              ||||| || |||||||||
                              AGGGT  TG CTCTTACCC
                                    AA A       IIIC
GAM464 TRIM9         TCCCATTACTGAGAATGGG      7334   GC A      II
                              TCCCA AT GAGAATGG
                              ||||| || ||||||||
                              AGGGT  TG CTCTTACC
                                    AA A      CI
GAM465 BACH1         TGGAGAACCAAGACTGTATCC    7347        C A  C GAG
                              TGGAGAACCAG GC GTA CC
                              |||||||||| || ||| ||
                              ACCTCTTGGTT TG CAT GG
                                    C A  A III
GAM465 BACH1         TGGAGAACCAAGACTGTATCC    7347        C A  CCI
                              GGAGAACCAG GC GTA
                              |||||||||| || |||
                              CCTCTTGGTT TG CAT
                                    C A   AGI
GAM465 GNA11         GGAGAACCAGTCTCGGTGCC     7343        CGCAGTACII
                              GGAGAACCAG
                              ||||||||||
                              CCTCTTGGTC
                                    AGAGCCACGG
GAM465 GNA11         GGAGAACCAGTCTCGGTGCC     7343 TG       CGCA_ A CGA
                              GAGAACCAG    GT CC
                              ||||||||    || ||
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                        CTCTTGGTC    CA GG
                        __    AGAGC  C  AII
GAM465 HUNK             AGAACCA--GCTGTAACCG    7340      GCAGT  CI
                        AGAACCAGC    ACC
                        |||||||||  |||
                        TCTTGGTCG   TGG
                        ACAT_  CI
GAM465 HUNK             AGAACCA--GCTGTAACCG    7340 TGGAGA    GCA  C
                        ACCAGC  GTA CCG
                        |||||| ||| |||
                        TGGTCG  CAT GGC
                        _____   A__  T
GAM465 KCNK5           AGAACCAGC-CAG-AGCTGAG    7341      G  TACCCGI
                        AGAACCAGC CAG
                        ||||||||| |||
                        TCTTGGTCG GTC
                        _ TCGACTC
GAM465 KCNK5           AGAACCAGC-CAG-AGCTGAG    7341 TGGAGA    G  TACCC
                        ACCAGC CAG    GA
                        |||||| |||    ||
                        TGGTCG GTC    CT
                        _____    _ TCGA_
GAM465 RAB5A           TGGAGACTACAATGCAGTACCC    7346     AC_  C      GAG
                        TGGAGA  CAG GCAGTACCC
                        ||||||  ||| |||||||||
                        ACCTCT  GTT CGTCATGGG
                        GAT  A      III
GAM465 RAB5A           TGGAGACTACAATGCAGTACCC    7346 G  AC_  C     I
                        GAGA  CAG GCAGTACC
                        ||||  ||| ||||||||
                        CTCT  GTT CGTCATGG
                        _ GAT  A     I
GAM465 SYNGR1         GGAGAAACAGATGGGCAGTACCCTGAG7344 AAC  C___     GAI
                        CAG   GCAGTACCC
                        |||    |||||||||
                        GTC   CGTCATGGG
                        TT_  TACC     III
GAM465 SYNGR1         GGAGAAACAGATGGGCAGTACCCTGAG7344 TG   C C___     _ III
                        GAGAA CAG   GCAGTACCC GAG
                        ||||| |||    ||||||||| |||
                        CTCTT GTC   CGTCATGGG CTC
                        __   T TACC      A CII
GAM465 TMPRSS3         AGAACGAA---AGTACCCGAG    7342 GAACC  C_
                        AGCG AGTACCCGA
                        |||| |||||||||
                        TTGC TCATGGGCT
                        TC___  TT
GAM465 TPMT           GGAGAACCA-C-CCGAACCCG    7345 _      GCGCAGT  I
                        GAGAACCA    ACCC
                        |||||||    ||||
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                          CTCTTGGT    TGGG
                          C      GGGCT__   I
GAM465  TPMT          GGAGAACCA-C-CCGAACCCG   7345 TG      GCGCAGT   A
                          GAGAACCA    ACCCG
                          |||||||    |||||
                          CTCTTGGT    TGGGC
                          __    GGGCT__    C
GAM466  CCND2         TAAGAAGTGGAGAGGAAGAAA   7360        C CAC  CTT
                          TAAGAAGTGGA AG  GAAA
                          ||||||||||| || ||||
                          ATTCTTCACCT TC  CTTT
                            C CTT  III
GAM466  CCR9          AAGA--TGGACATTTTCACGAAACTT 7350 TAAGAA    G___      I
                            GTGGACA   CACGAAACTT
                            |||||||   ||||||||||
                            TACCTGT   GTGCTTTGAA
                          TC____    AAAA     A
GAM466  ENO2          AAGAAGTGGAAAGTGCGGAAC   7353 TA      C CA A  T
                          AGAAGTGGA AG  CG AACT
                          ||||||||| || || ||||
                          TCTTCACCT TC  GC TTGG
                          __       T AC C  I
GAM466  ESR1          AGAAGTGGACTCTACTGAACCTT  7355 TAAG     AGC GA  I
                          AAGTGGAC  AC AACTT
                          ||||||||  || |||||
                          TTCACCTG  TG TTGGA
                          ____        AGA AC   A
GAM466  F8A           TAAGAAGTGAGGGGCAGGATGAAA  7359       ACA  C AACTTI
                          TAAGAAGTGG  GCA GA
                          ||||||||||  ||| ||
                          ATTCTTCACT  CGT CT
                            CCC  C ACTTTI
GAM466  NFYC          AAGAAGTGG-CAGTAACAAAC    7352 TA     A C_    ACT
                          AGAAGTGG CAG  ACGAA
                          |||||||| ||| |||||
                          TCTTCACC GTC  TGTTT
                          __       _ AT   GTI
GAM466  PLXNA2        GAACTGGCTATGACGAAACTT    7358 TAAGAAG  ACAGC
                          TGG    ACGAAACTT
                          |||    ||||||||||
                          ACC    TGCTTTGAA
                          G_____    GATAC
GAM466  RNF26         AAGAAGTGGGTAAGACGGAA     7351 TA     AC_ C AAACT
                          AGAAGTGG  AG ACG
                          ||||||||  || |||
                          TCTTCACC  TC TGC
                          __       CAT _ CTTCI
GAM466  SLC24A1       GAAGCTGGACAGCAGGGAAC     7356 TAAGAAG      C_ _
                          TGGACAGCA GAA ACT
                          ||||||||| ||| |||
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                            ACCTGTCGT CTT TGG
                        CG_____          CC  G
GAM466  SYK             AGAAGTGGAAAGACATGAAA    7354 TAAG    C _ C  CT
                            AAGTGGA AG CA GAAA
                            ||||||| || || ||||
                            TTCACCT TC GT CTTT
                        ____        T  T  A   CC
GAM466  TSN             GAAGTGGACGCCGCAGGCAAC    7357 TAAGAA    A__  CGA   T
                            GTGGAC  GCA  AACT
                            |||||| ||| ||||
                            CACCTG  CGT  TTGG
                        _____      CGG  CCG   T
GAM467  ANKRD3      TCAGTCCCCA-GCACTGAGGT    7373 TGTC      G C
                            AGTCCCCAG C CTGAGGT
                            |||||||||| | |||||||
                            TCAGGGGTC G GACTCCA
                        ____        _ T
GAM467  CRY2        TGGCAGTCCCCA-TCCCTGAG    7378 T      GG    GT
                            TG CAGTCCCCA CCCTGAG
                            || ||||||||| |||||||
                            AC GTCAGGGGT GGGACTC
                        C        A_     ||
GAM467  CSK             TCCCCAGGCCCCACAGGTG    7374 TGTCA    _   CCC  A
                            GTCCC CAGG  TG GGT
                            ||||| ||||  || |||
                            CGGGG GTCC  AC CCA
                        C____     T    ___ _
GAM467  CSK             TCAGTCCCCACAGGCCCATGA    7368 TGTC      __  _ GGTG
                            AGTCCCCA GGCCC TGA
                            |||||||| ||||| |||
                            TCAGGGGT CCGGG ACT
                        ____        GT   T  GGII
GAM467  EGFL3       TCAG--CCCAGGCCCAGAGCGTG   7371 TGTCAGTC     T  _
                            CCCAGGCCC GAG GTG
                            |||||||||| ||| |||
                            GGGTCCGGG CTC CAC
                        TC_____          T  G
GAM467  GADD45G     GTCTGTCCTTCCTGGCCCTGAGG   7366 __  AG  CCA      GI
                            TGTC TCC  GGCCCTGAGGT
                            |||| |||  |||||||||||
                            ACAG AGG  CCGGGACTCCG
                        AG  GA  A__         ||
GAM467  GMFG        TCAGTCCCCA-GCCCAGAG    7370 TGTC    G  T
                            AGTCCCCAG CCC GAGG
                            |||||||||| ||| ||||
                            TCAGGGGTC GGG CTCT
                        ____        _  T
GAM467  GRIK3       CAGCCCCCAGG-CCTGAGGT    7364 TGTCAGT      C
                            CCCCAGGCC TGAGGT
                            ||||||||| ||||||
```

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                    GGGGTCCGG ACTCCA
                G_____        _
GAM467 ITGAV        TCA-TCCCCAGGCCTTGAGG    7372 TGTCA       C    T
                    GTCCCCAGGCC TGAGG
                    IIIIIIIIIII IIIII
                    TAGGGGTCCGG ACTCC
                    _____        A    T
GAM467 MFGE8        CAGTCCCCA-GCCCTATGGTG    7365 TGTCAG     G    A
                    TCCCCAG CCCTG GGT
                    IIIIIII IIIII III
                    AGGGGTC GGGAT CCA
                    _____      _    A
GAM467 MYO1C        CAGCCCCCAGGCCCTTGAGG    7363 TGTCAGT      _    T
                    CCCCAGGCCCT GAGG
                    IIIIIIIIIII IIII
                    GGGGTCCGGGA CTCC
                G_____        A    C
GAM467 RBM8A        TGTTCGTCTCCGGGCCCTGAG    7379 CA   C  A       GTG
                    TGT GTC CC GGCCCTGAG
                    III III II IIIIIIIII
                    ACA CAG GG CCGGGACTC
                    AG   A   C        III
GAM467 SET          TCAATCCACATAGCCCTGAGGT    7369 TGTC    C  _        G
                    AGTCC CA GGCCCTGAGGT
                    IIIII II IIIIIIIIIII
                    TTAGG GT TCGGGACTCCA
                    ____      T  A        G
GAM467 SLC5A5       TGTCAGTCCCGCGGCTGGCCCTG  7376        CA____       AGGTGI
                    TGTCAGTCCC   GGCCCTG
                    IIIIIIIIII   IIIIIII
                    ACAGTCAGGG   CCGGGAC
                    CGCCGA    IIIGTG
GAM467 STS          TGTCTGGTCCCCAGGCGCTG    7375 A_      C AGGT
                    TGTC GTCCCCAGGC CTG
                    IIII IIIIIIIIII III
                    ACAG CAGGGGTCCG GAC
                    AC        C  IIIG
GAM467 TCF3         GTCAGTCCCC--TTCCTGAGG    7367 TG      AGGC     T
                    TCAGTCCCC  CCTGAGG
                    IIIIIIIII  IIIIIII
                    AGTCAGGGG  GGACTCC
                    __      AA__      C
GAM467 TNFAIP2      TGACAGTCCCCAGAGCCTG    7377 T      GC   AGGT
                    TG CAGTCCCCAG CCTG
                    II IIIIIIIIII IIII
                    AC GTCAGGGGTC GGAC
                    T      TC  IIIG
GAM468 ANK3         ACAGCAGCCTTATTAACCT      7382 TGAC    __  T  CTC
                    AGCAGCC ATTA CCTG
                    IIIIIII IIII IIII
```

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                        TCGTCGG  TAAT GGAT
                        ____       AA   T  TII
GAM468  ARHGEF7         CAGACGCATTTTTCCTGCTCC    7385 TGACA   GCCATTA
                        GCA      TCCTGCTCC
                        III      IIIIIIIII
                        CGT      AGGACGAGG
                        TG___    AAAA___
GAM468  FKBP1B          TGAGCAGCAGCCA-TCTCCAGC   7386  _       A  T TCC
                        TGA CAGCAGCCATT TCC GC
                        III IIIIIIIIIII III II
                        ACT GTCGTCGGTAG AGG CG
                         C      _   T  III
GAM468  HSPD1           TGACAGCAGTAAACCATTAT     7387     ____      CCTGCTC
                        TGACAGCAG   CCATTAT
                        IIIIIIIII   IIIIIII
                        ACTGTCGTC   GGTAATA
                        ATTT     IIICCTC
GAM468  MAP4K2          TGACAGCAGC--TCCCCTGGTCC  7393       CATTA   C
                        TGACAGCAGC    TCCTG TCC
                        IIIIIIIIII    IIIII III
                        ACTGTCGTCG    GGGAC AGG
                         AGG__    C
GAM468  MAPK8IP1        TGTCAGCAGCCAGCTGTCCTG    7389 TGA     _  A    CTCC
                        CAGCAGCCA TT TCCTG
                        IIIIIIIII II IIIII
                        GTCGTCGGT GA AGGAC
                        ACA     C  C   IIIC
GAM468  MASP2           TGACAGCAGCC-TCA-CCTG     7390       A  T   CT
                        TGACAGCAGCC TTA CCTG
                        IIIIIIIIIII III IIII
                        ACTGTCGTCGG AGT GGAC
                          _  _   II
GAM468  MLC1            TGACAGCAGCC--TCTCCT-CTCC 7394        ATTA  G
                        TGACAGCAGCC   TCCT CTCC
                        IIIIIIIIIII   IIII IIII
                        ACTGTCGTCGG   AGGA GAGG
                         AG__   _
GAM468  MS4A8B          TGCCAGCAGCCACGTATCTCTTGATCC7388 TGA      _  _ GC_  III
                        CAGCAGCCAT TATC CT  TCC
                        IIIIIIIIII IIII II  III
                        GTCGTCGGTG ATAG GA  AGG
                        ACG      C  A ACT  III
GAM468  NUDT1           CAGCAGCCACGTCTCCTGC     7383 TGACAG    TA_
                        CAGCCAT  TCCTGCTC
                        IIIIIII  IIIIIIII
                        GTCGGTG  AGGACGGG
                        _____     CAG
GAM468  PPP2R2B         TGACAGCAGGC-TTA-CTTGC    7391      CCA  CC TC
                        TGACAGCAG  TTAT TGC
                        IIIIIIIII  IIII III
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                    ACTGTCGTC  AATG  ACG
                      CG_   A_   II
GAM468 RAG1         TGACAGCAG--ATGA-CCTCCT   7392      CCATTA  GCTC
                    TGACAGCAG    TCCT
                    |||||||||    ||||
                    ACTGTCGTC    AGGA
                      TACTGG  IIIC
GAM468 RAG1         CATCAGCCATTATCACTGGTCC   7384 TGACAG      _  C
                      CAGCCATTATC CTG TCC
                      ||||||||||| ||| |||
                      GTCGGTAATAG GAC AGG
                      _____        T  C
GAM469 AKR1B1       TGACAGGGCTCTTGAGATCCAACA  7422      CCAT___  C  AGGI
                    TGACAGGGC     GTCC ACA
                    |||||||||     |||| |||
                    ACTGTCCCG     TAGG TGT
                      AGAACTC   T  IIIG
GAM469 APOBEC2        GACAGG---CATGTCCCAGATGG  7412 TG   GCC      CAA
                      ACAGG  CATGTCCCA  G
                      |||||  |||||||||  |
                      TGTCC  GTACAGGGT  C
                       __   ___       CTA
GAM469 ATP5J        GGGGCCTTTTCCCCCACAAGG    7417 TGACAGGGCCCATG
                            TCCCACAAGG
                            ||||||||||
                            GGGGTGTTCC
                    GAAAAG_____
GAM469 CDX1         TGACTGTCCACCATGTCCCAGAAGG 7420    AGGGC_     C  II
                    TGAC    CCATGTCCCA AAGG
                    ||||    |||||||||| ||||
                    ACTG    GGTACAGGGT TTCC
                      ACAGGT       C  II
GAM469 CYP4F3       TGTCAGGAGCACCTTGTCCCACA   7418 TGA  _ _  A      AGGI
                    CAGG GC CC TGTCCCACA
                    |||| || || |||||||||
                    GTCC CG GG ACAGGGTGT
                    ACA  T  T  A      IIIG
GAM469 DTX1         GACAGGGCC--TGTCACCCA      7410 TG    CA  _  A A
                    ACAGGGCC  TGTC CC CA
                    ||||||||  |||| || ||
                    TGTCCGG  ACAG GG GT
                      __     __   T _ C
GAM469 FUT3         CAGGGCCCAGGGCCCTCCAGG    7408 TGA_    ATG  CACA
                    CAGGGCCC  TCC   AGG
                    ||||||||  |||   |||
                    GTCCCGGG  AGG   TCC
                    CCGG       ___  ____
GAM469 FUT5         CAGGGCCCA-GTGCCTCCAGG    7407 TGACAG    _  _  CAAG
                      GGCCCA TGTC CCA
                      |||||| |||| |||
```

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                                    CCGGGT ACGG GGT
                          _____        C  A  CCCA
GAM469 FUT6        CAGGGCCCA-GTGCCTCCAGG   7407 TGACAG    _  _   CAAG
                          GGCCCA TGTC CCA
                          |||||| |||| |||
                          CCGGGT ACGG GGT
                          _____        C  A  CCCA
GAM469 GASC1       TGACAGGGCCCTAAGCCGCACAAGG 7421       AT_  C   II
                          TGACAGGGCCC  GTC CACAAGG
                          ||||||||||  ||| |||||||
                          ACTGTCCCGGG  CGG GTGTTCC
                               ATT  C   II
GAM469 GJA4        TGACAGGG-CCAAATCCGGCACAAG  7424       CAT  __   GI
                          TGACAGGGCC  GTCC CACAAG
                          ||||||||||  |||| ||||||
                          ACTGTCCCGG  TAGG GTGTTC
                               TT_  CC   II
GAM469 GLTSCR1       TGACAGGGCAGCCACGTTCAAGAA  7419       __   CCCA  I
                          TGACAGGGC CCATGT  CAAGG
                          ||||||||| ||||||  |||||
                          ACTGTCCCG GGTGCA  GTTCT
                               TC   A___   T
GAM469 HIF1A       TGTCAGGGCCCA-GCCCGACA   7427 TGA    T  C  AG
                           CAGGGCCCA GTCC ACA
                           ||||||||| |||| |||
                           GTCCCGGGT CGGG TGT
                           ACA      _  C  II
GAM469 IL8RA       GACAGGGCCC-TGTTCTCCAAGG   7413 TG      A  CCCA
                           ACAGGGCCC TGT   CAAGG
                           ||||||||| |||   |||||
                           TGTCCCGGG ACA   GTTCC
                            __    _ AGAG
GAM469 LAPTM5       TGGCAGGGTCAGTG-CCCACAAGG   7428 A   CC T _     I
                          TG CAGGG  CA GT CCCACAAGG
                          || |||||  || || |||||||||
                          AC GTCCC  GT CA GGGTGTTCC
                           C  A_ _  C    I
GAM469 M6PR        CAGAGCCCTCGATGTCCCAC     7402 TGACAG    ___    AAG
                           GGCCC  ATGTCCCAC
                           |||||  |||||||||
                           TCGGG  TACAGGGTG
                            _____    AGC     AAG
GAM469 MAD1L1       ACAGAGAC--TGTCCCACAA    7398 TGAC   CCCA
                            AGGG  TGTCCCACAA
                            ||||  ||||||||||
                            TCTC  ACAGGGTGTT
                            ____    TG__
GAM469 MAT1A       CAGGAGCCCAGG-CCCACAAGG   7401 TGACA     T T
                          GGGCCCA G CCCACAAGG
                          ||||||| | |||||||||
```

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                              CTCGGGT C GGGTGTTCC
                              _____        C _
GAM469  MUCDHL          CAGGGCCCAGTTGTTCCTCCAG   7403 TGACAG    __ _ CA AGG
                              GGCCCA TGT CC  CA
                              ||||||  ||| || ||
                              CCGGGT  ACA GG  GT
                              _____    CA  A AG CGG
GAM469  NAP1L4          ACAGGGCCC---TCCCACAGGG   7399 TGAC    ATG    A
                              AGGGCCC  TCCCACA G
                              |||||||  ||||||| |
                              TCCCGGG  AGGGTGT C
                              ____   ___      C
GAM469  NFRKB           TGACAGGG-CTGTGTCACCACA   7423      CCA  _   AGG
                              TGACAGGGC  TGTC CCACA
                              |||||||||  |||| |||||
                              ACTGTCCCG  ACAG GGTGT
                               AC_  T   |||
GAM469  PAX5            GGGCCTCAGTTTCCCACAAGG   7414 TGA  GGCCCATG
                              CAG      TCCCACAAGG
                              |||      ||||||||||
                              GTC      AGGGTGTTCC
                               A__  AA_____
GAM469  PRG2            TGACTCGTGCCATGTCCCAC   7426   AGG_ C    AAG
                              TGAC   GCC ATGTCCCAC
                              ||||   ||| |||||||||
                              ACTG   CGG TACAGGGTG
                               AGCA _      |||
GAM469  RALBP1          CAGGGCCCAGCCTCCCAGAAG   7404 TGACAG    TG_ C G
                              GGCCCA  TCCCA AAG
                              ||||||  ||||| |||
                              CCGGGT  AGGGT TTC
                              _____    CGG  C G
GAM469  RHO             GGGCCCATGAACATCCC-CAAGG   7416 TGACA  CCAT   A
                              GGGC  GTCCC CAAGG
                              ||||  ||||| |||||
                              CTTG  TAGGG GTTCC
                               GTA__   ____   _
GAM469  SH2D2A          CAGGGCCCA-GACTCAAAAGG   7406 TGACAG    TG CC C
                              GGCCCA T CA AAG
                              |||||| | || |||
                              CCGGGT G GT TTC
                              _____    CT A_ T
GAM469  SH3GL1          CAGGGCCCATCACCAGCACCAGG   7405 TGACAG    GT __ A |
                              GGCCCAT CC CAC AGG
                              ||||||| || ||| |||
                              CCGGGTA GG GTG TCC
                              _____    GT TC  G G
GAM469  SPOCK           GACAGGGCCCAT----CACAGAGG   7411 TG      GTCC   _
                              ACAGGGCCCAT  CACA AG
                              |||||||||||  |||| ||
```

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                            TGTCCCGGGTA   GTGT TC
                            __      ____       C
GAM469  STX1A       AGGGCCCATGGCAGAGAAGG     7400 TGACAGGG    TCCCAC
                            CCCATG    AAG
                            ||||||    |||
                            GGGTAC    TTC
                            _____       CGTCTC
GAM469  TAF1C       TGCCAGA-CCCATGTCCCA     7425 ACA        CAA
                            TG  GGGCCCATGTCCCA
                            ||  |||||||||||||
                            AC  TCTGGGTACAGGGT
                             GG_           |||
GAM469  UBE2G2        ACAGGGCCCCATTTCTTCAGAAGG  7397 TGAC    ATG_ C_ C  I
                            AGGGCCC   TC CA AAGG
                            |||||||   || || ||||
                            TCCCGGG   AG GT TTCC
                            ____      GTAA AA C  T
GAM469  WBP2        GGGCCCTAATGTCCCACAA      7415 TGACAGGGCCC      G
                            ATGTCCCACAA
                            |||||||||||
                            TACAGGGTGTT
                            GAT_____         A
GAM469  ZNF278      CAGGGCCCAGGTCCCCCAGGG    7409 TGACAG   T  ACA
                            GGCCCA GTCCC  AGG
                            |||||| |||||  |||
                            CCGGGT CAGGG  TCC
                            _____     C  GG_
GAM470  ARHG        TGCAGTTGCTGTAG-TGGAGGCAG  7451 CT   AT_  GA       I
                            GCAG  CTG GGTGGAGGCAG
                            ||||  ||| |||||||||||
                            CGTC  GAC TCACCTCCGTC
                            __  AAC  A_        A
GAM470  AXIN1       CTGCACAGCCGGCGGCTGGAGGCAG 7440    GAT  A _      II
                            CTGCA  CTGG GG TGGAGGCAG
                            |||||  |||| || |||||||||
                            GACGT  GGCC CC ACCTCCGTC
                             GTC  G G       II
GAM470  DDX26       AGATGGTAGAGGTGGAGGC      7431 CTGCAGATC        A
                            TGGAGGTGGAGGC
                            |||||||||||||
                            ATCTCCACCTCCG
                            CC_____         C
GAM470  FGFR1       TGGAGA---GGAGGTGGAGGGAG  7456 CTGCAGATCT       C
                            GGAGGTGGAGG A
                            ||||||||||| |
                            CCTCCACCTCC T
                            CCTCT_____         C
GAM470  FUT3        CTGAAGATCTGGA----GAGGCAG  7443 C       GGTG
                            CTG AGATCTGGA   GAGGCA
                            ||| ||||||||   ||||||
```

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                         GAC TCTAGACCT   CTCCGT
                           T          ____
GAM470 GBF1          CAGAGCTGCCGGGCTGGAGGCAG  7434 __   AGAT     TG   CAGI
                           CTGC   CTGGAGG GAGG
                           ||||   ||||||| ||||
                           GACG   GACCTCC CTCC
                         TC  GCCC     GT  IIIG
GAM470 GPR4          CTGGAGAGCCCAGGAGGTGGAGGC  7439  C  _  _        AGI
                           CTG AGA TCT GGAGGTGGAGGC
                           ||| ||| ||| |||||||||||
                           GAC TCT GGG CCTCCACCTCCG
                            C   C  T        III
GAM470 GRIA2         CTGCTAAAACCTGAAG-TGGAGGCAG 7436    __    G       II
                           CTGC  AGATCTG AGGTGGAGGCAG
                           ||||  ||||||| ||||||||||||
                           GACG  TTTGGAC TTCACCTCCGTC
                            AT        _       II
GAM470 HSF4         CTGCAGAGTCCGCAGAGGGGTGGAGGCA7437     _   G ____       GIII
                           CTGCAGA TCTG A   GGTGGAGGCA
                           ||||||| |||| |   ||||||||||
                           GACGTCT AGGC T   CCACCTCCGT
                            C   G CTCC       IIIG
GAM470 LAG3         CTGCAGAGAGGGAGGTGGAGGAAG  7444    TCT      C I
                           CTGCAGA  GGAGGTGGAGG AG
                           |||||||  ||||||||||| ||
                           GACGTCT  CCTCCACCTCC TC
                            CTC        T I
GAM470 MSN         CAGAGAAGGAGGTGGATGC     7435 CTGCAGATCT     G A
                             GGAGGTGGA GC
                             ||||||||| ||
                             CCTCCACCT CG
                         TCTT_____       A A
GAM470 MUC5B      CAGAGCATGGGGATGGAGGCAG   7433 CT  GATC  A
                           GCA  TGG GGTGGAGGCAG
                           |||  ||| |||||||||||
                           CGT  ACC CTACCTCCGTC
                         T_  ____   C
GAM470 PABPN1      GCA-ATCTGGAGGGGCAGGGAG   7450 CTGCA      T _ C
                           GATCTGGAGG GG AGG AG
                           |||||||||| || ||| ||
                           TTAGACCTCC CC TCC TC
                         ____       _ G  C
GAM470 PHEMX      TGCTGGTTTGAAGGTGGAGG     7452 CTGCAGATC       CA
                           TGGAGGTGGAGG
                           ||||||||||||
                           ACTTCCACCTCC
                         CGACCAA__        CI
GAM470 PLN          CTGCAGATCTAGAGGTTGTAGCAG 7445          GGA   I
                           CTGCAGATCTGGAGGT GGCAG
                           ||||||||||||||| |||||
```

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                        GACGTCTAGATCTCCA  TCGTC
                              ACA     I
GAM470 PRG2             TGCAG----GGAGGTGGAGGGAG   7455 CT   ATCT        C
                           GCAG   GGAGGTGGAGG A
                           ||||   ||||||||||| |
                           CGTC   CCTCCACCTCC T
                            __   ____           C
GAM470 RNF4             GATCTCAGGAAAATGGAGGCAG   7446 CTG  ATCT
                            CAG   GGAGGTGGAGGCAG
                            |||   ||||||||||||||
                            GTC   CTTTTACCTCCGTC

                            ___   ____
GAM470 RNF4             CTGCAGATCAATGATAAGGTGCAGGCAG7438         TG____   G   III
                           CTGCAGATC   GAGGTG AGGCAG
                           |||||||||   |||||| |||||
                           GACGTCTAG   TTCCAC TCCGTC
                              TTACTA       G     III
GAM470 RPS6KA2            AGA-CTGGAGGTGGACACAG    7432 CTGCAGATC        G
                             TGGAGGTGGA GCA
                             |||||||||| |||
                             ACCTCCACCT TGT
                             _____         G
GAM470 SHANK2            GCAG-TCTGCGAGGTGGAGAGCAG  7447 CTGC  A   _     _  I
                            AG TCTG GAGGTGGAG GCAG
                            || |||| ||||||||| ||||
                            TC AGAC CTCCACCTC CGTC
                            ___  _  G    T  G
GAM470 SPAG8            TGCAGGT--GGCGGTGGAGGCA    7453 CT   ATC  A
                           GCAG   TGG GGTGGAGGCA
                           ||||   ||| ||||||||||
                           CGTC   ACC CCACCTCCGT
                            __   C__  G
GAM470 SPTBN4           CTGCAGATC-GGGGCTGGGGGC    7441        T A  _  A  AG
                           CTGCAGATC GG GG TGG GGC
                           ||||||||| || || ||| |||
                           GACGTCTAG CC CC ACC CCG
                             _  _  G  C  II
GAM470 SRD5A2           TGGACATCTGG---TGGAGGCA    7454 CTGCAG   GGA
                             ATCT  GGTGGAGGCA
                             ||||  ||||||||||
                             TAGA  CCACCTCCGT
                           CCTG__   ___
GAM470 STAU            GCTGACCTGGGAGGTGGAGG    7449 CTGCA    _     CA
                            GATCTGG AGGTGGAGG
                            ||||||| |||||||||
                            CTGGACC TCCACCTCC
                             A____     C    AA
GAM470 SUV39H1          GCAGGTGGGGGCAGGTGGAGGCAG   7448 CTGCAGATCT _       I
                             GG AGGTGGAGGCAG
                             || |||||||||||
```

```
                              CC TCCACCTCCGTC
                         TCCACCC___ G        C
GAM470  UCP1             CTCCAGCCCCGAAGGTGGAGGAAG  7442  G  AT         C  I
                         CT CAG  CTGGAGGTGGAGG AG
                         || |||  |||||||||||| ||
                         GA GTC  GGCTTCCACCTCC TC
                          G  GG          T  I
GAM471  DIAPH2           CAACC-ACGCCGTTGCCACT    7459   T  _        II
                         CAACT AC CTGTTGCCAC
                         ||||| || ||||||||||
                         GTTGG TG GGCAACGGTG
                           _   C       AI
GAM471  DIAPH2           CAACC-ACGCCGTTGCCACT    7459 TCTCAACT  _        T
                         TAC CTGTTGCCACT
                         ||| ||||||||||
                         GTG GGCAACGGTGA
                          G_____  C       T
GAM471  JAK2            TCACATCTTGTTCCTGTTGCC    7461  T  A  A__      ACTTG
                        TC CA CTT  CCTGTTGCC
                        || || |||  |||||||||
                        AG GT GAA  GGACAACGG
                         T  A  CAA      IIIGT
GAM471  JAK2            TCACATCTTGTTCCTGTTGCC    7461  T  A  A__       III
                        TC CA CTT  CCTGTTGC
                        || || |||  ||||||||
                        AG GT GAA  GGACAACG
                         T  A  CAA      GII
GAM471  PRAME          TCTCAG-TCACTTGTTGCCAC    7462    AC  C       TT
                       TCTCA TTAC TGTTGCCAC
                       ||||| |||| ||||||||||
                       AGAGT AGTG ACAACGGTG
                        C_    A       II
GAM471  PRAME          TCTCAG-TCACTTGTTGCCAC    7462 _  AC  C        I
                        CTCA TTAC TGTTGCCA
                        |||| |||| |||||||||
                        GAGT AGTG ACAACGGT
                        A  C_   A        I
GAM471  RAI2          CTCAGCT---CTGATGCCACTTG   7460 TC  A  TAC   T
                       TCA CT  CTG TGCCACTT
                       ||| ||  ||| ||||||||
                       AGT GA  GAC ACGGTGAA
                        __    C ___    T
GAM471  RAI2          CTCAGCT---CTGATGCCACTTG   7460   A  TAC  T      I
                        CTCA CT  CTG TGCCACT
                        |||| ||  ||| ||||||||
                        GAGT GA  GAC ACGGTGA
                         C  ___  T     A
GAM472  CELSR2         GTCAAGCCCCCAAGC--CAGGGC   7471 TG       G  _  AG  C
                        TCAAGCCCC CA GC  CAG GC
                        |||||||||| || ||  ||| ||
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```
                         AGTTCGGGG GT CG  GTC CG
                         __       _ T __  C
GAM472 CNN1              GTCCAGCCAAGAGCAGCAGCAGC   7469 T___     CCCC       GCI
                          GTCAAG   GCAGCAGCAGC
                          IIIIII   IIIIIIIIIII
                          CGGTTC   CGTCGTCGTCG
                         AGGT    T___          GII
GAM472 CYB561           TCTAGCCACAGCCAGCAGCAGCG   7472 T_  _  CCGC      CI
                          GTCA AGCC   AGCAGCAGCG
                          IIII IIII   IIIIIIIIII
                          CGGT TCGG   TCGTCGTCGC
                         AT  G  ____          CA
GAM472 EGR3             AAGCGGCGGCAGCAGCACCGC   7465 TGTCAA CCC       G
                           GC  GCAGCAGCA CGC
                           II  IIIIIIIIII III
                           CG  CGTCGTCGT GCG
                         C_____  C__        G
GAM472 FGFR4            GTCAAGACGCTGGGGCAGCAGCAGC 7468 TG   _ CCC___      CII
                          TCAAG C   GCAGCAGCAGCG
                          IIIII I   IIIIIIIIIIII
                          AGTTC G   CGTCGTCGTCGT
                         __     T CGACCC         III
GAM472 GJB3            TCAAGCCC--CAGCTGCAGC     7476 TGTC    GC  A
                           AAGCCCC AGC GCAGC
                           IIIIIIII III IIIII
                           TTCGGGG TCG CGTCG
                         ____      __  A
GAM472 HAS2           TCAAGTCCC--AGCAGCAG     7475 TGTC  _  C    CAGC
                           AAG CCC GCAGCAG
                           III III IIIIIII
                           TTC GGG CGTCGTC
                         ____  A  T    ACII
GAM472 ICOS          TGTCAAGCCCAGAGGCACCA     7480       CGCA  G GCG
                          TGTCAAGCCC   GCA CA
                          IIIIIIIIII   III II
                          ACAGTTCGGG   CGT GT
                           TCTC  G III
GAM472 LDOC1          TCCAGCCCCGACCCCAGCAGCAG   7474 TGTCA    _ AG    CI
                          AGCCCCG C CAGCAGCG
                          IIIIIIII I IIIIIIII
                          TCGGGGC G GTCGTCGT
                         G____    T GG     CC
GAM472 LENG4          GTCTGGCCCCGCAGCAGCAGC   7470 TGTCAA          C
                          GCCCCGCAGCAGCAGCG
                          IIIIIIIIIIIIIIIII
                          CGGGGCGTCGTCGTCGT
                         AGAC__            I
GAM472 MASP1          TCAGGAGCAGCAGCAGCAGC     7477 TGTCA CCC
                          AGC  GCAGCAGCAGCG
                          III  IIIIIIIIIII
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                           TCG   CGTCGTCGTCGT
                       TCC__   T__
GAM472  TCF8           AGCCACAGAGCAGCAGCAGC     7466 TGTCA  CCC
                           AGC   GCAGCAGCAGCG
                           |||   ||||||||||||
                           TCG   CGTCGTCGTCGT
                       GTC__   T__
GAM472  TIC            TGTCA-GCCG-GCAGGCAGCAGCG  7479   A  CC  _      C
                       TGTCA GCC  GCAG CAGCAGCG
                       ||||| |||  |||| ||||||||
                       ACAGT CGG  CGTC GTCGTCGC
                            _  C_   C      I
GAM472  TNFAIP1        AGACCCAGGCAGCAGCAGC      7467 TGTCAAGCCCC
                             GCAGCAGCAGCG
                             ||||||||||||
                             CGTCGTCGTCGT
                       GTC_____
GAM472  TNFRSF5         TCACGCCACAGCAGCAGCAGC    7473 TGTCAA  C _
                            GCC C GCAGCAGCAGCGC
                            ||| | ||||||||||||||
                            CGG G CGTCGTCGTCGTG
                       TG____  T T
GAM472  WHSC1          TGTCCGAGACCTGCAGCAGCA    7478   A_ C C     GCGC
                       TGTC  AG CC GCAGCAGCA
                       ||||  || || |||||||||
                       ACAG  TC GG CGTCGTCGT
                        GC T A       IIIC
GAM473  ADAM12         CAGAGGCATCATGGCATTTTACC   7487 A  ACTG_        I
                           GAG   GTGGCATTTTGC
                           |||   |||||||||||
                           CTC   TACCGTAAAATG
                        _   CGTAG        I
GAM473  ADAM12         CAGAGGCATCATGGCATTTTACC   7487 A__  GAGACTG        I
                           GCA   GTGGCATTTTGCC
                           |||   ||||||||||||
                           CGT   TACCGTAAAATGG
                        CTC AG_____        A
GAM473  CHS1           AGCAGAGACT-TTGGAATT    7483      GG  CATI
                           AGCAGAGACT TGG
                           |||||||||| |||
                           TCGTCTCTGA ACC
                             A_ TTAA
GAM473  CHS1           AGCAGAGACT-TTGGAATT    7483      GG  CATTTTG
                           AGCAGAGACT TGG
                           |||||||||| |||
                           TCGTCTCTGA ACC
                             A_ TTAAIII
GAM473  FMN2           CAGAGACT--TGGCATTTT     7488      GG   I
                           CAGAGACT TGGCATTT
                           |||||||| ||||||||
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                         GTCTCTGA ACCGTAAA
                            __        A
GAM473  FMN2        CAGAGACT--TGGCATTTT    7488 AGCA    GG      G
                         GAGACT TGGCATTTT
                         |||||| |||||||||
                         CTCTGA ACCGTAAAA


GAM473  GALR1       AGCAGAGACTGGACGGATT    7484         _ CATII
                         ____    __     _
                         AGCAGAGACTGG TGG

                         |||||||||| |||
                         TCGTCTCTGACC GCC
                              T  TAAII
GAM473  GALR1       AGCAGAGACTGGACGGATT    7484         _ CATTTTGC
                         AGCAGAGACTGG TGG

                         |||||||||| |||
                         TCGTCTCTGACC GCC
                              T  TAAIIICC
GAM473  KAL1        GCAGAGACTCCCAGCATTTT    7491     GG      I
                         CAGAGACT TGGCATTT
                         |||||||| ||||||||
                         GTCTCTGA GTCGTAAA
                              GG      I
GAM473  KAL1        GCAGAGACTCCCAGCATTTT    7491 AG    GG      GC
                         CAGAGACT TGGCATTTT
                         |||||||| |||||||||
                         GTCTCTGA GTCGTAAAA
                            __      GG    AI
GAM473  LDB3        GAGACTGGTGGCTTCGTGC    7490         ATTTTGII
                         GAGACTGGTGGC
                         ||||||||||||
                         CTCTGACCACCG
                              AAGCACGI
GAM473  LDB3        GAGACTGGTGGCTTCGTGC    7490 AGCAGAGA    A T
                         CTGGTGGC TT TGC
                         |||||||| || |||
                         GACCACCG AG ACG
                         _____      A C
GAM473  NDRG3       AGCAGAGGCC--TGGCATTTTG  7486     A GG      C
                         AGCAGAG CT TGGCATTTTG
                         ||||||| || |||||||||||
                         TCGTCTC GG ACCGTAAAAC
                              C __      I
GAM473  NDRG3       AGCAGAGGCC--TGGCATTTTG  7486 _   A GG      I
                         GCAGAG CT TGGCATTT
                         |||||| || ||||||||
                         CGTCTC GG ACCGTAAAA
                              T   C __      I
GAM473  PRKY        AGCAG-GCC-GGTGGCATTT    7485 AGA      TG
                         AGCAG CTGGTGGCATTT
                         ||||| ||||||||||||
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                                 TCGTC  GGCCACCGTAAA
                                   C__        II
GAM473  PRKY          AGCAG-GCC-GGTGGCATTT   7485 _  AGA      I
                         GCAG  CTGGTGGCATT
                         IIII  IIIIIIIIII
                         CGTC  GGCCACCGTAA
                          T  C__        I
GAM473  SIRPB2          GAGGCTGGGACAGGCATTTG   7489  A  T___     III
                         GAG CTGG  GGCATTTT
                         III IIII  IIIIIIII
                         CTC GACC  CCGTAAAA
                           C  CTGT     CII
GAM473  SLC10A1          GCA-AGACTGGTG--TTTTGC   7492  G      GCATTTI
                         GCA AGACTGGTG
                         III IIIIIIIII
                         CGT TCTGACCAC
                          _       AAAAACG
GAM473  SLC10A1          GCA-AGACTGGTG--TTTTGC   7492 AGCA      GCA
                          GAGACTGGTG  TTTTGC
                          IIIIIIIIII  IIIIII
                          TTCTGACCAC  AAAACG
                         G___       A__
GAM474  BIG1          TGACAAAATATTATGGGTA   7509      GT  TII
                         TGACAAAATAT TGTG
                         IIIIIIIIIII IIII
                         ACTGTTTTATA ATAC
                           __    CCA
GAM474  BIG1          TGACAAAATATTATGGGTA   7509      GT  T GAGT
                         TGACAAAATAT TG GTA
                         IIIIIIIIIII II III
                         ACTGTTTTATA AC CAT
                          AT  C   IIIT
GAM474  CCNT2          AAAATATGTAGTGTAAAATT   7496      T    I
                         AAATATGT GTGTAGAGT
                         IIIIIIII IIIIIIIII
                         TTTATACA CACATTTTA
                           T      I
GAM474  CCNT2          AAAATATGTAGTGTAAAATT   7496 TGACAAAA   T
                            TATGT GTGTAGAGT
                            IIIII IIIIIIIII
                            ATACA CACATTTTA
                          _____  T
GAM474  CDKN2A          TGACGGAAAGGAAGCTTGTGTAGAG 7506   AAAATAT__  _      TTII
                         TGAC     GTT GTGTAGAG
                         IIII     III IIIIIIII
                         ACTG     CGA CACATCTC
                          CCTTTCCTT  A    IIIT
GAM474  CDKN2A          TGACGGAAAGGAAGCTTGTGTAGAG 7506 GACAAAATATG      I
                            TTGTGTAGA
                            IIIIIIIII
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                        AACACATCT
                        CCTTTCCTTCG        I
GAM474  CLDN14          TGAGAGAAAAT--TGTGTAGA    7510  CAAAATAT        GT
                        TGA      GTTGTGTAGA
                        |||      ||||||||||
                        ACT      TAACACATCT
                        CTCTTT__        II
GAM474  EYA4            GACAATTTATAT-GTGTAGAG    7505 _  AA   T   I
                        ACAA  TATGT GTGTAGA
                        ||||  ||||| |||||||
                        TGTT  ATATA CACATCT
                        C  AA   _   I
GAM474  EYA4            GACAATTTATAT-GTGTAGAG    7505 TG   AA   T
                        ACAA  TATGT GTGTAGAGT
                        ||||  ||||| |||||||||
                        TGTT  ATATA CACATCTCG
                        __   AA    _
GAM474  HMMR            TGAAGAAATA-GTTACATGTAGAGTT 7508  CA   T  __        II
                        TGA  AAATA GTT  GTGTAGAGTT
                        |||  ||||| |||  ||||||||||
                        ACT  TTTAT CAA  TACATCTCAA
                        TC   _  TG        II
GAM474  HMMR            TGAAGAAATA-GTTACATGTAGAGTT 7508 GACA   T  __        I
                        AAATA GTT  GTGTAGAGT
                        ||||| |||  |||||||||
                        TTTAT CAA  TACATCTCA
                        TTC_  _  TG        I
GAM474  KCND2           AAATATGTTGTGT-GAGTT    7500          A  I
                        AAATATGTTGTGT GAGT
                        ||||||||||||| ||||
                        TTTATACAACACA CTCA
                        _   A
GAM474  LDHB            AAAAGTTTATGTGTAGAGTT       7495 AAATATGT        I
                        TGTGTAGAGT
                        ||||||||||
                        ACACATCTCA
                        TTTCAAAT        I
GAM474  LDHB            AAAAGTTTATGTGTAGAGTT       7495 TGACAAAATATGT
                        TGTGTAGAGT
                        ||||||||||
                        ACACATCTCA
                        CAAAT_____
GAM474  MIPOL1          AAATATGTTGATTGGAATT    7499        TGTA_  II
                        AAATATGTTG   GAGT
                        ||||||||||   ||||
                        TTTATACAAC   CTTA
                        TAAAC   AI
GAM474  NR3C1           AAATATGTTAAGTTTTGAGTT    7498        T A__   III
                        AAATATGTTG GT  GAGT
                        ||||||||||| || ||||
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                          TTTATACAAT CA  CTCA
                             T AAA  AII
GAM474 OSCAR          CAAGATTTATTGTGTAGAG      7504  A A      II
                        CAA AT TGTTGTGTAGA
                        III II IIIIIIIIIII
                        GTT TA ATAACACATCT
                           C A      CI
GAM474 OSCAR          CAAGATTTATTGTGTAGAG      7504 TGACAAAATA
                            TGTTGTGTAGAGT
                            IIIIIIIIIIII
                            ATAACACATCTCG
                        CTAA_____
GAM474 RBBP9          ACAAAATAT-ATGTCCTAGA      7503        T GTAGII
                        ACAAAATATGT GT
                        IIIIIIIIIII II
                        TGTTTTATATA CA
                          _ GGATCT
GAM474 RFXAP          TGACAAAATACTGGAGTGT-TAGTT 7507       GTT_ AG  I
                        TGACAAAATAT GTGT AGTT
                        IIIIIIIIIII IIII IIII
                        ACTGTTTTATG CACA TCAA
                           ACCT A_  I
GAM474 RFXAP          TGACAAAATACTGGAGTGT-TAGTT 7507       GTT_ AG  I
                        GACAAAATAT GTGT AGT
                        IIIIIIIIII IIII III
                        CTGTTTTATG CACA TCA
                          ACCT A_ I
GAM474 RFXAP          AACAAATTTT-TGTAGAGTT      7497 A T G_     I
                        AATA GTT TGTAGAGT
                        IIII III IIIIIIII
                        TTGT TAA ACATCTCA
                         _ T AA     I
GAM474 ZNF22          AATATGTTGAATCTAGAGT       7501       __G  III
                        AATATGTTG T TAGAG
                        IIIIIIIII I IIIII
                        TTATACAAC A ATCTC
                          TT G  AII
GAM474 ZNF8           ACAAAATATGTCGCTAAAGAG      7502 C       GT_ I
                        AAAATATGTTGT AGA
                        IIIIIIIIIII III
                        TTTTATACAGCG TCT
                         _      ATT I
GAM474 ZNF8           ACAAAATATGTCGCTAAAGAG      7502 TGAC      GT_ TT
                        AAAATATGTTGT AGAG
                        IIIIIIIIIII IIII
                        TTTTATACAGCG TCTC
                        ____      ATT CC
GAM475 C18orf1        ACACCACTCCCACACGAAG       7514        AGAAIII
                        ACACCACTCCCA
                        IIIIIIIIIIII
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                              TGTGGTGAGGGT
                                GTGCTTC
GAM475  C18orf1         ACACCACTCCCACACGAAG      7514 TA        A__    AATAA
                              CACCACTCCCA  GAAG
                              |||||||||| ||||
                              GTGGTGAGGGT  CTTC
                                     GTG   AIIIG
                                  __
GAM475  CARPX          CCAATCCCAAGAATGAATGAG      7529 CCAC       _   AI
                              TCCCAAGAA GAAT
                              ||||||||| ||||
                              AGGGTTCTT CTTA
                                T___     A  CT
GAM475  CARPX          CCAATCCCAAGAATGAATGAG      7529 TACACCAC      _   AAG
                              TCCCAAGAA GAAT
                              ||||||||| ||||
                              AGGGTTCTT CTTA
                              _____      A  CTC
GAM475  CDK10          CACCACTCCTCCCAAGAAG       7522 ___  CA       III
                              CAC CTCCCAAGAA
                              ||| |||||||||
                              GTG GAGGGTTCTT
                              GTG AG      CII
GAM475  CDK10          CACCACTCCTCCCAAGAAG       7522 TA CA        AATAA
                              CAC CTCCCAAGAAG
                              ||| ||||||||||
                              GTG GAGGGTTCTTC
                              G_ AG        GTIII
GAM475  DHCR24         CCACTCCCACCAAGACAAAG      7530        AG   ATAAI
                              CACTCCCA AAGA
                              |||||||| ||||
                              GTGAGGGT TTCT
                                GG   GTTTI
GAM475  DHCR24         CCACTCCCACCAAGACAAAG      7530 TACACCA  _   A  TAA
                              CTC CCAAGA GAA
                              ||| |||||| |||
                              GGG GGTTCT TTT
                              A_____  T  G  CAC
GAM475  DYRK1A         AGAATTCCAAGTGGTGCTA       7521 C GT       II
                              AGA TTC GGTGGTGCT
                              ||| ||| ||||||||||
                              TCT AAG TCACCACGA
                              T GT      TI
GAM475  DYRK1A         AGAATTCCAAGTGGTGCTA       7521 TGAGAC GT      AG
                              TTC GGTGGTGCTA
                              ||| |||||||||||
                              AAG TCACCACGAT
                              TT____ GT      GT
GAM475  FZD4           ACAGCAGCAGCCAAGAAGA       7513 C CTC_    II
                              ACA CA  CCAAGAAG
                              ||| || |||||||||
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                          TGT GT   GGTTCTTC
                           C CGTC      TI
GAM475 FZD4        ACAGCAGCAGCCAAGAAGA      7513 TACACCACTC      ATAA
                          CCAAGAAGA
                          |||||||||
                          GGTTCTTCT
                       GTCGTCGTC_      CIII
GAM475 GOCAP1       TACACTGCTCCCAAGAACAAT   7536   CA     G   AAG
                       TACAC CTCCCAAGAA AAT
                       ||||| |||||||||| |||
                       ATGTG GAGGGTTCTT TTA
                         AC      G  III
GAM475 GOCAP1       TACACTGCTCCCAAGAACAAT   7536   CA     G  I
                        ACAC CTCCCAAGAA AA
                        |||| |||||||||| ||
                        TGTG GAGGGTTCTT TT
                         AC       G  I
GAM475 HNF3G       AGAGCTTCGTGGTGTGAGCT     7519  _      GT_ III
                       AGA CTTCGTGGTG  GC
                       ||| ||||||||||  ||
                       TCT GAAGCACCAC  CG
                        C      ACT AII
GAM475 HNF3G       AGAGCTTCGTGGTGTGAGCT     7519 TG  A      GT_ AAG
                        AG CTTCGTGGTG  GCT
                        || ||||||||||  |||
                        TC GAAGCACCAC  CGA
                        __ _       ACT GGI
GAM475 MAT1A       TGAGACTTCCTGG-GCTGC      7539    G  TGG   TAA
                       TGAGACTTC TGG  TGC
                       ||||||||| |||  |||
                       ACTCTGAAG ACC  ACG
                          G  CG_  III
GAM475 MAT1A       TGAGACTTCCTGG-GCTGC      7539    G  TG_ GI
                       TGAGACTTC TGG  GT
                       ||||||||| |||  ||
                       ACTCTGAAG ACC  CG
                          G  CGA II
GAM475 MXI1        GACTTAGACTTGGGTGCTAAG    7533 ___   CGTGGT   I
                        GACTT   GGTGCTA
                        |||||   |||||||
                        CTGAA   CCACGAT
                        AAT  C_____   T
GAM475 MXI1        GACTTAGACTTGGGTGCTAAG    7533 TG    CGTGGT    A
                        AGACTT   GGTGCTAAG
                        ||||||   |||||||||
                        TCTGAA   CCACGATTC
                        AA  C_____     C
GAM475 NDN         CATCAGTCCCATATAAAAGAATAAG 7523 ACCAC   ___     I
                        TCCCA AGAAGAATAA
                        ||||| |||||||||
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                              AGGGT   TTTTCTTATT
                        TC___       ATA          I
GAM475 NDN              CATCAGTCCCATATAAAAGAATAAG 7523 TACAC  C    ___          II
                            CA TCCCA  AGAAGAATAAG
                            || ||||| |||||||||||
                            GT AGGGT  TTTTCTTATTC
                        A____   C  ATA       TA
GAM475 OLFM1            CTTAGTGAAATGGTGCTAAG    7531  C  __        III
                            CTT GTG  GTGGTGCTAA
                            ||| ||| ||||||||||
                            GAA CAC  TACCACGATT
                            T   TT       CII
GAM475 OLFM1            CTTAGTGAAATGGTGCTAAG     7531 TGAGACTTCGT
                              GGTGGTGCTAAG
                              ||||||||||||
                              TTACCACGATTC
                        ACT_____
GAM475 OTOF            CACCACTCCAAGAAAAGAAAAA  7524 A     C     ATAI
                           CCACTCC AAGAAGA
                           ||||||| |||||||
                           GGTGAGG TTCTTTT
                           _    _     CTTT
GAM475 OTOF            CACCACTCCAAGAAAAGAAAAA  7524 TACA    C      ATAAG
                           CCACTCC AAGAAGA
                           ||||||| |||||||
                           GGTGAGG TTCTTTT
                           ____     _    CTTTT
GAM475 PKNOX1          CACCACTCCTAAGTAAACAAT    7525     C  A  AIII
                          CACCACTCC AAG AGA
                          ||||||||| ||| |||
                          GTGGTGAGG TTC TTT
                              A  A  GTTA
GAM475 PKNOX1          CACCACTCCTAAGTAAACAAT    7525 TACA     C  AA    G
                           CCACTCC AAG  GAATAA
                           ||||||| ||| |||||||
                           GGTGAGG TTC  TTTGTT
                           ____    A  A_    A
GAM475 PLOD2         ACC-CTCCCCCCAAAAAAGAATAAG 7517 CCA        _     I
                           CTCCCAAGAA GAATAA
                           |||||||||| ||||||
                           GGGGGTTTTT CTTATT
                        AG_      T   I
GAM475 PLOD2         ACC-CTCCCCCCAAAAAAGAATAAG 7517 TACACCA       _     I
                           CTCCCAAGAA GAATAAG
                           |||||||||| |||||||
                           GGGGGTTTTT CTTATTC
                        GAG____      T   C
GAM475 PON1         ACAACACTCCCAAGAATTTTAAG  7516 C          GAATAAI
                           CA CACTCCCAAGAA
                           || |||||||||||
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                    GT GTGAGGGTTCTT
                    T         AAAATTI
GAM475 PON1         ACAACACTCCCAAGAATTTTAAG   7516 TA  C        GAA   I
                    CA CACTCCCAAGAA  TAAG

                    II IIIIIIIIIII  IIII
                    GT GTGAGGGTTCTT  ATTC
                    __ T        AAA  T
GAM475 PPIH         ACACCAC---CAAGAAGAA      7515     CTC
                    ACACCA  CCAAGAAGA

                    IIIIII  IIIIIIIII
                    TGTGGT  GGTTCTTCT

                              ___
GAM475 PPIH         ACACCAC---CAAGAAGAA      7515 TA  CTC       T
                    CACCA  CCAAGAAGAA

                    IIIII  IIIIIIIIII
                    GTGGT  GGTTCTTCTT
                    __  ___      C
GAM475 RAB18        CTTCCCGTGGTGCTAGGA      7532    GTG      AGII
                    CTTC  GTGGTGCTA

                    IIII  IIIIIIIII
                    GAAG  CACCACGAT
                    GGG       CCTI
GAM475 RCN1         TACACCACTTACAGTAAGTAATAA 7534    CC AG _  GI
                    TACACCACT CA AAG AATAA

                    IIIIIIIII II III IIII
                    ATGTGGTGA GT TTC TTATT
                      AT CA A   II
GAM475 RCN1         TACACCACTTACAGTAAGTAATAA 7534 A   CC AG _  I
                    CACCACT CA AAG AATA

                    IIIIIII II III IIII
                    GTGGTGA GT TTC TTAT
                    _   AT CA A  I
GAM475 RRM2B        TGATAATTAGTAGTGGTGCTAA   7540  GACTTC      GA
                    TGA   GTGGTGGTGCTAA

                    III   IIIIIIIIIIII
                    ACT   CATCACCACGATT
                     ATTAAT         II
GAM475 RRM2B        TGATAATTAGTAGTGGTGCTAA   7540 GAGACTTC      I
                    GTGGTGGTGCTA

                    IIIIIIIIIIII
                    CATCACCACGAT
                    CTATTAAT        I
GAM475 SCA7         TGAGACA-CGATCCTGGTGCTAA  7538    TT TGG_    GA
                    TGAGAC CG  TGGTGCTAA

                    IIIIII II  IIIIIIIII
                    ACTCTG GC  ACCACGATT
                     T_ TAGG       II
GAM475 SCA7         TGAGACA-CGATCCTGGTGCTAA  7538    TT TGG_   I
                    GAGAC CG  TGGTGCTA

                    IIIII II  IIIIIIII
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                          CTCTG GC   ACCACGAT
                           T_  TAGG        I
GAM475 SEDL            CACTCCCAACTGCAGAATA    7526      GA__    III
                          CACTCCCAA  AGAAT
                          ||||||||| |||||
                          GTGAGGGTT  TCTTA
                             GACG   TII
GAM475 SMARCC1           CCACTCCCAAGAGTCCAGAACAA  7528          ____    IIIT
                          CCACTCCCAAGA  AGAATA
                          |||||||||||  ||||||
                          GGTGAGGGTTCT  TCTTGT
                              CAGG    TIII
GAM475 SPOCK          ACTATTTCCAAGAAGAAGAA     7518 ACCACTC       TI
                          CCAAGAAGAA
                          ||||||||||
                          GGTTCTTCTT
                         ATAAA__       CT
GAM475 SPOCK          ACTATTTCCAAGAAGAAGAA     7518 TACACCACTC      TAA
                          CCAAGAAGAA
                          ||||||||||
                          GGTTCTTCTT
                         TAAA_____       CTT
GAM475 TBX3          TAAACCACGC-CAAGAAGA    7535 TAC   TC     ATA
                          ACCAC  CCAAGAAGA
                          |||||  |||||||||
                          TGGTG  GGTTCTTCT
                         ATT   C_       III
GAM475 TBX3          TAAACCACGC-CAAGAAGA    7535 TAC   TC    I
                          ACCAC  CCAAGAAG
                          |||||  ||||||||
                          TGGTG  GGTTCTTC
                         ATT   C_      T
GAM475 TP63          CCACTATCCCAAGAAGAAAAA    7527    __      TAIII
                          CCAC  TCCCAAGAAGAA
                          ||||  |||||||||||
                          GGTG  AGGGTTCTTCTT
                           AT        TTTII
GAM475 TP63          CCACTATCCCAAGAAGAAAAA    7527 TACACCAC      TAAG
                           TCCCAAGAAGAA
                          ||||||||||||
                          AGGGTTCTTCTT
                         AT_____        TTTT
GAM475 WHSC1         TATACCTTTTTCAAGAAGAAT   7537 AC  ACTCC      I
                          ACC   CAAGAAGAA
                          |||   |||||||||
                          TGG   GTTCTTCTT
                         TA AAAAA     I
GAM475 WHSC1         TATACCTTTTTCAAGAAGAAT   7537 TAC  ACTCC       AAG
                          ACC   CAAGAAGAAT
                          |||   ||||||||||
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                          TGG    GTTCTTCTTA
                          ATA  AAAAA        III
GAM475  ZNF80          AGACCTTCGTGGTGAGTGTTA    7520  _       _   CTIII
                          AGAC TTCGTGGTG GTG
                          |||| ||||||||| |||
                          TCTG AAGCACCAC CAC
                            G       T  AATII
GAM475  ZNF80          AGACCTTCGTGGTGAGTGTTA    7520 TGAGA       _   CTAAGA
                          CTTCGTGGTG GTG
                          |||||||||| |||
                          GAAGCACCAC CAC
                          TG___          T  AATGTI
GAM476  ADORA2B           GGTGGCCGGGACCCACGGGTC    7557 _  A  T  AG      I
                          GGT GG GGC  CCACGGG
                          ||| || |||  |||||||
                          CCG CC CTG  GGTGCCC
                            A  G _  __      A
GAM476  ADORA2B           GGTGGCCGGGACCCACGGGTC    7557 TAG  A  T  AG
                          GGT GG GGC  CCACGGGTC
                          ||| || |||  |||||||||
                          CCG CC CTG  GGTGCCCAG
                          ___   G _  __
GAM476  APPBP2         AGGGGCGGTGGCAGCCACG    7545    TA           II
                          AGGG  GGTGGCAGCCAC
                          ||||  ||||||||||||
                          TCCC  CCACCGTCGGTG
                            CG         CI
GAM476  APPBP2         AGGGGCGGTGGCAGCCACG    7545 TA  A         GGT
                          GGGT GGTGGCAGCCACG
                          |||| |||||||||||||
                          CCCG CCACCGTCGGTGC
                          C_   _         GII
GAM476  BAI2        AGGGTAGGTAGCTGCAGCCGCG    7544           ___    ACIII
                          AGGGTAGGTGGC  AGCC
                          |||||||||||  ||||
                          TCCCATCCATCG  TCGG
                            ACG    CGCII
GAM476  BAI2        AGGGTAGGTAGCTGCAGCCGCG    7544 TA           ___    A GGTC
                          GGGTAGGTGGC  AGCC CG
                          |||||||||||  |||| ||
                          CCCATCCATCG  TCGG GC
                            __       ACG   C GIII
GAM476  BLK        AGGTGGCAGCACCCCCGGTC    7549           CA___   GTIII
                          AGGTGGCAGC    CGG
                          ||||||||||    |||
                          TCCACCGTCG    GCC
                          TGGGG  AGIII
GAM476  BLK        AGGTGGCAGCACCCCCGGTC    7549 TAGGGTAGGT   G  A  GT
                          GGCA CC CGG
                          |||| || |||
```

```
                              TCGT GG GCC
                         G_____      G  G  AG
GAM476  CXorf6           GGCAGGTGGCAGCTCAGGGG    7555        _  C  II
                         GGTAGGTGGCAGC CA GG
                         IIIIIIIIIII II II
                         CCGTCCACCGTCG GT CC
                                  A  C  CI
GAM476  CXorf6           GGCAGGTGGCAGCTCAGGGG    7555 TAGGGT      _  C  T
                              AGGTGGCAGC CA GGG
                              IIIIIIIIII II III
                              TCCACCGTCG GT CCC
                         _____            A  C  C
GAM476  CYP24            TAGGGCTTGCTGG-AGCCACGGG   7559     AG _  C      TC
                         TAGGGT  G TGG AGCCACGGG
                         IIIIII I III IIIIIIIII
                         ATCCCG  C ACC TCGGTGCCC
                              AA G  _       II
GAM476  CYP24            TAGGGCTTGCTGG-AGCCACGGG   7559     AG _  C      I
                              AGGGT  G TGG AGCCACGG
                              IIIII I III IIIIIIII
                              TCCCG  C ACC TCGGTGCC
                              AA G  _      I
GAM476  DCK             AGGGCTGGGAGGCGGCCACGGGT   7543 ____  T      AGC    I
                              GGG AGGTGGC  CACGGG
                              III IIIIIIII  IIIIII
                              CCC TCCGCCG  GTGCCC
                         CCGA  _    ___      I
GAM476  DCK             AGGGCTGGGAGGCGGCCACGGGT   7543 TA  A_ T  A      CI
                              GGGT GG GGC GCCACGGGT
                              IIII II III IIIIIIIII
                              CCCG CC CCG CGGTGCCCA
                         __  AC T  C       CI
GAM476  EPHX1           GGGGAGGTGGCAGGCGGGGG    7552 _  T      CCA  I
                              GG AGGTGGCAG  CGG
                              II IIIIIIIII  III
                              CC TCCACCGTC  GCC
                         C _      C__  C
GAM476  EPHX1           GGGGAGGTGGCAGGCGGGGG    7552 TAG T      CCA  T
                              GG AGGTGGCAG  CGGG
                              II IIIIIIIII  IIII
                              CC TCCACCGTC  GCCC
                              ___  _      C__  C
GAM476  FOXM1           GGGGAGGTGGCAGGGAGGGG    7553 _  T      CCAC I
                              GG AGGTGGCAG   GG
                              II IIIIIIII   II
                              CC TCCACCGTC   CC
                         C _         CCTC I
GAM476  FOXM1           GGGGAGGTGGCAGGGAGGGG    7553 TAG T      CCAC
                              GG AGGTGGCAG   GGGT
                              II IIIIIIIII   IIII
```

```
                          CC TCCACCGTC   CCCG
                          ___ _           CCTC
GAM476  GRIK3        GGCAGGTGGCAG-CTCTGGTC   7556 _          CACG  I
                         GTAGGTGGCAGC  GGT
                         |||||||||||  |||
                         CGTCCACCGTCG  CCA
                         C         AGA_  I
GAM476  GRIK3        GGCAGGTGGCAG-CTCTGGTC   7556 TAGGGT       CACG
                          AGGTGGCAGC  GGT
                          ||||||||||  |||
                          TCCACCGTCG  CCA
                          _____         AGA_
GAM476  KCNA7         AGGGTAGGTGACAGGCCTGGTTC   7548         _ AC  GTI
                         GGGTAGGTGGCAG CC  GG
                         |||||||||||| ||  ||
                         CCCATCCACTGTC GG  CC
                              C A_  AAI
GAM476  KCNA7         AGGGTAGGTGACAGGCCTGGTTC   7548 TA       _ ACG  CI
                         GGGTAGGTGGCAG CC  GGT
                         |||||||||||| ||  |||
                         CCCATCCACTGTC GG  CCA
                             __         C A__  AG
GAM476  LZTS1        GGGCTGGTGGCAGCCCAGGG   7551  A      A  I
                         GGT GGTGGCAGCC CGG
                         ||| |||||||||| |||
                         CCG CCACCGTCGG GTC
                              A      _   C
GAM476  LZTS1        GGGCTGGTGGCAGCCCAGGG   7551 TAGGGTA      A  T
                          GGTGGCAGCC CGGG
                          |||||||||| ||||
                          CCACCGTCGG GTCC
                         CGA____        _  C
GAM476  MBP          GGGTGTGTGGGCAGCCACGG   7550  AG  _     II
                         GGGT GTGG CAGCCACG
                         |||| |||| ||||||||
                         CCCA CACC GTCGGTGC
                           CA   C     CI
GAM476  MBP          GGGTGTGTGGGCAGCCACGG   7550 TAGGGTAG  _    GT
                          GTGG CAGCCACGG
                          |||| |||||||||
                          CACC GTCGGTGCC
                         CACA____  C     GG
GAM476  PARK2        GGGTAGGTGGCGGCTGCGGG   7554        A CA  I
                         GGTAGGTGGC GC  CGG
                         |||||||||| ||  |||
                         CCATCCACCG CG  GCC
                             C AC  I
GAM476  PARK2        GGGTAGGTGGCGGCTGCGGG   7554 TAGG      A CA
                          GTAGGTGGC GC  CGGGT
                          |||||||| ||  |||||
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                        CATCCACCG CG  GCCCG
                        ____          C  AC
GAM476  PLXNB3          AGGGGAGGTGGCAGGCAGGG     7546 _  T      C  CGI
                             GGG AGGTGGCAG CA
                             ||| |||||||||| ||
                             CCC TCCACCGTC GT
                             C  _        C  CCI
GAM476  PLXNB3          AGGGGAGGTGGCAGGCAGGG     7546 TA T      C  C  T
                             GGG AGGTGGCAG CA GGG
                             ||| |||||||||| || |||
                             CCC TCCACCGTC GT CCC
                             C_  _      C  _  T
GAM476  SGCD           TAGCTGGCAGCCA-GTGTC     7560  G      CGGGTI
                             TAG TGGCAGCCA
                             ||| |||||||||
                             ATC ACCGTCGGT
                              G      CACAGI
GAM476  SOX12          TAGGCTGTAGA-GGCAGCCACG   7558  __   T      GGTC
                             TAGG  GTAGG GGCAGCCACG
                             ||||  ||||| ||||||||||
                             ATCC  CATCT CCGTCGGTGC
                              GA    _       IIIC
GAM476  SOX12          TAGGCTGTAGA-GGCAGCCACG   7558 AGG_  T      I
                                 GTAGG GGCAGCCAC
                                 ||||| |||||||||
                                 CATCT CCGTCGGTG
                                 CCGA    _       I
GAM476  UMOD           AGGTGAGATGGCAGCCATGG     7547 G  _       CGI
                             GGT AGGTGGCAGCCA
                             ||| |||||||||||
                             CCA TCTACCGTCGGT
                             _  C      ACI
GAM476  UMOD           AGGTGAGATGGCAGCCATGG     7547 TAG _      C  T
                             GGT AGGTGGCAGCCA GGG
                             ||| ||||||||||| |||
                             CCA TCTACCGTCGGT CCT
                             ___  C      A  I
GAM477  ACTN2          AGCAGTATGAGCAAAAGAA      7564      AATGAIII
                             AGCAGTATGAG
                             |||||||||||
                             TCGTCATACTC
                              GTTTTCT
GAM477  ACTN2          AGCAGTATGAGCAAAAGAA      7564 TA      AAT  CTAAC
                             GCAGTATGAG  GAA
                             ||||||||||  |||
                             CGTCATACTC  TTT
                             __       GTT  CTTTI
GAM477  AGL            AGCAATGAAAGAGAATGAA      7563      AT__      III
                             AGCAGT  GAGAATGA
                             ||||||  ||||||||
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                    TCGTTA  CTCTTACT
                     CTTT      TII
GAM477 AGL          AGCAATGAAAGAGAATGAA    7563 TA   AT__      CTAAC
                     GCAGT   GAGAATGAA
                     |||||   |||||||||
                     CGTTA   CTCTTACTT
                      __   CTTT    AIIIA
GAM477 COL17A1      TAG-AGAATGCAGAATGAAC    7576   C T  _     II
                    TAG AG ATG AGAATGAA
                    ||| || ||| ||||||||
                    ATC TC TAC TCTTACTT
                      _  T  G    GI
GAM477 COL17A1      TAG-AGAATGCAGAATGAAC    7576   C T  _    TAAC
                    TAG AG ATG AGAATGAAC
                    ||| || ||| |||||||||
                    ATC TC TAC TCTTACTTG
                      _  T  G    IIIA
GAM477 GABRA3       AGAAGGATGA--ATGAACTGAAACA 7565 CAGTATGA       AI
                      GAATGAACT
                      |||||||||
                      CTTACTTGA
                    TCCTA___      CT
GAM477 GABRA3       AGAAGGATGA--ATGAACTGAAACA 7565 TAGCAGTATGA      __  I
                      GAATGAACT AACA
                      ||||||||| ||||
                      CTTACTTGA TTGT
                    CTTCCTA____      CT  T
GAM477 HS3ST4       TAGCAGAAGATAAGAATGAAC    7573    T__       TAACA
                    TAGCAG  ATGAGAATGAAC
                    ||||||  |||||||||||||
                    ATCGTC  TATTCTTACTTG
                     TTC        IIIAC
GAM477 HS3ST4       TAGCAGAAGATAAGAATGAAC    7573    T__       III
                    TAGCAG  ATGAGAATGAA
                    ||||||  ||||||||||||
                    ATCGTC  TATTCTTACTT
                     TTC        GII
GAM477 IGFBP3       AGCATGAGAATGACTCTAA    7568       A AII
                    AGTATGAGAATGA CT
                    ||||||||||||| ||
                    TCGTACTCTTACT GA
                      _ GAT
GAM477 IGFBP3       AGCATGAGAATGACTCTAA    7568 TAGCAGTA      A_  C
                      TGAGAATGA CTAA
                      ||||||||| ||||
                      ACTCTTACT GATT
                    _____      GA  C
GAM477 IMPG2        GTTTGAGAATGAACAACCA    7572 GTA        T II
                     TGAGAATGAAC AAC
                     ||||||||||| |||
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                        ACTCTTACTTG TTG
                     CAA          _  GT
GAM477 ITSN1         TAGGATTATGAGAAT--ATTAACA  7577  CAG        __  TAAI
                         TAG  TATGAGAATG AAC
                         |||  ||||||||| |||
                         ATC  ATACTCTTAT TTG
                       CTA          AA  TIII
GAM477 ITSN1         TAGGATTATGAGAAT--ATTAACA  7577  CAG       AAC
                         TAG  TATGAGAATG  TAACA
                         |||  ||||||||||  |||||
                         ATC  ATACTCTTAT  ATTGT
                       CTA          A__
GAM477 KLRD1         TAGCAAAAATAGAGAATGAA     7574     TAT__      CTAAC
                        TAGCAG   GAGAATGAA
                        ||||||   |||||||||
                        ATCGTT   CTCTTACTT
                         TTTAT        IIIAC
GAM477 KLRD1         TAGCAAAAATAGAGAATGAA     7574     TAT__      III
                        TAGCAG   GAGAATGA
                        ||||||   ||||||||
                        ATCGTT   CTCTTACT
                         TTTAT        TII
GAM477 MAN2A2        GCAGTCTCTGTGAATGAACT     7571    A__  A      III
                         GCAGT  TG GAATGAAC
                         |||||  || |||||||||
                         CGTCA  AC CTTACTTG
                          GAG  A        AII
GAM477 MAN2A2        GCAGTCTCTGTGAATGAACT     7571  TAGCAGTA  A      AAC
                            TG GAATGAACT
                            || |||||||||
                            AC CTTACTTGA
                        TCAGAG__  A        AAI
GAM477 PIM2          AGTAAGAGCATATGAACTAA     7566   T A__     III
                         AGTA GAG  ATGAACTA
                         |||| |||  ||||||||
                         TCAT CTC  TACTTGAT
                          T  GTA        TII
GAM477 PIM2          AGTAAGAGCATATGAACTAA     7566 T C    GAGA     C
                           AG AGTAT   ATGAACTAA
                           || |||||   ||||||||||
                           TC TCGTA   TACTTGATT
                         _ _  ____           C
GAM477 RFXAP           AGTATGAGAATAAACTAACA    7569              I
                          GTATGAGAATGAACTAAC
                          ||||||||||||||||||
                          CATACTCTTATTTGATTG
                                   I
GAM477 RFXAP           AGTATGAGAATAAACTAACA    7569  TAGCAGTA
                           TGAGAATGAACTAAC
                           |||||||||||||||
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                           ACTCTTATTTGATTG
                           ‾‾‾‾‾‾‾‾‾
GAM477  SLC4A10      AGTATGAGAATACAAACTA      7567        __      III
                     AGTATGAGAAT GAACT
                     |||||||||| |||||
                     TCATACTCTTA TTTGA
                         TG   TII
GAM477  SNX6         TACCAGGATACATGAATGAACTAA  7575  G  __   A       CAI
                     TA CAG  TATG GAATGAACTAA
                     || ||| |||| |||||||||||
                     AT GTC  ATGT CTTACTTGATT
                      G  CT   A        III
GAM477  SNX6         TACCAGGATACATGAATGAACTAA  7575 AGCA   A      I
                         GTATG GAATGAACTA
                         ||||| |||||||||||
                         TATGT CTTACTTGAT
                         GTCC    A       I
GAM477  WNT5A        CATTCTGCAGAATGAACTAA      7570  GTA _      II
                     CA  TG AGAATGAACTA
                     ||  || |||||||||||
                     GT  AC TCTTACTTGAT
                      AAG  G       TI
GAM477  WNT5A        CATTCTGCAGAATGAACTAA      7570 TAGCAGTA _      C
                        TG AGAATGAACTAA
                        || |||||||||||
                        AC TCTTACTTGATT
                     AG‾‾‾‾‾‾  G        C
GAM478  ABCC1        TGAGAGGGAAAGAAAAGAGGT    7595     A  ___    CCAGAG
                     TGAGAG GAAA  AAGAGGT
                     |||||| |||| |||||||
                     ACTCTC CTTT  TTCTCCA
                         C   CTT      IIIGAG
GAM478  ABCC1        TGAGAGGGAAAGAAAAGAGGT    7595     A  ___    III
                     TGAGAG GAAA  AAGAGG
                     |||||| |||| ||||||
                     ACTCTC CTTT  TTCTCC
                         C   CTT   AII
GAM478  APBA1        GAGAGAGTAAA-GAGGTCC      7591     AA      I
                     GAGAGAG AAAGAGGTC
                     ||||||| ||||||||||
                     CTCTCTC TTTCTCCAG
                        A_       G
GAM478  APBA1        GAGAGAGTAAA-GAGGTCC      7591 TG  AA      AG
                      AGAGAG AAAGAGGTCC
                      |||||| ||||||||||
                      TCTCTC TTTCTCCAGG
                        __    A_      AI
GAM478  BECN1        TGAGAGAGATAAAAA--TCCAG   7601      AAA      A
                     TGAGAGAGA AGAGGTCCAG
                     ||||||||| |||||||||||
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                        ACTCTCTCT  TTTTTAGGTC
                           A__       I
GAM478  BECN1           TGAGAGAGATAAAAA--TCCAG  7601 _    AAA    I
                           GAGAGAGA  AGAGGTCCA
                           |||||||| |||||||||
                           CTCTCTCT TTTTTAGGT
                           A     A__     I
GAM478  CENTD2          GAGAGAGAAAGACAGAGGGAGAGAG 7588    AAA  TCC  I
                           AGAGAGA  AGAGG  AGA
                           ||||||| |||||  |||
                           TCTCTTT TCTCC  TCT
                            CTG    CTC  I
GAM478  CENTD2          GAGAGAGAAAGACAGAGGGAGAGAG 7588 T    AAA  TCC  II
                           GAGAGAGA  AGAGG  AGAG
                           |||||||| |||||  ||||
                           CTCTCTTT  TCTCC  TCTC
                           T    CTG   CTC  TI
GAM478  CYP4A11         TGAGAGAGAGAAGGGCAGG--CAGA 7597    AA  A  C__   GI
                           TGAGAGAGA  AAG GGT  CAGA
                           ||||||||| ||| |||  ||||
                           ACTCTCTCT TTC CCG  GTCT
                              C_  _  TCC   II
GAM478  CYP4A11         TGAGAGAGAGAAGGGCAGG--CAGA 7597 _    AAAG  CCAI
                           GAGAGAGAA  AGGT
                           ||||||||| ||||
                           CTCTCTCTT  TCCG
                           T    CCCG   TCII
GAM478  CYP4A11         TGAGAGAGAAAGTG-GGTCCAG    7600    AAGA    AG
                           TGAGAGAGAAA  GGTCCAG
                           |||||||||||  ||||||||
                           ACTCTCTCTTT  CCAGGTC
                              CAC_    II
GAM478  CYP4A11         TGAGAGAGAAAGTG-GGTCCAG    7600 _    AAGA    I
                           GAGAGAGAAA  GGTCCA
                           ||||||||||  ||||||
                           CTCTCTCTTT  CCAGGT
                           A     CAC_   I
GAM478  DPYSL2          GAGAGAGAAAGAGAGAGT-GAGAG  7590    A  TCC  I
                           AGAGAGAAA AGAGG  AGA
                           ||||||||| |||||  |||
                           TCTCTCTTT TCTCT  TCT
                              C    CAC  I
GAM478  DPYSL2          GAGAGAGAAAGAGAGAGT-GAGAG  7590 TG    A  TCC  I
                           AGAGAGAAA AGAGG  AGAG
                           ||||||||| |||||  ||||
                           TCTCTCTTT TCTCT  TCTC
                           __     C   CAC  G
GAM478  FSTL1           GAG-GAAACTGAGGTCCAGA      7585 _ A  AA     I
                           AG GAAA  GAGGTCCAG
                           || |||| |||||||||
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```
                      TC CTTT  CTCCAGGTC
                      C  _   GA        I
GAM478 FSTL1          GAG-GAAACTGAGGTCCAGA     7585 TGAGAGA   AA
                          GAAA  GAGGTCCAGA
                          ||||  ||||||||||
                          CTTT  CTCCAGGTCT
                      _____      GA
GAM478 HSPA2          GAGAGAGAAAGGCAAAGAGGT    7587        ____    IIIA
                          GAGAGAGAAA  AAGAGG
                          ||||||||||  ||||||
                          CTCTCTCTTT  TTCTCC
                          CCGT    AIII
GAM478 HSPA2          GAGAGAGAAAGGCAAAGAGGT    7587 T__     AA      CCAGAG
                          GAGAGAG  AAAGAGGT
                          |||||||  ||||||||
                          CTCTTTC  TTTCTCCA
                      TCT      CG     AIIIGA
GAM478 IL18R1         GAGGGAGAAAAAGAATAGCTCCA  7589 AGA        ___G  I
                          GAGAAAAAGA  G TCC
                          ||||||||||  | |||
                          CTCTTTTTCT  C AGG
                          ___       TAT G  I
GAM478 IL18R1         GAGGGAGAAAAAGAATAGCTCCA  7589 TG  A      ___G  GAGI
                          AG GAGAAAAAGA  G TCCA
                          || ||||||||||  | |||
                          TC CTCTTTTTCT  C AGGT
                          __  C      TAT G  AIII
GAM478 KCND2          AGTGAGAAAC-GTGGTCCAGAG   7584 GA_    AAGA     I
                          GAGAAA  GGTCCAGA
                          ||||||  ||||||||
                          CTCTTT  CCAGGTCT
                      TCA     GCA_      I
GAM478 KCND2          AGTGAGAAAC-GTGGTCCAGAG   7584 TGAGA    AAGA
                          GAGAAA  GGTCCAGAG
                          ||||||  |||||||||
                          CTCTTT  CCAGGTCTC
                      A____     GCA_
GAM478 LYZ            TGAGAGAGACAAAATGAGCTGAAGA 7594    G   A  GTCCAGI
                          GAGAGA AAAA GAG
                          |||||| |||| |||
                          CTCTCT TTTT CTC
                           G   A  GACTTCI
GAM478 LYZ            TGAGAGAGACAAAATGAGCTGAAGA 7594         _  _  GTCC  GII
                          TGAGAGAGA AAAA GAG   AGA
                          ||||||||| |||| |||   |||
                          ACTCTCTCT TTTT CTC   TCT
                           G   A  GACT  III
GAM478 NDP           TGAGAGCTAGAAAGAGGTCC       7599     AGAA      AGA
                          TGAGAG  AAAGAGGTCC
                          ||||||  ||||||||||
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                        ACTCTC   TTTCTCCAGG
                         GATC         III
GAM478 NDP              TGAGAGCTAGAAAGAGGTCC    7599    AGAA      I
                        GAGAG   AAAGAGGTC
                        IIIII  IIIIIIIII
                        CTCTC   TTTCTCCAG
                         GATC        I
GAM478 PLSCR1          GAGCGAGACAA---GGTCCAGAG   7593   A   AAAA       I
                        GAG GAGA   GAGGTCCAG
                        III IIII  IIIIIIIII
                        CTC CTCT   TTCCAGGTC
                          G   G___      T
GAM478 PLSCR1          GAGCGAGACAA---GGTCCAGAG   7593 TG  A   AAAA
                         AG GAGA   GAGGTCCAGA
                         II IIII  IIIIIIIIII
                         TC CTCT   TTCCAGGTCT
                         __  G   G___
GAM478 SERPINA5         AGAGGGAAACTGAGGTCCAGAG   7583   A  AA         I
                        GAG GAAA  GAGGTCCAGA
                        III IIII  IIIIIIIII
                        CTC CTTT  CTCCAGGTCT
                          C   GA       I
GAM478 SERPINA5         AGAGGGAAACTGAGGTCCAGAG    7583 TGAG  A   AA
                         AG GAAA  GAGGTCCAGAG
                         II IIII  IIIIIIIIII
                         TC CTTT  CTCCAGGTCTC
                         ____  C   GA
GAM478 SFRS2IP         GAGAGAGAAAA--TGGTCAAG    7592         AGA   CI
                        GAGAGAGAAAA  GGTC
                        IIIIIIIIII  IIII
                        CTCTCTCTTTT  CCAG
                           A__  TT
GAM478 SFRS2IP         GAGAGAGAAAA--TGGTCAAG    7592 TG       AGA   C A
                         AGAGAGAAAA  GGTC AG
                         IIIIIIIIII  IIII II
                         TCTCTCTTTT  CCAG TC
                          __       A__  T A
GAM478 SH3BP4         AGGGAGTGAAAGAGGTCCA      7582  A  AA        II
                        AG GAG  AAAGAGGTCC
                        II III  IIIIIIIIII
                        TC CTC  TTTCTCCAGG
                          C  AC       TI
GAM478 SH3BP4         AGGGAGTGAAAGAGGTCCA      7582 TGAGA  AA        A
                         GAG  AAAGAGGTCCAG
                         III IIIIIIIIIIII
                         CTC  TTTCTCCAGGTT
                         C____  AC        G
GAM478 SIRT6         GAGAGAAAAAGA-ATCCACAG      7586          G  GI
                        AGAGAAAAAGAG TCCA
                        IIIIIIIIIIII IIII
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                          TCTCTTTTTCTT AGGT
                             _     GT
GAM478  SIRT6        GAGAGAAAAAGA-ATCCACAG    7586 TGAGAG      G  G
                          AGAAAAAGAG TCCA A
                          |||||||||| |||| |
                          TCTTTTTCTT AGGT T
                           _____    _  G
GAM478  SOX10        TGAGAGAGAAAACAGGAGTC    7596        _ AG  CAGA
                          TGAGAGAGAAAA AG  GTC
                          ||||||||||| || |||
                          ACTCTCTCTTTT TC  CAG
                              G CT  IIIG
GAM478  SOX10        TGAGAGAGAAAACAGGAGTC    7596        AG  TII
                          TGAGAGAGAAAA  AGG
                          ||||||||||| |||
                          ACTCTCTCTTTT  TCC
                              G_    TCA
GAM478  TG           AGAGAAAAAGATGACCATAG    7580        GGT  GAI
                          GAGAAAAAGA  CCA
                          |||||||||| |||
                          CTCTTTTTCT  GGT
                              ACT    ATI
GAM478  TIMM17B      TGAGAGAGAAAAAGGGGACC    7598        A T AGA
                          TGAGAGAGAAAAAG GG CC
                          ||||||||||||| || ||
                          ACTCTCTCTTTTTC CC GG
                              C T  III
GAM478  TIMM17B      TGAGAGAGAAAAAGGGGACC    7598        A TCI
                          GAGAGAGAAAAAG GG
                          ||||||||||||| ||
                          CTCTCTCTTTTTC CC
                             _ CTG
GAM478  WNT10B       AGAAGGAAAAAGAGGCTCCAAGAG  7581 A       _    AI
                          AG GAAAAAGAGG TCCAG
                          || |||||||||| |||||
                          TC CTTTTTCTCC AGGTT
                           _    G   CI
GAM478  WNT10B       AGAAGGAAAAAGAGGCTCCAAGAG  7581 TGA  A     _  _  I
                          GAG GAAAAAGAGG TCCA GAG
                          ||| |||||||||| |||| |||
                          TTC CTTTTTCTCC AGGT CTC
                           ___  _    G  T  A
GAM479  CALM1        GCGGGGGTACCT-CCG-ATGC    7610 TAGC     GTGG  C
                          GGGGGTAC   CG ATGC
                          ||||||||   || ||||
                          CCCCCATG   GC TACG
                           ____    GAG_  _
GAM479  CBFA2T2      GGGCGTG-GTGGCGCATGC    7611 TAGCGGGGGTAC
                          GTGGCGCATG
                          ||||||||||
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                              CACCGCGTAC
                     CAC_____
GAM479 DMD           TGCTGCTTCCCAAACTTAGAAA    7619 GT    _ G        CC
                     GCTGTT T CAAACTTAGGAA
                     |||||| | |||||||||||
                     CGACGA G GTTTGAATCTTT
                        __      A G        TI
GAM479 DMP1          GTGCT-TTTGCAAACTAAG    7612   G      T GAA
                     GTGCT TTTGCAAACT AG
                     ||||| |||||||||| ||
                     CACGA AAACGTTTGA TC
                        _          T III
GAM479 GATA6         TGCAGTCTTGCAAACTGAGTAA    7618 GT TG_       T GAACC
                     GC  TTTGCAAACT AG
                     ||  |||||||||| ||
                     CG  GAACGTTTGA TC
                        __ TCA       C ATTAI
GAM479 GDF2          TGCTGTTTGC--TCTGAAGGAACC  7620 GT      AAACTT
                     GCTGTTTGC    AGGAACC
                     |||||||||    |||||||
                     CGACAAACG    TCCTTGG
                        __          AGACT_
GAM479 GOT2          GTGCTGTTT-CTCAC-GAGGAACC  7614       G_ AACTT
                     GTGCTGTTT CA    AGGAACC
                     ||||||||| ||    |||||||
                     CACGACAAA GT    TCCTTGG
                        GA GC___
GAM479 HCS           AGCTGGGCATGGTGGCGCATGC    7606 TA GG   C_       G
                     GC GGGTA GTGGCGCATGC
                     || ||||| |||||||||||
                     CG CCCGT CACCGCGTACG
                        __ A_    AC        G
GAM479 LTB4R         GTGCTGTTTGCTAAATCAG       7613        A C  GAAC
                     GTGCTGTTTGC AA TTAG
                     ||||||||||| || ||||
                     CACGACAAACG TT AGTC
                         A T   IIIC
GAM479 MCM4          TAGCTGGGATTACA-GGCGCATGC  7616  _ GG   T       GI
                     TAGC GGG  TACG GGCGCATGC
                     |||| |||  |||| |||||||||
                     ATCG CCC  ATGT CCGCGTACG
                         A TA  _       II
GAM479 MYBPH         AGCGGGGGT-CTTGG-GCAT      7605 TA     ACG  C  G
                     GCGGGGGT  TGG GCAT
                     ||||||||  ||| ||||
                     CGCCCCCA  ACC CGTA
                        __     GA_ _ G
GAM479 NCOA6         TAGCAGGGCATGGTGGCGCATGC   7617       GTAC       GI
                     TAGCGGGG  GTGGCGCATGC
                     ||||||||  |||||||||||
```

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                         ATCGTCCC   CACCGCGTACG
                           GTAC          II
GAM479  PTGIS            GCTGGAGTGCCGTGGCGCA    7609 TAGCG   A_       TGC
                           GGGGT CGTGGCGCA
                           IIIII IIIIIIIII
                           CCTCA GCACCGCGT
                           A____   CG     CAI
GAM479  PTPN2            CGGGGAGAGCGCTGGCGC-TGCG   7607 TAGCG  TA _    A
                           GGGG CG TGGCGC TGCG
                           IIII II IIIIII IIII
                           CCTC GC ACCGCG ACGC
                           _____   TC G    _
GAM479  PTPN2            AGCGCTGGCGCTGCGGCGCATGCG  7604 TA G G AC         I
                           GC GG GT GTGGCGCATGCG
                           II II II IIIIIIIIIIII
                           CG CC CG CGCCGCGTACGC
                           CG A G A_      G
GAM479  RP2              TAGCCAGGTGTA-GTGGCGCATGC   7615 G _ C      GI
                           TAGC GGG GTA GTGGCGCATGC
                           IIII III III IIIIIIIIII
                           ATCG TCC CAT CACCGCGTACG
                            G  A  _       II
GAM479  SORCS1           TGCTGTTTG-GAACTTCTGAA    7621 GT   CA   AG  C
                           GCTGTTTG AACTT GAA
                           IIIIIIII IIIII III
                           CGACAAAC TTGAA CTT
                            __     C_   GA  T
GAM479  SPON1            CTGATTTGCAAACTT--GAAC    7608 GTGCT        AG
                           GTTTGCAAACTT GAAC
                           IIIIIIIIIIII IIII
                           TAAACGTTTGAA CTTG
                           _____      __
GAM480  DMD              GCTGCCCAATGCCATCCTG     7626 GG     GGAAG_  CATA
                           CTGCCCAA    CCTG
                           IIIIIIII    IIII
                           GACGGGTT    GGAC
                           __      ACGGTA  CIII
GAM480  EIF2B5           CTTCCGCAAGGAAG-CTGC    7624 GGCTG _     C  AT
                           CC CAAGGAAGC TGC
                           II IIIIIIIII III
                           GG GTTCCTTCG ACG
                           A____  C    _  GT
GAM480  MBNL             GGCTTTGCAAGGAAGCCGGCA   7627   GCC     T TAG
                           GGCT CAAGGAAGCC GCA
                           IIII IIIIIIIIII III
                           CCGA GTTCCTTCGG CGT
                            AAC      C  III
GAM480  ROM1             CTGCCCAAGGGAG--TGCAGAG   7625 GGCT    A CC  TA
                           GCCCAAGG AG TGCA
                           IIIIIIII II IIII
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                              CGGGTTCC TC  ACGT
                       ____        C __    CT
GAM481  AMD1           AAAGGACTAATAAAATTTTC    7630 TAGCAAAG    GAT_
                              GACTAA   ATTTTC
                              ||||||   ||||||
                              CTGATT   TAAAAG
                       _____         ATTT
GAM481  BAT1           AGCAAAGGAAAACAAAGATACTATTTCT7631 TA      CT___    __    III
                              GCAAAGGA    AAGATAT TTTCT
                              ||||||||    |||||||  |||||
                              CGTTCCT    TTCTATG AAAGA
                         __       TTTGT     AT  TII
GAM481  GLRA3           AGCAAAGG---AAGA-ATGTTC   7632 TA      CTA  TATT
                              GCAAAGGA  AGA    TT
                              ||||||||  |||    ||
                              CGTTTCCT  TCT    AA
                         __       ____  TAC_
GAM481  KCNMB3          AGCAAAGGA-TGAGATACATTCT   7633 TA      CTA    T
                              GCAAAGGA   AGATAT TTCT
                              ||||||||   |||||| ||||
                              CGTTTCCT   TCTATG AAGA
                         __      AC_     T
GAM482  IFNW1           TAGAA--GCAAAATTTTAAC   7636   AT G       AT
                              TAGA  AG AAAATTTTAAC
                              ||||  || |||||||||||
                              ATCT  TC TTTTAAAATTG
                         __     G       II
GAM483  ALPL            CCTCTGGGTCTGGAGAAATA     7640  G      TGCTATI
                              CT TGGGTCTGG
                              || ||||||||||
                              GA ACCCAGACC
                               G      TCTTTAI
GAM483  ATRN           CTGTGGGTCATGGTGCATGATAT   7643 TGT   _    TATAI
                              GGGTC TGGTGC
                              ||||| |||||||
                              CCCAG ACCACG
                              ___    T    TACTA
GAM483  CYP8B1         CTCCCATGTGGGTCTGGGGATA   7641 T _       TGCTI
                              CC TGTGGGTCTGG
                              || ||||||||||||
                              GG ACACCCAGACC
                              _ T        CCTAI
GAM483  HPCA           CTCC-GTGGGTCTGTGTG-TAT   7642 TC       _  CTI
                              CTGTGGGTCTG GTG
                              |||||||||||| |||
                              GGCACCCAGAC CAC
                              A_      A ATI
GAM483  KCNA7          TCCTTTGGGTCCTGGTGCTA     7646  G    _    II
                              TCCT TGGGTC TGGTGCT
                              |||| |||||| |||||||
```

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                    AGGA ACCCAG ACCACGA
                      A      G      TI
GAM483 MHC2TA        TCCTGTGGGCACTGGGGCT    7645        _   T II
                     TCCTGTGGGT CTGG GC
                     |||||||||| |||| ||
                     AGGACACCCG GACC CG
                         T   C  AI
GAM483 TGM4          TGTGGGTCTGGCTGCT-TAT    7648        _  ATAII
                     TGTGGGTCTGG TGCT
                     |||||||||| ||||
                     ACACCCAGACC ACGA
                         G   ATAII
GAM483 TRO          CCTGTGGGTCCTG--GCTAT    7639        GGT  I
                    CCTGTGGGTCT  GCTA
                    ||||||||||   ||||
                    GGACACCCAGG  CGAT
                        AC_   A
GAM483 VASP         TCCTGTGGGGTTCATTGGTGC   7644       __  __    IIIG
                    TCCTGTGGG TC TGGTG
                    ||||||||| || |||||
                    AGGACACCC AG ACCAC
                        CA  TA     GIII
GAM483 WHSC1        TCTCCTGTGTTTCTCGGGCT    7647      GG _ T  I
                    CTCCTGTG TCT GG GC
                    |||||||| ||| || ||
                    GAGGACAC AGA CC CG
                        AA   G  _  I
GAM484 COLQ         GGGAGCCAGCCAAGGCTGTCCT    7658 GA   A  T_     I
                     AGCCA CC GGCTGTCC
                     ||||| || |||||||||
                     TCGGT GG CCGACAGG
                     C_    C TT      I
GAM484 COLQ         GGGAGCCAGCCAAGGCTGTCCT    7658 T A   A  T_     GA
                     GGA GCCA CC GGCTGTCCT
                     ||| |||| || |||||||||
                     CCT CGGT GG CCGACAGGA
                     _  _   C TT      AI
GAM484 FCN2         GGAGGCCAACCT-GTTCTCCT    7661 _  A      GCTG  I
                     GA GCCAACCTG  TCC
                     || ||||||||   |||
                     CT CGGTTGGAC  AGG
                     C C       AAG_  I
GAM484 FCN2         GGAGGCCAACCT-GTTCTCCT    7661 TG  A      GCTG   G
                     GA GCCAACCTG   TCCT
                     || ||||||||    ||||
                     CT CGGTTGGAC   AGGA
                     __  C      AAG_  G
GAM484 GAS7         GCCAACCTGAGCTACCCTG     7655         _  GT  II
                    GCCAACCTG GCT CCT
                    ||||||||| ||| |||
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                         CGGTTGGAC CGA  GGA
                             T  TG  CI
GAM484  GJB1         GCCACACCTGGCTGCTGCTG    7654    _        CCTIII
                        GCCA ACCTGGCTGT
                        IIII IIIIIIIIII
                        CGGT TGGACCGACG
                           G      ACGACI
GAM484  HLCS         GGAAGCC---CTGGCTGTCC    7660    AAC     I
                        GGAAGCC CTGGCTGT
                        IIIIIII IIIIIIII
                        CCTTCGG GACCGACA
                            ___       G
GAM484  HLCS         GGAAGCC---CTGGCTGTCC    7660 TG    AAC
                         GAAGCC CTGGCTGTCCT
                         IIIIII IIIIIIIIII
                         CTTCGG GACCGACAGGG
                           __     ___
GAM484  MEN1          GCCAACCTGGGCATACTGA    7656      CT C  II
                        GCCAACCTGG GT CTG
                        IIIIIIIIII II III
                        CGGTTGGACC TA GAC
                           CG T  TI
GAM484  OTX1         GGCAGCCAACCT---TGTC     7659  A     GGCTGT
                         GG AGCCAACCT
                         II IIIIIIIII
                         CC TCGGTTGGA
                           G     ACAGII
GAM484  OTX1         GGCAGCCAACCT---TGTC     7659 TGGA     GGC  C
                          AGCCAACCT  TGTC
                          IIIIIIIII  IIII
                          TCGGTTGGA  ACAG
                         CG__      ___   C
GAM484  PLXNA1       TGGAAGCCACCCAGG-AGT-CTGA  7666      A TG CT  C
                        TGGAAGCCA CC G GTC TGA
                        IIIIIIIII II I III III
                        ACCTTCGGT GG C CAG ACT
                          _ GT CT  _
GAM484  PLXNA1       TGGAAGCCACCCAGG-AGT-CTGA  7666      A TG CT  CTI
                        TGGAAGCCA CC G GTC
                        IIIIIIIII II I III
                        ACCTTCGGT GG C CAG
                          _ GT CT  ACT
GAM484  PMM2         TGAAAGC--ACCTGGCTGT    7664      CA      CCT
                        TGGAAGC ACCTGGCTGT
                        IIIIIII IIIIIIIIII
                        ACTTTCG TGGACCGACA
                            __          III
GAM484  PMM2         TGAAAGC--ACCTGGCTGT    7664      CA      I
                        TGGAAGC ACCTGGCTG
                        IIIIIII IIIIIIIII
```

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                       ACTTTCG  TGGACCGAC
                          __          A
GAM484  RANBP17        AGCCAACATCACTGTCCTGA    7652    CTG        I
                       GCCAAC  GCTGTCCTG
                       ||||||  |||||||||
                       CGGTTG  TGACAGGAC
                          TAG         I
GAM484  SERPINA4       GCCAGCACCTG-CTGTCCTG    7653    __   G     II
                       GCCA  ACCTG CTGTCCT
                       ||||  ||||| |||||||
                       CGGT  TGGAC GACAGGA
                          CG     _       CI
GAM484  SLC12A7        GGAGGGCAGTCCTGGCTGTCGTG  7657 AA CAA       CI
                       GC  CCTGGCTGTC
                       ||  ||||||||||
                       CG  GGACCGACAG
                          CC  TCA        CI
GAM484  SLC12A7        GGAGGGCAGTCCTGGCTGTCGTG  7657 T_ AA CAA      C AI
                       GG  GC  CCTGGCTGTC TG
                       || ||  |||||||||| ||
                       CC  CG  GGACCGACAG AC
                          CT __  TCA        C CI
GAM484  TCF7           TGAAAGACAGGCTCTGGCTGTCATGA 7663    C AC__      C II
                       TGGAAG CA   CTGGCTGTC TGA
                       |||||| ||   |||||||||| |||
                       ACTTTC GT   GACCGACAG ACT
                          T CCGA         T  II
GAM484  TCF7           TGAAAGACAGGCTCTGGCTGTCATGA 7663   AGCCAAC       CTI
                       GGA      CTGGCTGTC
                       |||      ||||||||||
                       TCT      GACCGACAG
                          GTCCGA_       TAC
GAM484  TK2            TGGAAGCCAGGGCTGGCTGCCC    7662         AC_       TGA
                       TGGAAGCCA  CTGGCTGTCC
                       |||||||||  ||||||||||
                       ACCTTCGGT  GACCGACGGG
                          CCC        III
GAM484  TK2            TGGAAGCCAGGGCTGGCTGCCC    7662 G     AC_       I
                       GAAGCCA  CTGGCTGTC
                       |||||||  ||||||||||
                       CTTCGGT  GACCGACGG
                          _      CCC         I
GAM484  TMEPAI         AGACAACCTGCTGGCTGTCTTG    7651 C      ___        CTIII
                       AG CAACCT  GGCTGTC
                       || ||||||  |||||||
                       TC GTTGGA  CCGACAG
                          T    CGA      AACII
GAM484  TMEPAI         AGACAACCTGCTGGCTGTCTTG    7651 TGGA   AAC        C A
                       AGCC  CTGGCTGTC TG
                       ||||  |||||||||| ||
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                              TTGG  GACCGACAG AC
                              ____      AC_      A C
GAM484 ZNF142        TGGAAGCCACTCTCTCT-TCCT   7665      AC GG G  GA
                     TGGAAGCCA CT CT TCCT
                     |||||||| || || ||||
                     ACCTTCGGT GA GA AGGA
                        GA  GA _   II
GAM484 ZNF142        TGGAAGCCACTCTCTCT-TCCT   7665 _     AC GG G  I
                      GGAAGCCA CT CT TCC
                      |||||||| || || |||
                      CCTTCGGT GA GA AGG
                       A   GA GA _   I
GAM485 ATP7B         TGAAATGCACACTCCAGAGCA   7675      T  CGT  GCA
                     TGAAATGCAC TTCC  GCA
                     |||||||||| ||||   |||
                     ACTTTACGTG GAGG  CGT
                        T   TCT  III
GAM485 BCLG          TGTAACGCACTTTCCC-TACAGCA  7676 A       G    I
                     TG AATGCACTTTCCC TGCAGCA
                     || ||||||||||||| |||||||
                     AC TTGCGTGAAAGGG ATGTCGT
                        A        _    I
GAM485 DIAPH2        GAAATGCACTTATTTCCTTTCCAGC 7674 TG      ___  CGTG  AII
                     AAATGCACTT TCC  CAGC
                     |||||||||| |||  ||||
                     TTTACGTGAA AGG  GTCG
                        __       TAA  AAAG  GII
GAM485 JAG2          AAATGCACTTTCACGAGGAG   7670 TGAA      C TGC C
                     ATGCACTTTC CG  AG
                     |||||||||| ||  ||
                     TACGTGAAAG GC  TC
                     ____       T TCC  C
GAM485 NRIP1         ATGCACTTT-TCATGCAGCA    7672 TGAAATGC   CC
                     ACTTT  CGTGCAGC
                     |||||  ||||||||
                     TGAAA  GTACGTCG
                     _____     A_
GAM485 RIMS2         GAAGATTCAGTA-CCCGTGCAGC  7673 TGAAATG CTTT     A
                       CA  CCCGTGCAGC
                       ||   |||||||||
                       GT  GGGCACGTCG
                     TTCTAA_ CAT_      A
GAM485 UBQLN2        AAAAGCACTTTCCTG-GCA    7669 TGAAAT     CGT  G
                      GCACTTTCC  GCA
                      |||||||||  |||
                      CGTGAAAGG  CGT
                     TT____       AC_  A
GAM485 ZNF131        AATGCACTTTTCATCATGCAGC  7671 TGAAAT    _ C_    A
                      GCACTTT C CGTGCAGC
                      ||||||| | |||||||
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                              CGTGAAA G GTACGTCG
                              _____      A TA    G
GAM486 BCRP2           TGAGAACACC----ACAGCCTC  7688      GTGT   A
                              TGAGAACACC  ACAGC
                              ||||||||||  |||||
                              ACTCTTGTGG  TGTCG
                                  ____      G
GAM486 BCRP2           TGAGAACACC----ACAGCCTC  7688      GTGT   A
                              TGAGAACACC  ACAGC TC
                              ||||||||||  ||||| ||
                              ACTCTTGTGG  TGTCG AG
                                  ___      G
GAM486 FABP2          TGAGAACACGCAGTATTCAGC   7685      _ _  A  III
                              TGAGAACAC C GTGT CAG
                              ||||||||| | |||| |||
                              ACTCTTGTG G CATA GTC
                                  C T   A  GII
GAM486 FABP2          TGAGAACACGCAGTATTCAGC   7685      _ _  A  ATCGG
                              TGAGAACAC C GTGT CAGC
                              ||||||||| | |||| ||||
                              ACTCTTGTG G CATA GTCG
                                  C T   A  IIIGG
GAM486 FOSB          GAGAACCACAAGTACAGCATGGG   7683   AC T     CGI
                              AGAAC CG GTACAGCAT
                              ||||| || |||||||||
                              TCTTG GT CATGTCGTA
                                  GT T     CCI
GAM486 FOSB          GAGAACCACAAGTACAGCATGGG   7683 TG  AC T     C I
                              AGAAC CG GTACAGCAT GG
                              ||||| || ||||||||| ||
                              TCTTG GT CATGTCGTA CC
                                  __   GT T     C C
GAM486 GAD1          TGAGAACACCAGACGTACAGC   7686          __     ATCGG
                              TGAGAACACCG TGTACAGC
                              |||||||||| ||||||||
                              ACTCTTGTGGT GCATGTCG
                                  CT      IIIGG
GAM486 GAD1          TGAGAACACCAGACGTACAGC   7686          __     III
                              TGAGAACACCG TGTACAG
                              |||||||||| |||||||
                              ACTCTTGTGGT GCATGTC
                                  CT      GII
GAM486 HEPH          TGAGGCACGCTGGGT-CAGCATCGG 7684   AA  C ___ A     I
                              TGAG CAC GT  GT CAGCATCGG
                              |||| ||| ||  || |||||||||
                              ACTC GTG CG  CA GTCGTAGCC
                                  C_ _ ACC _     I
GAM486 HEPH          TGAGGCACGCTGGGT-CAGCATCGG 7684   AA  C ___ A     I
                              GAG CAC GT  GT CAGCATCG
                              ||| ||| ||  || |||||||||
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                              CTC  GTG CG   CA GTCGTAGC
                              C_  _ ACC _      I
GAM486  INMT              AGAGCCCC-TGTACAGCAT       7679  ACA  G       I
                              AGA   CC TGTACAGCA
                              |||   || |||||||||
                              TCT   GG ACATGTCGT
                              CG_  G       A
GAM486  INMT              AGAGCCCC-TGTACAGCAT       7679 TGAGAACA  G       C
                                 CC TGTACAGCAT
                                 || ||||||||||
                                 GG ACATGTCGTA
                              TCG_____  G      A
GAM486  ITSN1            GAGAACACCATCTAGTACAG        7680          ___      III
                              GAGAACACCGT  GTACA
                              ||||||||||  |||||
                              CTCTTGTGGTA  CATGT
                                GAT    CII
GAM486  ITSN1            GAGAACACCATCTAGTACAG        7680 TG       ___      CATCG
                              AGAACACCGT  GTACAG
                              |||||||||  ||||||
                              TCTTGTGGTA  CATGTC
                                __         GAT      CIIIG
GAM486  KCNJ15           TGAGAACACTGTCCAGAGCA        7687       C  G  C   TCG
                              TGAGAACAC GT TA AGCA
                              ||||||||| || || ||||
                              ACTCTTGTG CA GT TCGT
                                A G  C   III
GAM486  KCNJ15           TGAGAACACTGTCCAGAGCA        7687       C  G  C  I
                              GAGAACAC GT TA AGC
                              |||||||| || || |||
                              CTCTTGTG CA GT TCG
                                A G  C  I
GAM486  RBM8A            GAGAACACC-TGGACAACA        7681         G  T   I
                              GAGAACACC TG ACAGC
                              ||||||||| || |||||
                              CTCTTGTGG AC TGTTG
                               _  C   T
GAM486  RBM8A            GAGAACACC-TGGACAACA        7681 TG      G  T   TC
                              AGAACACC TG ACAGCA
                              |||||||| || ||||||
                              TCTTGTGG AC TGTTGT
                               __    _ C   CI
GAM486  SCAMP1            GAGTACA---TGTACAGCA        7682 GAGAACAC
                                 CGTGTACAGC
                                 ||||||||||
                                 GTACATGTCG
                              CTCAT___
GAM486  SCAMP1            GAGTACA---TGTACAGCA        7682 TGAGAACAC        T
                                 CGTGTACAGCA
                                 |||||||||||
```

```
                              GTACATGTCGT
                       TCAT_____           T
GAM487 ACCN2           TGCGCGTGTCGTCTCCTTGTG    7696 _ TT  C _      I
                           GC GTG CG CTCCTTGT
                           || ||| || |||||||
                           CG CAC GC GAGGAACA
                           G __  A A       I
GAM487 ACCN2           TGCGCGTGTCGTCTCCTTGTG    7696 TGGTGCTT  C _      G
                              GTG CG CTCCTTGTG
                              ||| || |||||||||
                              CAC GC GAGGAACAC
                       CG_____ A A       G
GAM487 BCL7A           TGGTGCTTGGGGCGTGCCT      7701       T_ C_ T____ TTGT
                       TGGTGCTTG GC GC   CC  G
                       ||||||||| || ||   ||  |
                       ACCACGAAC CG CG   GG  C
                           CC  CA GA||| TGTT
GAM487 BCL7A           TGGTGCTTGGGGCGTGCCT      7701       _____   GCTCC||
                       TGGTGCTT   GTGCC
                       ||||||||   |||||
                       ACCACGAA   CACGG
                           CCCCG   A|||CCT
GAM487 DDX19           CTTGTGCCGTTGTCCTTGGGG    7692       C__    TG|||
                       CTTGTGCCG  TCCTTG
                       |||||||||  ||||||
                       GAACACGGC  AGGAAC
                           AAC    CCC||
GAM487 GALR1           TGTTGCTCGGAGCCGCTCCTT    7698 G    T_       GTGG
                       TG TGCTTG GCCGCTCCTT
                       || |||||| ||||||||||
                       AC ACGAGC CGGCGAGGAA
                          A   CT    |||G
GAM487 GALR1           TGTTGCTCGGAGCCGCTCCTT    7698 GG    T_      I
                         TGCTTG GCCGCTCCT
                         |||||| |||||||||
                         ACGAGC CGGCGAGGA
                         A_    CT    I
GAM487 GPR86           TGGTGCTTGTGC--CTCCT      7702           G CC|
                       TGGTGCTTGTGCC CT
                       |||||||||||| ||
                       ACCACGAACACGG GG
                             A A||
GAM487 GPR86           TGGTGCTTGTGC--CTCCT      7702           GC  TGT
                       TGGTGCTTGTGCC TCCT
                       |||||||||||| ||||
                       ACCACGAACACGG AGGA
                             __  |||
GAM487 IL19           TGGTGCTTGCGGGCTGCTCCTTGTG 7699         __ C     G||
                       TGGTGCTTGT GC GCTCCTTGTG
                       |||||||||| || |||||||||
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```
                        ACCACGAACG CG CGAGGAACAC
                           CC  A          III
GAM487 IL19             TGGTGCTTGCGGGCTGCTCCTTGTG 7699 GG      __   C      I
                        TGCTTGT GC GCTCCTTGT
                        IIIIIII II IIIIIIIII
                        ACGAACG CG CGAGGAACA
                           __   CC  A      I
GAM487 LNK             TGGTGCTTGTAATCCCAGCTACTTG 7697          ___ _  C  TGGII
                        TGGTGCTTGTG  CC GCT CTTG
                        IIIIIIIIII  II III IIII
                        ACCACGAACAT  GG CGA GAAC
                           TAG  T  T  IIIGG
GAM487 M11S1           CTTGCTGCCGCTCCCGCTGTGG   7691 _        __     III
                        CTTG TGCCGCTCCT TGTG
                        IIII IIIIIIIIII IIII
                        GAAC ACGGCGAGGG ACAC
                          G     CG   CII
GAM487 MAN2A2            GTGCAGG-GCCAGCTCCTTGT    7694  TTGT _      I
                        TGC   GCC GCTCCTTG
                        III   III IIIIIIIII
                        ACG   CGG CGAGGAAC
                         TCC_  T       I
GAM487 MAN2A2            GTGCAGG-GCCAGCTCCTTGT    7694 TGGT TTGT _      G
                          GC   GCC GCTCCTTGT
                          II   III IIIIIIIII
                          CG   CGG CGAGGAACA
                        ____  TCC_  T         A
GAM487 MBNL          TGGAACTTGT-CAGCTCCTTGT   7703  T    GCC        GG
                        TGG GCTTGT  GCTCCTTGT
                        III IIIIII  IIIIIIIII
                        ACC TGAACA  CGAGGAACA
                         T   GT_      II
GAM487 MBNL          TGGAACTTGT-CAGCTCCTTGT   7703 _ T    GCC      I
                         GG GCTTGT  GCTCCTTG
                         II IIIIII  IIIIIIII
                         CC TGAACA  CGAGGAAC
                         A T   GT_     I
GAM487 MYO1C            TGATGCCCCTGCCGCTCCT     7700       G      TGTG
                        TGGTGCTT TGCCGCTCCT
                        IIIIIIII IIIIIIIIII
                        ACTACGGG ACGGCGAGGA
                           G      IIIG
GAM487 MYO1C            TGATGCCCCTGCCGCTCCT     7700       G      II
                        TGGTGCTT TGCCGCTCC
                        IIIIIIII IIIIIIIII
                        ACTACGGG ACGGCGAGG
                           G      AI
GAM487 SPTBN2         TGCTCCTGTGCTCCGCTCTCCTTGTGG7695 __   G  CG        I
                        GCTT TGC CTCCTTGTG
                        IIII III IIIIIIIII
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                              CGAG GCG  GAGGAACAC
                              CA   _  A_      I
GAM487  SPTBN2       TGCTCCTGTGCTCCGCTCTCCTTGTGG7695 TG__    G  CG       III
                        GTGCTT TGC CTCCTTGTGG
                        ||||||| ||| ||||||||||
                        CACGAG GCG  GAGGAACACC
                        AGGA    _  A_      GGT
GAM487  TCF7         GTGCTTGTGACCATGCTCACATGT 7693   C TG  _   TCCTTI
                        GTG T TGC CGC
                        ||| | ||| |||
                        CAC G ACG GTG
                         T GT  A  TACAII
GAM487  TCF7         GTGCTTGTGACCATGCTCACATGT 7693 TGGT     _ __   CT_  GGI
                        GCTTGTG CC GCTC  TGT
                        ||||||| || |||| |||
                        CGAACAC GG CGAG  ACA
                        ____      T TA  TGT ACI
GAM488  CDH10         GACATGTACCTAACA-GAAGCG  7718 A    __      ACCI
                        CATGTAC AACAGGA
                        ||||||| |||||||
                        GTACATG TTGTCTT
                         _   GA    CGII
GAM488  CDH10         GACATGTACCTAACA-GAAGCG  7718 AG      __      ACC  T
                        ACATGTAC AACAGGA  GTG
                        |||||||| ||||||| |||
                        TGTACATG TTGTCTT  CGC
                        __    GA    ___   C
GAM488  CYP1B1     AGAC--GT-CAACAGGAACC    7712  AT A       GT
                        AGAC GT CAACAGGAACC
                        |||| || |||||||||||
                        TCTG CA GTTGTCCTTGG
                         __ _       II
GAM488  CYP1B1     AGAC--GT-CAACAGGAACC    7712 _ AT A
                        GAC GT CAACAGGAAC
                        ||| || |||||||||||
                        CTG CA GTTGTCCTTG
                        T __ _
GAM488  DCTN1     AGACTTGT----CAGGAACCGTG  7716   A ACAA
                        AGAC TGT   CAGGAACCGTG
                        |||| |||   ||||||||||||
                        TCTG ACA   GTCCTTGGCAC
                         A ____
GAM488  DCTN1     AGACTTGT----CAGGAACCGTG  7716 _ A ACAA
                        GAC TGT   CAGGAACCGT
                        ||| |||   |||||||||||
                        CTG ACA   GTCCTTGGCA
                        T A ____
GAM488  DIA1     AGAC-TGTACA---GGAACC    7713  A ACA       G
                        AGAC TGT  ACAGGAACC
                        |||| |||  ||||||||||
```

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                        TCTG ACA  TGTCCTTGG
                          _  ___           I
GAM488 DIA1         AGAC-TGTACA---GGAACC    7713 _  A  ACA
                           GAC TGT  ACAGGAAC
                           ||| |||  ||||||||
                           CTG ACA  TGTCCTTG
                           T   _  ___
GAM488 FUT8         AGAAACGGA-AACAGGAACCG    7714   C  TAC      TG
                           AGA ATG  AACAGGAACCG
                           ||| |||  |||||||||||
                           TCT TGC  TTGTCCTTGGC
                            T  CT_       II
GAM488 FUT8         AGAAACGGA-AACAGGAACCG    7714 _  C  TAC       I
                            GA ATG  AACAGGAACC
                            || |||  ||||||||||
                            CT TGC  TTGTCCTTGG
                            T  T CT_       I
GAM488 GOCAP1       ACATGAACACATGACAGGAACCG  7706 AG____   TACA      GTI
                           ACATG  ACAGGAACCGT
                           |||||  ||||||||||||
                           TGTAC  TGTCCTTGGCG
                           TACTTG  ____       AII
GAM488 GOCAP1       ACATGAACACATGACAGGAACCG  7706   T  ____       IIIC
                           ACATG ACA  ACAGGAACC
                           ||||| |||  |||||||||
                           TGTAC TGT  TGTCCTTGG
                            T  GTAC       CIII
GAM488 GRLF1        AGACA-GACCAACAGGAA--GTGT  7717    TGTA      CC
                           AGACA  CAACAGGAA GTGT
                           |||||  ||||||||| ||||
                           TCTGT  GTTGTCCTT CACA
                            CTG_        __
GAM488 GRLF1        AGACA-GACCAACAGGAA--GTGT  7717    TGTA      CCGI
                           AGACA  CAACAGGAA
                           |||||  |||||||||
                           TCTGT  GTTGTCCTT
                            CTG_       CACA
GAM488 IL17R        AGACATGTACACACAGATGAATACGTG7711         _  __  C_  TIII
                           AGACATGTACA ACAG GAA CGTG
                           ||||||||||| |||| ||| ||||
                           TCTGTACATGT TGTC CTT GCAC
                            G  TA  AT  IIIT
GAM488 IL17R        AGACATGTACACACAGATGAATACGTG7711 A    _    AACCGTI
                           TGTACA ACAGG
                           |||||| |||||
                           ACATGT TGTCT
                           _   G  ACTTATI
GAM488 PIGA         AGA-ATGCATACAACAGGAAC    7710   C  __       CGTG
                           AGA ATGT ACAACAGGAAC
                           ||| |||| |||||||||||
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                          TCT TACG  TGTTGTCCTTG
                           _  TA        IIIT
GAM488  PIGA          AGA-ATGCATACAACAGGAAC   7710  C  __        II
                      AGA ATGT  ACAACAGGAA
                      III IIII  IIIIIIIIII
                      TCT TACG  TGTTGTCCTT
                       _  TA        GI
GAM488  PTPRF         AGACTGTGTACAACAGTGAAC   7709  A_      _   CGTGT
                      AGAC  TGTACAACAG GAAC
                      IIII  IIIIIIIIII IIII
                      TCTG  ACATGTTGTC CTTG
                        AC        A   IIITG
GAM488  PTPRF         AGACTGTGTACAACAGTGAAC   7709  A_      _   III
                      AGAC  TGTACAACAG GAA
                      IIII  IIIIIIIIII III
                      TCTG  ACATGTTGTC CTT
                        AC        A   GII
GAM488  RET          AGGCATG--CAAAAGGAACCGT   7715  A   CAAC      G
                      AG CATGTA  AGGAACCGT
                      II IIIIII   IIIIIIIII
                      TC GTACGT   TCCTTGGCA
                       C   TT__     I
GAM488  RET          AGGCATG--CAAAAGGAACCGT   7715 GA_   CAAC   I
                         CATGTA  AGGAACCG
                          IIIIII   IIIIIIII
                         GTACGT   TCCTTGGC
                      TCC   TT__    I
GAM488  WHSC1        ACATGTAC-ACAGACACTGTGT   7707 _      A GA C  I
                      CATGTACA CAG AC GTG
                      IIIIIIII III II III
                      GTACATGT GTC TG CAC
                      T     _  TG A  I
GAM488  WHSC1        ACATGTAC-ACAGACACTGTGT   7707 AGAC    A GA  C
                      ATGTACA CAG AC GTGT
                      IIIIIII III II IIII
                      TACATGT GTC TG CACA
                      ____      _  TG  A
GAM488  XRCC5        ACATGTACAA----AACTGTGT   7708 _      ACAG   C
                      CATGTACA  GAAC GTG
                      IIIIIIII   IIII III
                      GTACATGT   TTTG CAC
                      T     ____   A
GAM488  XRCC5        ACATGTACAA----AACTGTGT   7708 AGAC    ACAG   C
                      ATGTACA   GAAC GT
                      IIIIIII    IIII II
                      TACATGT   TTTG CA
                      ____      ____   A
GAM489  AKAP2        CACACAGGCAGGGGAAAGAGGA   7724 AC   TCA      I
                      CAGGT  GGAAAGAGG
                      IIIII  IIIIIIIII
```

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                              GTCCG  CCTTTCTCC
                            GT    TCC        I
GAM489  AKAP2        CACACAGGCAGGGGAAAGAGGA   7724 TGACAC    TCA
                            CAGGT  GGAAAGAGGA
                            |||||  |||||||||
                            GTCCG  CCTTTCTCCT
                            T_____    TCC
GAM489  AMD1         GACACCAGGGAGAGGGAAGA    7730      TTCA_  AGI
                            ACACCAGG   GGAA
                            ||||||||   ||||
                            TGTGGTCC   CCTT
                            CTCTC  CII
GAM489  AMD1         GACACCAGGGAGAGGGAAGA    7730 TG      TTC A   G
                            ACACCAGG  AGG AAGAG
                            ||||||||  ||| |||||
                            TGTGGTCC  TCC TTCTT
                            __      CTC  C   I
GAM489  ARHC        CCAGAT-CGGGAAAGAGGA    7727     CA       I
                            CCAGGTT GGAAAGAGG
                            ||||||| |||||||||
                            GGTCTAG CCTTTCTCC
                              C_      T
GAM489  CNGB3        GACATCA---TCAGGAAAGA    7731 ACAC GGT
                              CA  TCAGGAAAG
                              ||  |||||||||
                              GT  AGTCCTTTC
                            CT__  AGT
GAM489  CNGB3        GACATCA---TCAGGAAAGA    7731 TGACAC GGT
                              CA  TCAGGAAAGAG
                              ||  |||||||||||
                              GT  AGTCCTTTCTT
                            T_____  AGT
GAM489  FMOD        ACCCCACCTACAGGAAAGAAGA   7723 ___  AGGTT        I
                            CACC   CAGGAAAGAGG
                            ||||   |||||||||||
                            GTGG   GTCCTTTCTTC
                            GGG  AT___        I
GAM489  FMOD        ACCCCACCTACAGGAAAGAAGA   7723 TGA  AGGTT
                            CACC   CAGGAAAGAGGA
                            ||||   ||||||||||||
                            GTGG   GTCCTTTCTTCT
                            GG_  AT___
GAM489  GLRA3       CAACAG---CCGGAAAGAGGA    7725 AC_  GTTCA
                            CAG   GGAAAGAGG
                            |||   |||||||||
                            GTC   CCTTTCTCC
                            GTT  GG___
GAM489  GLRA3       CAACAG---CCGGAAAGAGGA    7725 TGACACCA   CA
                            GGTT  GGAAAGAG
                            ||||  ||||||||
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                         TCGG  CCTTTCTC
                       G_____  __
GAM489 HAP1            CCAGGTTCATGAACACAGAGG   7726      G  ___   III
                        CCAGGTTCA GAA  AGAG
                        |||||||| ||| ||||
                        GGTCCAAGT CTT  TCTC
                          A  GTG   CII
GAM489 KCNA7           TGACAGGCCTGGTTCAGGA    7733   __ A      AAGAGG
                        TGACA CC GGTTCAGGA
                        ||||| || |||||||||
                        ACTGT GG CCAAGTCCT
                          CC A      IIIAGG
GAM489 KCNA7           TGACAGGCCTGGTTCAGGA    7733   __ A      III
                        TGACA CC GGTTCAGG
                        ||||| || ||||||||
                        ACTGT GG CCAAGTCC
                          CC A      TII
GAM489 KCNK4          GACTACCGGGTG-AGGAAAGAG   7728 AC_ A TC      I
                        ACC GGT AGGAAAGA
                        ||| ||| |||||||||
                        TGG CCA TCCTTTCT
                       TGA  C  C_     I
GAM489 KCNK4          GACTACCGGGTG-AGGAAAGAG   7728 TGAC A TC       A
                        ACC GGT AGGAAAGAGG
                        ||| ||| |||||||||||
                        TGG CCA TCCTTTCTCT
                       TGA_  C  C_       I
GAM489 MCC           TGA-AGCAGG---AGGAAAGAGGA 7735   CAC   TTC
                        TGA  CAGG  AGGAAAGAGG
                        |||  ||||  ||||||||||
                        ACT  GTCC  TCCTTTCTCC
                         TC_  ___
GAM489 MCC           TGA-AGCAGG---AGGAAAGAGGA 7735 _ CAC   TTC
                         GA  CAGG  AGGAAAGAGG
                         ||  ||||  ||||||||||
                         CT  GTCC  TCCTTTCTCC
                        A TC_  ___
GAM489 PRG2          ACACCAGGTGCCAGGCAAAG     7721     _    AAAIII
                        ACACCAGGT TCAGG
                        ||||||||| |||||
                        TGTGGTCCA GGTCC
                          C   GTTTCI
GAM489 PRG2          ACACCAGGTGCCAGGCAAAG     7721 TGAC    _  _  AGG
                         ACCAGGT TCAGG AAAG
                         ||||||| ||||| ||||
                         TGGTCCA GGTCC TTTC
                         ____    C  G  GCI
GAM489 RAB23          TGAC-CCAATTTCAGGAAA      7734  A  G      GAG
                        TGAC CCAG TTCAGGAAA
                        |||| |||| ||||||||||
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                         ACTG GGTT AAGTCCTTT
                           _    A       III
GAM489  RAB23      TGAC-CCAATTTCAGGAAA      7734   A   G      I
                         TGAC CCAG TTCAGGAA
                         IIII IIII IIIIIIII
                         ACTG GGTT AAGTCCTT
                            _    A      T
GAM489  SCD        ACAACAGCTCAAGGAAAGAG     7722 CACCA    _       I
                          GGTTCA GGAAAGA
                          IIIIIII IIIIIII
                          TCGAGT CCTTTCT
                          GTTG_     T   I
GAM489  SCD        ACAACAGCTCAAGGAAAGAG     7722 TGACACCA      _
                          GGTTCA GGAAAGAGG
                          IIIIII IIIIIIIII
                          TCGAGT CCTTTCTCT
                          TTG_____     T
GAM489  STARD4     GACATCCAG-TTCAGGAAA      7729    _   G      II
                         GACA CCAG TTCAGGAA
                         IIII IIII IIIIIIII
                         CTGT GGTC AAGTCCTT
                            A    _     TI
GAM489  STARD4     GACATCCAG-TTCAGGAAA      7729 TG   _  G       GAG
                          ACA CCAG TTCAGGAAA
                          III IIII IIIIIIIII
                          TGT GGTC AAGTCCTTT
                           __   A   _     AII
GAM489  TCL1B      GACACCAGG-CCAG--AAGAGG   7732       T   A  AI
                         GACACCAGGT CAGGA AG
                         IIIIIIIIII IIIII II
                         CTGTGGTCCG GTCTT TC
                               _      C  CI
GAM489  TCL1B      GACACCAGG-CCAG--AAGAGG   7732 TG      T   AA
                          ACACCAGGT CAGG AGAGG
                          IIIIIIIII IIII IIIII
                          TGTGGTCCG GTCT TCTCC
                            __    _   __
GAM490  ABCC3      AGGATGCGGAACAGGCAAAG     7741 _  T  T        I
                          GGT TGG AACAGGCAAA
                          III III IIIIIIIIII
                          CTA GCC TTGTCCGTTT
                           C   C   _       I
GAM490  ABCC3      AGGATGCGGAACAGGCAAAG     7741 TGA  T  T       T
                          GGT TGG AACAGGCAAAG
                          III III IIIIIIIIII
                          CTA GCC TTGTCCGTTTC
                           ___    C  _       C
GAM490  ALPP       AGGTTTGGTGTCATGGGCTCAGTC 7740 GG     AA __  AA I
                          TTTGGT CA GGC AGT
                          IIIIII II III III
```

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                              AAACCA GT CCG TCA
                               __  CA  AC  AG   I
GAM490 ALPP        AGGTTTGGTGTCATGGGCTCAGTC  7740 TGAG      AA __  AA   I
                              GTTTGGT CA GGC AGTC
                              ||||||| || ||| ||||
                              CAAACCA GT CCG TCAG
                              ____    CA  AC  AG   G
GAM490 ARF3        TGAGGCAGGAGAAGAGGCAAAGTC  7748     TT T_  C       I
                              TGAGGT GG AA AGGCAAAGTC
                              |||||| || || |||||||||
                              ACTCCG CC TT TCCGTTTCAG
                                T_ TC C       I
GAM490 ARF3        TGAGGCAGGAGAAGAGGCAAAGTC  7748     TT T_  C       I
                              GAGGT GG AA AGGCAAAGT
                              ||||| || || |||||||||
                              CTCCG CC TT TCCGTTTCA
                                T_ TC C       I
GAM490 ARHA        TTTGGTAACATACATTAAGT      7750       G  AAGIII
                              TTTGGTAACA GCA
                              |||||||||| |||
                              AAACCATTGT TGT
                               A  AATTCA
GAM490 CAPN10      GGTGGGGTATGAGGCAAAGT       7744 GTTT  AC      I
                              GGTA AGGCAAAG
                              |||| ||||||||
                              CCAT TCCGTTTC
                        CACC  AC      I
GAM490 CAPN10      GGTGGGGTATGAGGCAAAGT       7744 TGAGGTTT  AC
                              GGTA AGGCAAAGT
                              |||| |||||||||
                              CCAT TCCGTTTCA
                        CC_____   AC
GAM490 CYP1B1      TTGGGGACCTGGCAAAGTC        7751 T  TA A_      II
                              TTGG AC GGCAAAGT
                              |||| || ||||||||
                              AACC TG CCGTTTCA
                              _  CC GA     GI
GAM490 GRM4        AGGTTTGGTGAACTGGGGAAG      7739 G    _ A CAAAI
                              GTTTGGT AAC GG
                              ||||||| ||| ||
                              CAAACCA TTG CC
                              _   C  A CCTTI
GAM490 GRM4        AGGTTTGGTGAACTGGGGAAG      7739 TGAG    _ A CA TC
                              GTTTGGT AAC GG AAG
                              ||||||| ||| || |||
                              CAAACCA TTG CC TTC
                              ____    C  A CC CC
GAM490 HSD3B1      TGAGATTTGGTAACA-GCAAA      7747              G  GT
                              TGAGGTTTGGTAACAG CAAA
                              |||||||||||||| ||||
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                              ACTCTAAACCATTGTC GTTT
                                      II
GAM490  HSD3B1         TGAGATTTGGTAACA-GCAAA    7747 _          G  I
                              GAGGTTTGGTAACAG CAA
                              IIIIIIIIIIIIII III
                              CTCTAAACCATTGTC GTT
                              A          _  I
GAM490  HSD3B2         TGAGATTTGGTAACA-GCAAA    7747          G  GT
                              TGAGGTTTGGTAACAG CAAA
                              IIIIIIIIIIIIII IIII
                              ACTCTAAACCATTGTC GTTT
                                      _  II
GAM490  HSD3B2         TGAGATTTGGTAACA-GCAAA    7747 _          G  I
                              GAGGTTTGGTAACAG CAA
                              IIIIIIIIIIIIII III
                              CTCTAAACCATTGTC GTT
                              A          _  I
GAM490  IAPP          TGAGGTTTGCTGAAAGCCA      7746       GTAAC   AAAGT
                              TGAGGTTTG  AGGC
                              IIIIIIIII   IIII
                              ACTCCAAAC   TTCG
                                GACT_  GTIII
GAM490  IAPP          TGAGGTTTGCTGAAAGCCA      7746       GTAAC  II
                              TGAGGTTTG  AGGC
                              IIIIIIIII   IIII
                              ACTCCAAAC   TTCG
                                GACT_  GT
GAM490  LOH11CR2A         AGGTTCAGGTCCCAGGCAAAG     7738 G  _  AA        I
                              GTTT GGT  CAGGCAAA
                              IIII III  IIIIIIII
                              CAAG CCA  GTCCGTTT
                              _  T  GG        I
GAM490  LOH11CR2A         AGGTTCAGGTCCCAGGCAAAG     7738 TGAG   _  AA         C
                              GTTT GGT  CAGGCAAAGT
                              IIII III  IIIIIIIIII
                              CAAG CCA  GTCCGTTTCG
                              ____    T  GG         A
GAM490  NAV2          GGTTTGATTGGAACAGGCAAA     7742     ___        III
                              GGTTTGGT  AACAGGCAA
                              IIIIIIII  IIIIIIIII
                              CCAAACTA  TTGTCCGTT
                                ACC       TII
GAM490  NAV2          GGTTTGATTGGAACAGGCAAA     7742 TGA  T T        C
                              GGTT GG AACAGGCAAAGT
                              IIII II IIIIIIIIIII
                              CTAA CC TTGTCCGTTTTA
                              AA_  _ _        T
GAM490  PKIB         TGAGGTTTGGGAA-----AAAGTC  7749       T C CAI
                              TGAGGTTTGG AA AGG
                              IIIIIIIII II III
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                         ACTCCAAACC TT TTC
                            C  T  AGI
GAM490 PKIB        TGAGGTTTGGGAA-----AAAGTC  7749        TAACA C
                     TGAGGTTTGG   GG AAAGT
                     IIIIIIIII   II IIIII
                     ACTCCAAACC   CT TTTCA
                         _____  T
GAM490 SLC6A1      GGGTGGGTAACAGGCACAG     7743 _ TT       AAII
                     GGT GGTAACAGGCA
                     III IIIIIIIIII
                     CCA CCATTGTCCGT
                       C  C_       GTCI
GAM490 SLC6A1      GGGTGGGTAACAGGCACAG     7743 TGAGGTTT      A T
                        GGTAACAGGCA AG
                        IIIIIIIIIII II
                        CCATTGTCCGT TC
                       AC_____        G T
GAM490 SRD5A1      TTTTTTAAATGGCAAAGTC      7752 TTTGGTAACA      II
                        GGCAAAGT
                        IIIIIIII
                        CCGTTTCA
                       AAAAAATTTA       GI
GAM490 SREBF1      GTTTGCAAA-AGGCAAAGT     7745    G  C      I
                        GTTTG TAA AGGCAAAG
                        IIIII III IIIIIIII
                        CAAAC GTT TCCGTTTC
                        _  T      A
GAM490 SREBF1      GTTTGCAAA-AGGCAAAGT      7745 TGAGGTTTG   C
                        GTAA AGGCAAAG
                        IIII IIIIIIII
                        CGTT TCCGTTTC
                       _____  T
GAM491 AGM1        AAAACAGATCTAGAGACAAT     7755 TGAGAAAA       AAT
                        CAGATTTAGAGA
                        IIIIIIIIIIII
                        GTCTAGATCTCT
                        _____     GTT
GAM491 BRCA1       TGTGAACACAGGGTTTTAGAGAAGTA 7773 TGA  A  A__     ATAII
                        GAA ACAG  TTTAGAGAA
                        III IIII  IIIIIIIII
                        CTT TGTC  AAATCTCTT
                       ACA  G  CCA      CATII
GAM491 CBFB        AGAAAAAATGAT-TAGAGAAA    7758 TGAGAAAACA   T    T
                        GATT AGAGAAA
                        IIII IIIIIII
                        CTAA TCTCTTT
                       TTTTTTA___  _    T
GAM491 CBFB        AGAAAAAATGATT-AGAGAAA    7759 TGAGAAAACA   T    T
                        GATT AGAGAAA
                        IIII IIIIIII
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                         CTAA TCTCTTT
                      TTTTTTA___   _      T
GAM491  COL19A1       AAAACAGATTCATAAAAAT     7756 TGAGAAAA     G
                         CAGATTTA AGAAAT
                         ||||||||| ||||||
                         GTCTAAGT TTTTTA
                      _____        A
GAM491  EIF2C1        GAGAAAAAGAACCAGATTTAGAAAAA 7770 T____    AA         TAII
                         GAGAA  CAGATTTAGAGAAA
                         ||||| |||||||||||||
                         TTCTT  GTCTAAATCTTTTT
                      TCTTT   G_        CIII
GAM491  EPHA3         TGGGATAACAGATTTGAGAGA     7774 A A       _    AATA
                         TG GA AACAGATT AGAGA
                         || || ||||||||| |||||
                         AC CT TTGTCTAAA TCTCT
                        C A      C   IIIA
GAM491  FGF7          AGAAAACAGTCCACTTAAAGAAAT  7760 TGAG        ___        AI
                         AAAACAG  ATTTAGAGAAAT
                         ||||||| ||||||||||||
                         TTTTGTC  TGAATTTCTTTA
                        ____      AGG        GA
GAM491  FPRL1         AGAAAACAGAATCAGAGGAAT     7766 TGAG     T    A  A
                         AAAACAGA TTAGAG AAT
                         ||||||||| |||||| |||
                         TTTTGTCT AGTCTC TTA
                        ____       T    C  A
GAM491  HHEX          GAGATAAACAGA-TTACAGAAA    7769 TG  _     _     ATA
                         AGA AAACAGATT TAGAGAA
                         ||| ||||||||| |||||||
                         TCT TTTGTCTAA GTCTTTT
                        __   A    T    III
GAM491  MAPK14        AGTAATCATATTTAGAGAAA      7765 TGAGAAAA  G       T
                         CA ATTTAGAGAAA
                         || |||||||||||
                         GT TAAATCTCTTT
                      ATTA____  A        C
GAM491  MBL2          AGAAAACAGAGTTCATAGAGAAA   7761 TGAG      TT___      TAI
                         AAAACAGA    TAGAGAAA
                         ||||||||    ||||||||
                         TTTTGTCT    ATCTCTTT
                          ____       CAAGT       CAI
GAM491  PDE6H         AGATAAACAAAATGTAGAGAAATA  7757 TGAGA      TT_     I
                         AAACAGA   TAGAGAAATA
                         |||||||  ||||||||||
                         TTTGTTT  ATCTCTTTAT
                      TA___      TAC      A
GAM491  PSA           AGAAAACAG---TAGAGAA       7763 TGAG     ATT
                         AAAACAG  TAGAGAA
                         ||||||| |||||||
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                              TTTTGTC  ATCTCTT
                              ____      __
GAM491  PTEN         TGAGAAAACATATTTA-ATAAAT  7777       G    A  ATA
                     TGAGAAAACA ATTTAG GAA
                     |||||||||| |||||| |||
                     ACTCTTTGT TAAATT TTT
                            A    A  AII
GAM491  RAD23B        GAAAACAGATTT-GAAAAA      7768 TGAGAA      A
                      AACAGATTT GAGAAA
                      ||||||||| ||||||
                      TTGTCTAAA CTTTT

                            _____  _
GAM491  RAG1          GAAACCTAGATTTAGAAAAAT     7767 TGAGAAAAC       A
                      AGATTTAGAGAAAT
                      ||||||||||||||
                      TCTAAATCTTTTTA
                     TGGA_____          A
GAM491  RIG        TGAGGAAGCA--TTTAGAGAA     7776   AAAAC  _      AT
                   TGAG   AG ATTTAGAGAA
                   ||||   || |||||||||
                   ACTC   TC TAAATCTCTT
                      CT___  G       II
GAM491  SFRP1        TGAGAATTCCCATTTAGAGA     7775    AACAG     AAT
                     TGAGAA    ATTTAGAGA
                     ||||||    |||||||||
                     ACTCTT    TAAATCTCT
                         AAGGG      III
GAM491  SH3BP4       AGAAAGCAGTTTTAGAGAA      7764 TGAGAAAA A    AT
                     CAG TTTAGAGAA
                     ||| |||||||||
                     GTC AAATCTCTT
                    TTTC____   A    AC
GAM491  SRGAP1       GAGAACACAGGGATTTAGAG     7771 TG  A  __     AAAT
                     AGAA ACA GATTTAGAG
                     |||| ||| |||||||||
                     TCTT TGT CTAAATCTC
                      __  G  CC      CIII
GAM491  TIMP4        AGAAAACAGACTAAGCCAGAA     7762 TGAG     T __   ATA
                     AAAACAGATT AG AGAA
                     |||||||||| || ||||
                     TTTTGTCTGA TC TCTT
                        ____     T GG  CTI
GAM491  UBE2B         TGAAAAAAGTACAGATTTACA-AAAT 7772       ___    G  ATAII
                      TGAGAAA ACAGATTTA AGAA
                      ||||||| ||||||||| ||||
                      ACTTTTT TGTCTAAAT TTTT
                         TCA      G  AIIIA
GAM492  ADAM12        TGCCCAAGCCACATCTCATAA     7798 GA  _     GAAAI
                      CCA GCCACATCT
                      ||| |||||||||
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```
                         GGT CGGTGTAGA
                         G_  T       GTATI
GAM492 ADAM12            TGCCCAAGCCACATCTCATAA      7798 TGA  _        GAAAAGGAA
                         CCA GCCACATCT
                         ||| |||||||||
                         GGT CGGTGTAGA
                         ACG  T       GTATTIIIA
GAM492 ADSS         CCAGCCACA--TGCAGAGGAA      7790 _      TC AAA   I
                         CAGCCACA TG  AGGA
                         |||||||| ||  ||||
                         GTCGGTGT AC  TCCT
                         G     __  GTC   I
GAM492 ADSS         CCAGCCACA--TGCAGAGGAA      7790 TGACCA     CT_ AA
                         GCCACAT GA AGGA
                         ||||||| || ||||
                         CGGTGTA CT TTCT
                         _____      CGT CC
GAM492 B3GALT5       TGACCAGCCA-GTCAATAACGGAA  7802       CA TGAAAA  I
                         TGACCAGCCA TC   GGAA
                         |||||||||| ||   ||||
                         ACTGGTCGGT AG   CCTT
                            C_ TTATTG   I
GAM492 B3GALT5       TGACCAGCCA-GTCAATAACGGAA  7802 _       CA TGAAAA  I
                         GACCAGCCA TC   GGA
                         ||||||||| ||   |||
                         CTGGTCGGT AG   CCT
                         A     C_ TTATTG   I
GAM492 BRCA1         TGACCAGCCGACGTTTTTAAAG   7799       _ ATCTGAAAAI
                         ACCAGCC AC
                         ||||||| ||
                         TGGTCGG TG
                            C CAAAAATTII
GAM492 C11orf8       CCACATCTGCAAAAAGAA       7787        __      III
                         CCACATCTG AAAAGGA
                         ||||||||| |||||||
                         GGTGTAGAC TTTTTCT
                            GT    TII
GAM492 CANX         TGACCACAGAACAACAGATGAAAAGGAA7797      ____ C TC      III
                         TGACCA  GC ACA TGAAAAGGAA
                         ||||||  || ||| |||||||||||
                         ACTGGT  TG TGT ACTTTTCCTT
                            GTCT T CT      III
GAM492 CANX         TGACCACAGAACAACAGATGAAAAGGAA7797 GACC  C TC     I
                         AGC ACA  TGAAAAGGA
                         ||| |||  |||||||||
                         TTG TGT  ACTTTTCCT
                         TGTC  T CT      I
GAM492 CHC1L         TGACCTTAGTCACATCTGA      7796 __ C       AAAGGA
                         TGACC AG CACATCTGA
                         ||||| || |||||||||
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                      ACTGG  TC GTGTAGACT
                      AA  A        IIIAAG
GAM492 CHC1L        TGACCTTAGTCACATCTGA    7796  __  C      III
                      TGACC  AG CACATCTG
                      IIIII II IIIIIIII
                      ACTGG  TC GTGTAGAC
                      AA  A        TII
GAM492 DMD         TGACCAGCCTCA-C--AAAAG    7800      A  CT AI
                      TGACCAGCC CAT  GA
                      IIIIIIIII III  II
                      ACTGGTCGG GTG  TT
                        A  TT  CI
GAM492 DMD         TGACCAGCCTCA-C--AAAAG    7800      A  CTG    G
                      TGACCAGCC CAT  AAAAG
                      IIIIIIIII III  IIIII
                      ACTGGTCGG GTG  TTTTC
                        A  ___   I
GAM492 ED1         CCCCATCTCCTGAAAAGGAA    7786 __  CA_        III
                       CCA  TCTGAAAAGGA
                       III  IIIIIIIIIII
                       GGT  GGACTTTTCCT
                       GG  AGA        TII
GAM492 EHD2       CCA-CGACATCCCTGAAAAGGA   7788 CA  C      __      I
                       GC ACATCT GAAAAGG
                       II IIIIII IIIIIII
                       TG TGTAGG CTTTTCC
                       __  C   GA      I
GAM492 EHD2       CCA-CGACATCCCTGAAAAGGA   7788 T  CAG ACAT        A
                       GAC  CC  CTGAAAAGGA
                       III  II  IIIIIIIIII
                       CTG  GG  GACTTTTCCT
                       G  TA_  ____        C
GAM492 FCRH3        ACCAGCCACA-CAAAAAAGG    7780 _        CT    I
                       CCAGCCACAT GAAAAG
                       IIIIIIIIII IIIIII
                       GGTCGGTGTG TTTTTC
                       T      T_  I
GAM492 FCRH3        ACCAGCCACA-CAAAAAAGG    7780 TGAC      CT    A
                        CAGCCACAT GAAAAGG
                        IIIIIIIII IIIIIII
                        GTCGGTGTG TTTTTCC
                        ____      T_    C
GAM492 FEN1        GACTAGC-ACTACTGAAAAGG    7795 _  C  C AT      I
                        AC AGC AC CTGAAAAG
                        II III II IIIIIIII
                        TG TCG TG GACTTTTC
                        C  A  _ AT    I
GAM492 FEN1        GACTAGC-ACTACTGAAAAGG    7795 TG  C  C AT        A
                        AC AGC AC  CTGAAAAGG
                        II III II  IIIIIIIII
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                              TG TCG TG  GACTTTCC
                              __  A  _ AT        C
GAM492 FLRT2          GAACATCCACGATG-GAAAAGGAA  7794 AC G   ATCT      I
                              CA CCAC   GAAAAGGA
                              || ||||   ||||||||
                              GT GGTG   CTTTTCCT
                              TT A   CTAC        I
GAM492 FLRT2          GAACATCCACGATG-GAAAAGGAA  7794 T  CAG   ATCT       I
                              GAC  CCAC   GAAAAGGAA
                              |||  ||||   |||||||||
                              TTG  GGTG   CTTTTCCTT
                              _  TA_  CTAC        G
GAM492 FVT1           CAGCCACATTCCTGAAGAG       7783       __    AAIII
                              CAGCCACAT CTGAA
                              ||||||||| |||||
                              GTCGGTGTA GACTT
                                 AG    CTCII
GAM492 GLUD1          GACCATGCCACCTTCTGAAAAGG  7791 ACCA    A_       I
                              GCCAC TCTGAAAAG
                              ||||| ||||||||||
                              CGGTG AGACTTTC
                              GTA_   GA       I
GAM492 GLUD1          GACCATGCCACCTTCTGAAAAGG  7791 TG  _   A_       AAI
                              ACCA GCCAC  TCTGAAAAGG
                              |||| |||||  ||||||||||
                              TGGT CGGTG  AGACTTTTCC
                              __   A  GA        GII
GAM492 LZTS1          CCAGCCACA---GAAAAGG      7789       TCT
                              CCAGCCACA  GAAAAG
                              |||||||||  ||||||
                              GGTCGGTGT  CTTTTC
                                      ___
GAM492 LZTS1          CCAGCCACA---GAAAAGG       7789 TGACCA     TCT
                              GCCACA  GAAAAG
                              ||||||  ||||||
                              CGGTGT  CTTTTC
                              _____    ___
GAM492 PIP5K1A        GACCAAGCCACATCTGAAAA      7792     _         II
                              GACCA GCCACATCTGAAA
                              ||||| |||||||||||||
                              CTGGT CGGTGTAGACTTT
                                 T      TI
GAM492 PIP5K1A        GACCAAGCCACATCTGAAAA      7792 TG  _        GA
                              ACCA GCCACATCTGAAAAG
                              |||| ||||||||||||||
                              TGGT CGGTGTAGACTTTTT
                              __    T       II
GAM492 POLG           ACCAGCCA-AGAAGAAAAGGAA   7781 _    CATCT      I
                              CCAGCCA   GAAAAGGA
                              |||||||   ||||||||
```

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                        GGTCGGT   CTTTTCCT
                      T     TCTT_        I
GAM492 POLG           ACCAGCCA-AGAAGAAAAGGAA   7781 TGAC    CATCT
                        CAGCCA    GAAAAGGAA
                        ||||||    |||||||||
                        GTCGGT    CTTTTCCTT
                      ____        TCTT_
GAM492 RB1CC1         CAGGCAC-TGTGAAAAGGA    7785  C ATC      I
                        CAG CAC  TGAAAAGG
                        ||| |||  ||||||||
                        GTC GTG  ACTTTTCC
                         C  AC_      T
GAM492 RB1CC1         CAGGCAC-TGTGAAAAGGA     7785 TGACCAGC  ATC
                           CAC  TGAAAAGG
                           |||  ||||||||
                           GTG  ACTTTTCC
                      _____     AC_
GAM492 SWAP70         CAGC-ACATACTCGGAAAAGGAA   7784 AGC   _ __      I
                        CACAT CT  GAAAAGGA
                        ||||| ||  ||||||||
                        GTGTA GA  CTTTTCCT
                      ___      T GC      I
GAM492 SWAP70         CAGC-ACATACTCGGAAAAGGAA   7784 TGACCAGCC  A  T
                        AC TC  GAAAAGGAA
                        || ||  |||||||||
                        TG AG CTTTTCCTT
                      TGTA_____ _  C
GAM492 TSSC4          TGACCAGCCCCA-CTGGGAAGG   7801      A  T  AA   AA
                        TGACCAGCC CA CTG  AAGG
                        ||||||||| || ||| ||||
                        ACTGGTCGG GT GAC  TTCC
                           G _ CC  II
GAM492 TSSC4          TGACCAGCCCCA-CTGGGAAGG   7801_      A  T  AA   I
                        GACCAGCC CA CTG  AAG
                        |||||||| || ||| |||
                        CTGGTCGG GT GAC  TTC
                         A      G _  CC  I
GAM492 VCL            AGCTCACTTCTGAAAAGGA      7782 _  A       II
                        AGC CAC TCTGAAAAGG
                        ||| ||| ||||||||||
                        TCG GTG AGACTTTTCC
                         A  A       TI
GAM492 VCL            AGCTCACTTCTGAAAAGGA      7782 TGACCAGCC  A
                          AC TCTGAAAAGGA
                          || ||||||||||
                          TG AGACTTTTCCT
                      _____     A
GAM492 ZNF132         GACCAGCCAAGCAACAGAATAAGG  7793 TG     __  TCT  _  AAI
                        ACCAGCCA CA  GAA AAGG
                        |||||||| ||  ||| ||||
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                    TGGTCGGT GT  CTT TTCC
                       TC  TGT  A   CII
GAM493  ABCA1         AATGTT-GTGTTTTCTTCA    7807   GTAGA        GGC
                      AATG    GTTTTCTTCA
                      ||||    ||||||||||
                      TTAC    CAAAAGAAGT
                       AACA_          III
GAM493  ABCA1         AATGTT-GTGTTTTCTTCA    7807   GTAGA       I
                      AATG    GTTTTCTTC
                      ||||    |||||||||
                      TTAC    CAAAAGAAG
                       AACA_        T
GAM493  BHMT2        TGGTAGAGTCTGTTGCAGTGCTT  7818 AATG      TCTT _   I
                     GTAGAGTTT  CAG GCTT
                     |||||||||  ||| ||||
                     CATCTCAGA  GTC CGAA
                      ____         CAAC  A   T
GAM493  BHMT2        TGGTAGAGTCTGTTGCAGTGCTT  7818 G        TCTT _   I
                     GTAGAGTTT  CAG GCT
                     |||||||||  ||| |||
                     CATCTCAGA  GTC CGA
                      _        CAAC  A   I
GAM493  C8A          ATGGATTGAGTTTTC-TCAG    7811   TA_       CAII
                     ATGG  GAGTTTTCTT
                     ||||  ||||||||||
                     TACC  CTCAAAAGAG
                      TAA      TCII
GAM493  C8A          ATGGATTGAGTTTTC-TCAG    7811 AA  TA_      T GCT
                      TGG  GAGTTTTCT CAG
                      |||  ||||||||| |||
                      ACC  CTCAAAAGA GTC
                       __  TAA       _  AII
GAM493  CAPN10        TGGTAGAGT----TTCAGGTCTT  7819 _         TTCT    _
                      GGTAGAGTT  TCAGG CT
                      |||||||||  ||||| ||
                      CCATCTCAA  AGTCC GA
                      A        ____     A
GAM493  CAPN10        TGGTAGAGT----TTCAGGTCTT  7819 AATG        TTCT   _
                      GTAGAGTT  TCAGG CT
                      ||||||||  ||||| ||
                      CATCTCAA  AGTCC GA
                       ____       ____    A
GAM493  CDH7          TACAGTTTTCTT---GCTT     7816  G      CAG
                      TA AGTTTTCTT  GCT
                      || |||||||||  |||
                      AT TCAAAAGAA  CGA
                       G        ___
GAM493  CENTD1        AATGTTA---TTTTCTTCA    7808   GTAGA       GG
                      AATG    GTTTTCTTCA
                      ||||    ||||||||||
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                          TTAC    TAAAAGAAGT
                          AA___          II
GAM493 EGFL5         AATGGTAGA---ACCTTCAGG    7809        TT TTCI
                         AATGGTAGAG TTC
                         |||||||||| |||
                         TTACCATCTT AAG
                            GG  TCCI
GAM493 EGFL5         AATGGTAGA---ACCTTCAGG    7809        TTT      C
                         AATGGTAGAG TCTTCAGG
                         |||||||||| ||||||||
                         TTACCATCTT GGAAGTCC
                             ___          I
GAM493 FBXL11       TGGGAAAGCCTTCTTCAGGC     7820 _ T           I
                         GG AGAGTTTCTTCAGG
                         || ||||||||||||||
                         CC TTTCGGAAGAAGTCC
                            C _          I
GAM493 FBXL11       TGGGAAAGCCTTCTTCAGGC     7820 AAT T          T
                           GG AGAGTTTCTTCAGGC
                           || ||||||||||||||
                           CC TTTCGGAAGAAGTCCG
                              ___ _           T
GAM493 KCNJ16       AATGGTAGAGAATGCTCTTTAG    7806        TT__  C GCTT
                         AATGGTAGAG   TTCTT AG
                         ||||||||||   ||||| ||
                         TTACCATCTC   GAGAA TC
                           TTAC    A IIIT
GAM493 KCNJ16       AATGGTAGAGAATGCTCTTTAG    7806 AT      TT__   CAI
                          GGTAGAG   TTCTT
                          |||||||   |||||
                          CCATCTC   GAGAA
                          __      TTAC    ATI
GAM493 LNK         ATGG--GAGTTTTCTGTCAG      7813    TA      _ I
                         ATGG GAGTTTTCT TCA
                         |||| |||||||||| |||
                         TACC CTCAAAAGA AGT
                           __         C  C
GAM493 LNK         ATGG--GAGTTTTCTGTCAG      7813 AA  TA      _  GC
                          TGG GAGTTTTCT TCAG
                          ||| |||||||||| ||||
                          ACC CTCAAAAGA AGTC
                           __  __         C  GI
GAM493 MEN1         ATGGTAGAG--ATGTTCAG      7814        TT_ TTCAI
                         ATGGTAGAG TTC
                         ||||||||| |||
                         TACCATCTC AAG
                            TAC  TCIII
GAM493 MEN1         ATGGTAGAG--ATGTTCAG      7814 AA       TTTTC   GC
                          TGGTAGAG   TTCAG
                          ||||||||   |||||
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                        ACCATCTC    AAGTC
                        __      TAC__   AI
GAM493 POLK             AGAGTCTCGCTCTTCAGGCT    7810      ___        III
                        AGAGTTT  TCTTCAGGC
                        ||||||| |||||||||
                        TCTCAGA  AGAAGTCCG
                             GCG       AII
GAM493 POLK             AGAGTCTCGCTCTTCAGGCT    7810 AATGGTAGAGTT
                               TTCTTCAGGCT
                               ||||||||||
                               GAGAAGTCCGA
                        AGC_____
GAM493 RERE             AATGGTAGATGTTGTGTTC      7805      _  TTC  AGGCT
                        AATGGTAGA GTT  TTC
                        ||||||||| |||  |||
                        TTACCATCT CAA  AAG
                           A  CAC  IIITT
GAM493 RERE             AATGGTAGATGTTGTGTTC      7805      _  TTCTTII
                        AATGGTAGA GTT
                        ||||||||| |||
                        TTACCATCT CAA
                            A  CACAAGI
GAM493 SYNGR1           TGGTACAGGTTTCACTCTTCAGGC 7817 __  AGAGTT        I
                            GGT    TTCTTCAGG
                            |||    |||||||||
                            CCA    GAGAAGTCC
                        GT  AAGT__         I
GAM493 SYNGR1           TGGTACAGGTTTCACTCTTCAGGC 7817 AAT__  AGAGTT         TI
                            GGT    TTCTTCAGGCT
                            |||    |||||||||||
                            CCA    GAGAAGTCCGG
                        CATGT  AAGT__          TI
GAM493 VCAM1            ATGGCAGTTACTGTTCTTCAGGC  7812 AA      AGTT__        TTI
                            TGGTAG    TTCTTCAGGC
                            ||||||    ||||||||||
                            ACCGTC    AAGAAGTCCG
                            __     AATGAC        TII
GAM493 VCAM1            ATGGCAGTTACTGTTCTTCAGGC  7812 TG  AGTT__           I
                            GTAG    TTCTTCAGG
                            ||||    |||||||||
                            CGTC    AAGAAGTCC
                            __     AATGAC       I
GAM493 ZNFN2A1          GGGAGAATTCCCTTCAGGCT     7815 AATGGT     TT
                            AGAGTT CTTCAGGCT
                            |||||| |||||||||
                            TCTTAA GAAGTCCGA
                            _____        GG
GAM493 ZNFN2A1          GGGAGAATTCCCTTCAGGCT     7815 GT     TT    I
                            AGAGTT CTTCAGGC
                            |||||| |||||||||
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                                TCTTAA GAAGTCCG
                                 CC    GG      I
GAM494 ADCY2          AGGAGCA-CAGTGAGTTGG    7826  _ T      II
                            AGGA CA CAGTGAGTTG
                            IIII II IIIIIIIIII
                            TCCT GT GTCACTCAAC
                               C _      CI
GAM494 ADCY2          AGGAGCA-CAGTGAGTTGG    7826 TACCAGGA T
                              CA CAGTGAGTTGG
                              II IIIIIIIIIII
                              GT GTCACTCAACC
                            C_____ _
GAM494 ARF1         CAGCACTGAACAGTGAGTTG    7828  G AT__      III
                            CAG AC  CAGTGAGTT
                            III II  IIIIIIIII
                            GTC TG  GTCACTCAA
                             G ACTT      CII
GAM494 ARF1         CAGCACTGAACAGTGAGTTG    7828 TACCA   TCA
                              GGACA  GTGAGTTGGT
                              IIIII  IIIIIIIIII
                              CTTGT  CACTCAACTA
                            GTGA_   ___
GAM494 CISH        TACCAGGACATCCAGGATTGCCTTGGT7833        AG____  AG   AIII
                            TACCAGGACATC    TG TTGGT
                            IIIIIIIIIIII    II IIIII
                            ATGGTCCTGTAG    AC AACCA
                              GTCCTA GG    IIIA
GAM494 CISH        TACCAGGACATCCAGGATTGCCTTGGT7833 ACCA      AG____  AG  I
                            GGACATC    TG TTGG
                            IIIIIII    II IIII
                            CCTGTAG    AC AACC
                            ____      GTCCTA GG  I
GAM494 COL8A1       GACTTCAAGGGTGAGTTGGT    7830  A ___        III
                            GAC TCA GTGAGTTGG
                            III III IIIIIIIII
                            CTG AGT CACTCAACC
                             A TCC      AII
GAM494 COL8A1       GACTTCAAGGGTGAGTTGGT    7830 TACCAGGACATCA
                               GTGAGTTGGT
                               IIIIIIIIII
                               CACTCAACCA
                            TTCC_____
GAM494 FN14        CAGGACATCTGAGTGAGTGGG    7829        __    TGIII
                            CAGGACATC AGTGAGT
                            IIIIIIIII IIIIIII
                            GTCCTGTAG TCACTCA
                               AC      CCCII
GAM494 FN14        CAGGACATCTGAGTGAGTGGG    7829 TACCAG    __    T_ A
                              GACATC AGTGAGT GGT
                              IIIIII IIIIIII III
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                    CTGTAG TCACTCA CCG
                    _____    AC    CC G
GAM494 GK           GGA-ATCCATGAGTTGGTA    7831   C  A      I
                    GGA ATC GTGAGTTGGT
                    ||| ||| ||||||||||
                    CCT TAG TACTCAACCA
                    _   G       T
GAM494 GNB1         ACCAGGACAATCTGTGTGT    7823      _ A  AGII
                    ACCAGGACA TC GTG
                    ||||||||| || |||
                    TGGTCCTGT AG CAC
                        T  A  ACAI
GAM494 GNB1         ACCAGGACAATCTGTGTGT    7823 TA    _ A  A TGGT
                    CCAGGACA TC GTG GT
                    |||||||| || ||| ||
                    GGTCCTGT AG CAC CA
                    __     T  A  A CIII
GAM494 HAP1         TACCAGGACAGCACTAGAG    7834      T  G  AII
                    TACCAGGACA CA TG
                    |||||||||| || ||
                    ATGGTCCTGT GT AT
                        C  G  CTC
GAM494 HAP1         TACCAGGACAGCACTAGAG    7834      T  G _ TTGGT
                    TACCAGGACA CA T GAG
                    |||||||||| || | |||
                    ATGGTCCTGT GT A CTC
                        C  G T  IIIAT
GAM494 MME          GGACATCAGCAAACTGGTA    7832      TG GT  II
                    GGACATCAG A TGGT
                    ||||||||| | ||||
                    CCTGTAGTC T ACCA
                        GT TG   TI
GAM494 PXF          ACCAGGACAGCCAGCTGAGCTG    7824 CC    _  _      I
                    AGGACA TCAG TGAGTT
                    |||||| |||| ||||||
                    TCCTGT GGTC ACTCGA
                    __     C  G    I
GAM494 PXF          ACCAGGACAGCCAGCTGAGCTG    7824 TA    _  _      TA
                    CCAGGACA TCAG TGAGTTGG
                    |||||||| |||| |||||||||
                    GGTCCTGT GGTC ACTCGACT
                    __        C  G    II
GAM494 SFRP4        AGCACTGCAGTGAGTTGTTA    7827 G  AT      GTI
                    G AC CAGTGAGTTG
                    | || ||||||||||
                    C TG GTCACTCAAC
                    G  AC      AAI
GAM494 SFRP4        AGCACTGCAGTGAGTTGTTA    7827 TACCAGGACAT      GT
                    CAGTGAGTTG
                    ||||||||||
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                         GTCACTCAAC
                 GAC_____        AA
GAM494  VCL          ACCAGGACA-CAGTGTGTT    7825      T   A  I
                     ACCAGGACA CAGTG GT
                     |||||||| |||| ||
                     TGGTCCTGT GTCAC CA
                       _     A A
GAM494  VCL          ACCAGGACA-CAGTGTGTT    7825 TA    T  A  GG
                       CCAGGACA CAGTG GTT
                       |||||||| |||| |||
                       GGTCCTGT GTCAC CAA
                       __    _  A  GI
GAM495  CACNG8         GACTCCAGTTTGACCACGGGCAG   7838   A___      C _ AAGGI
                       GACTC   TTGACCACG GG AG
                       |||||   |||||||| || ||
                       CTGAG   AACTGGTGC CC TC
                        GTCA       _  G  IIIGG
GAM495  SNX9          CATGTGACTCCCCGGAGAAGG    7837 _  ATTGA ACG
                       GACTC   CC CGGAGAAGG
                       |||||   || |||||||||
                       CTGAG   GG GCCTCTTCC
                       A     _____ ___
GAM496  ABCC3         GGCAGCATCTCCA-GGTCAGCT    7851 _     A T  CAACI
                       GCAGCATCT CA GTT
                       ||||||||| || |||
                       CGTCGTAGA GT CAG
                       C   G C  TCGII
GAM496  ABCC3         GGCAGCATCTCCA-GGTCAGCT    7851 TG     A T T A
                       GCAGCATCT CA GT CA CTG
                       ||||||||| || || || |||
                       CGTCGTAGA GT CA GT GAT
                       __    G C _ C
GAM496  ADAMTS1      CAGCATCTA-ATGCTTC-ACTG    7843 _     C   CA  I
                       AGCATCTA ATGTT  ACT
                       |||||||| |||||  |||
                       TCGTAGAT TACGA  TGA
                       G     _  AG  I
GAM496  ADAMTS1      CAGCATCTA-ATGCTTC-ACTG    7843 TGGCAG    C   CA
                       CATCTA ATGTT  ACT
                       |||||| |||||  |||
                       GTAGAT TACGA  TGA
                       _____   _  AG
GAM496  CCNDBP1       TGGCAGCATGGACTTGTTCA     7854     CT A    ACT
                       TGGCAGCAT AC TGTTCA
                       ||||||||| || ||||||
                       ACCGTCGTA TG ACAAGT
                        CC  A    III
GAM496  CCNDBP1       TGGCAGCATGGACTTGTTCA     7854     CT A   I
                       GGCAGCAT AC TGTTC
                       |||||||| || |||||
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                        CCGTCGTA TG ACAAG
                         CC  A     I
GAM496 CR1          GGCAGCATCTTCAAGTGCA      7850        A  T TCII
                        GGCAGCATCT CA GT
                        |||||||||| || ||
                        CCGTCGTAGA GT CA
                          A  T  CGTI
GAM496 CR1          GGCAGCATCTTCAAGTGCA      7850 TG      A  T T ACT
                         GCAGCATCT CA GT CA
                         |||||||| || || ||
                         CGTCGTAGA GT CA GT
                         __        A  T C GII
GAM496 CSNK1A1        GCAACATACATACATGTTCA      7846      C__        III
                        GCAGCAT  TACATGTTC
                        |||||||  |||||||||
                        CGTTGTA  ATGTACAAG
                          TGT      TII
GAM496 CSNK1A1        GCAACATACATACATGTTCA      7846 T  _ TC       ACT
                         GGCA GCA  TACATGTTCA
                         |||| |||  ||||||||||
                         TTGT TGT  ATGTACAAGT
                         _  A  __       CAI
GAM496 DLG5        GCAGCATCT-C-TGATCAGCTG      7848       ACA  T  ACI
                        GCAGCATCT  TG TCA
                        |||||||||  || |||
                        CGTCGTAGA  AC AGT
                          G__  T  CGA
GAM496 DLG5        GCAGCATCT-C-TGATCAGCTG      7848 TGGC     ACA  T  A
                         AGCATCT  TG TCA CT
                         |||||||  || ||| ||
                         TCGTAGA  AC AGT GA
                         ____     G__ T  C
GAM496 GALNT7        GCAACAGGT-CATGTTCAA      7847      TCTA       I
                        GCAGCA  CATGTTCA
                        ||||||  ||||||||
                        CGTTGT  GTACAAGT
                          CCA_      T
GAM496 GALNT7        GCAACAGGT-CATGTTCAA      7847 T    CATCTA      C
                         GGCAG   CATGTTCAA
                         |||||   |||||||||
                         TTGTC   GTACAAGTT
                         _  CA____       C
GAM496 HTLF        TGGCAGCATCAACAGCTTCA      7853       T  TG  ACT
                        TGGCAGCATC ACA TTCA
                        |||||||||| ||| ||||
                        ACCGTCGTAG TGT AAGT
                          T  CG  III
GAM496 HTLF        TGGCAGCATCAACAGCTTCA      7853      T  T CI
                        GGCAGCATC ACA GTT
                        ||||||||| ||| |||
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```
                    CCGTCGTAG TGT CGA
                       T  _  AG
GAM496  MAML1       GGCAACAT--ACATGTTCA      7849      TC        I
                    GGCAGCA  TACATGTTC
                    ||||||| |||||||||
                    CCGTTGT  ATGTACAAG
                        __        T
GAM496  MAML1       GGCAACAT--ACATGTTCA      7849 TG    TC       AC
                     GCAGCA  TACATGTTCA
                     |||||| |||||||||||
                     CGTTGT  ATGTACAAGT
                        __   __       CI
GAM496  NPC1        TGGCACCATCCGG-TGTTCAACT  7857   G   ACA      G
                    TGGCA CATCT  TGTTCAACT
                    ||||| |||||  |||||||||
                    ACCGT GTAGG  ACAAGTTGA
                        G    CC_      I
GAM496  NPC1        TGGCACCATCCGG-TGTTCAACT  7857 _  G   ACA     I
                     GGCA CATCT  TGTTCAAC
                     |||| |||||  ||||||||
                     CCGT GTAGG  ACAAGTTG
                        A   G   CC_      I
GAM496  NRCAM       AGCATCTACAT-TTTAAGTG     7841 _       GTTCAACTI
                    GCATCTACAT
                    ||||||||||
                    CGTAGATGTA
                    T       AAATTCAII
GAM496  SOX11       TGGCTGCATTAGTCTACATGTT   7852   A  ____      CAACTG
                    TGGC GCA   TCTACATGTT
                    |||| |||  |||||||||
                    ACCG CGT   AGATGTACAA
                        A  AATC       IIIGTC
GAM496  SOX11       TGGCTGCATTAGTCTACATGTT   7852   A  ____      IIIA
                    TGGC GCA   TCTACATGT
                    |||| |||  ||||||||
                    ACCG CGT   AGATGTACA
                        A  AATC       AIII
GAM496  STMN1       CAGCATCTAACA-GTTCAA      7842         _ T  II
                    CAGCATCTA CA GTTCA
                    ||||||||| || |||||
                    GTCGTAGAT GT CAAGT
                        T  _  TI
GAM496  STMN1       CAGCATCTAACA-GTTCAA      7842 TGGCAG    _ T    C
                      CATCTA CA GTTCAA
                      |||||| || ||||||
                      GTAGAT GT CAAGTT
                    _____     T _  T
GAM496  TBX1        CAGTATCTACATGTATCTAC     7844  C       _ AAII
                    CAG ATCTACATGT TC
                    ||| |||||||||| ||
```

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                              GTC TAGATGTACA AG
                               A       T ATGI
GAM496  TBX1        CAGTATCTACATGTATCTAC    7844 TGGCAGC      _ A T
                          ATCTACATGT TC AC
                          |||||||||| || ||
                          TAGATGTACA AG TG
                          A_____      T A T
GAM496  TCP10       TGGGGGCATCTACAT-TTCA    7855  CA      G  ACT
                       TGG GCATCTACAT TTCA
                       ||| |||||||||| ||||
                       ACC CGTAGATGTA AAGT
                         CC     _    |||
GAM496  TCP10       TGGGGGCATCTACAT-TTCA    7855 _ CA      GTTCI
                         GG GCATCTACAT
                         || ||||||||||
                         CC CGTAGATGTA
                       A CC      AAGII
GAM496  TMEM1       TGACAGTATTTACATGTTCCAC    7856   C C     A TG
                       TGGCAG AT TACATGTTC AC
                       |||||| || ||||||||| ||
                       ACTGTC TA ATGTACAAG TG
                         A A      G ||
GAM496  TMEM1       TGACAGTATTTACATGTTCCAC    7856   C C     AAI
                        GGCAG AT TACATGTTC
                        ||||| || ||||||||||
                        CTGTC TA ATGTACAAG
                          A A      GTI
GAM496  TRPM7       CAGCAT-T-CATGTTCAAATG    7845    CTA      CI
                        CAGCAT  CATGTTCAA
                        ||||||  |||||||||
                        GTCGTA  GTACAAGTT
                          A__      TA
GAM496  TRPM7       CAGCAT-T-CATGTTCAAATG    7845 TGGCAGCATCTA      C
                           CATGTTCAA T
                           ||||||||| |
                           GTACAAGTT A
                        GTAA_____      T
GAM497  AP1M1       GCTGGCTGGCTGGCAAGCGT    7860  G  GCG     CA
                        TGGC GGCT  GGCAAGCGT
                        |||| ||||  |||||||||
                        ACCG CCGA  CCGTTCGCA
                         A    ___     AC
GAM497  AP1M1       GCTGGCTGGCTGGCAAGCGT    7860  G  _G     II
                        GC GGCTG C GGCAAGCG
                        || ||||| | ||||||||
                        CG CCGAC G CCGTTCGC
                         A    C A     AI
GAM497  BRF1        TGGCCTGCTGCGGGCCAAG    7874   GG      _ CGTCA
                        TGGC GCTGCGGGC AAG
                        |||| |||||||||| |||
```

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                              ACCG  CGACGCCCG TTC
                               GA       G  IIICA
GAM497   BRF1        TGGCCTGCTGCGGGCCAAG     7874  GG      AAII
                         TGGC GCTGCGGGC
                         IIII IIIIIIIII
                         ACCG CGACGCCCG
                           GA       GTTC
GAM497   CDH23       GCGGGCTGCCAGGGCCAAGC    7861       __ _   III
                         GCGGGCTGC GGGC AAG
                         IIIIIIIII IIII III
                         CGCCCGACG CCCG TTC
                            GT  G  GII
GAM497   CDH23       GCGGGCTGCCAGGGCCAAGC    7861 TGGC    __ _    GTCA
                         GGGCTGC GGGC AAGC
                         IIIIIII IIII IIII
                         CCCGACG CCCG TTCG
                          ____     GT  G  GTII
GAM497   CMAR        GGGCGGTCGTGCAAGCGTC     7870  TG_ G      II
                         GGGC  CG GCAAGCGT
                         IIII  II IIIIIIII
                         CCCG  GC CGTTCGCA
                          CCA  A       GI
GAM497   G6PD        GGCTGGCGGGCAAG-GCCAC    7869 T__  _  TG    AGCGTCA
                         GGCG GGC CGGGCA
                         IIII III IIIIII
                         CCGT CCG GTCCGT
                          CGC  T  GT    IIICACT
GAM497   G6PD        GGCTGGCGGGCAAG-GCCAC    7869     _     C  II
                         GGCTG CGGGCAAG GTCA
                         IIIII IIIIIIII IIII
                         CCGAC GCCCGTTC CGGT
                           C     _   GI
GAM497   GRB7        GGCGGGCTG-AGGCATGAGCCA   7867 _     C   __  GTCI
                         GCGGGCTG GGGCA AGC
                         IIIIIIII IIIII III
                         CGCCCGAC TCCGT TCG
                          C     _    AC   GIII
GAM497   GRB7        GGCGGGCTG-AGGCATGAGCCA   7867 TG    C  AGC  C
                         GCGGGCTG GGGCA GTCA
                         IIIIIIII IIIII IIII
                         CGCCCGAC TCCGT CGGT
                           __     _  ACT   C
GAM497   GRM4        GGCGGGGCAGGCGGGCAAG     7863    _T_     III
                         GGCGGG C GCGGGCAA
                         IIIIII I IIIIIIII
                         CCGCCC G CGCCCGTT
                           C TC     CII
GAM497   GRM4        GGCGGGGCAGGCGGGCAAG     7863 TG   _T_     CGTCA
                         GCGGG C GCGGGCAAG
                         IIIII I IIIIIIIII
```

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                         CGCCC G  CGCCCGTTC
                         __     C TC      TIIIC
GAM497 GRM4              GGCAGGCTGCGGGCCACAGGGACAC 7865 G_     TG   CAA GI
                         GCGGGC CGGG  GC
                         |||||| |||| ||
                         CGCCCG GTCC  TG
                         GA     GT   CTG  II
GAM497 GRM4              GGCAGGCTGCGGGCCACAGGGACAC 7865 TG          AA  TCACII
                         GCGGGCTGCGGGC GCG
                         ||||||||||||| |||
                         CGTCCGACGCCCG TGT
                         __          G_ CCCTGT
GAM497 LHB               TGGAAGGCTGCGGG-GAGGGTC  7875  C       CA C  AC
                         TGG GGGCTGCGGG AG GTC
                         ||| ||||||||||| || |||
                         ACC TCCGACGCCC  TC CAG
                          T       C_ C  II
GAM497 LHB               TGGAAGGCTGCGGG-GAGGGTC  7875 _ C      CA C  I
                         GG GGGCTGCGGG AG GT
                         || ||||||||||| || ||
                         CC TCCGACGCCC  TC CA
                         A  T       C_ C  I
GAM497 POU3F1           GGCGGGCTGCGCGCCCGCG      7866        G AA  II
                         GGCGGGCTGCG GC GC
                         |||||||||| || ||
                         CCGCCCGACGC CG CG
                           G  GG  CI
GAM497 POU3F1           GGCGGGCTGCGCGCCCGCG      7866 TG     G AA   CA
                         GCGGGCTGCG GC GCGT
                         |||||||||| || ||||
                         CGCCCGACGC CG CGCG
                         __        G GG  II
GAM497 PTTG1IP          GGCTGGGCTGCGG---AGCGTGCAC 7862 _ _     GCA   _ I
                         GC GGGCTGCGG  AGCGT CA
                         || ||||||||  ||||| ||
                         CG CCCGACGCC  TCGCA GT
                         C A       ___   C  I
GAM497 PTTG1IP          GGCTGGGCTGCGG---AGCGTGCAC 7862 TG _     GCA   _
                         GC GGGCTGCGG  AGCGT CAC
                         || ||||||||  ||||| |||
                         CG CCCGACGCC  TCGCA GTG
                         __ A       ___   C
GAM497 RTN2            GGCGTCCTGCGGGC-AGAGACAC  7868 _ GG     AGCGTCAI
                         GCG CTGCGGGCA
                         ||| ||||||||||
                         CGC GACGCCCGT
                         C AG      CTCTGTII
GAM497 RTN2            GGCGTCCTGCGGGC-AGAGACAC  7868 TG GG     _ _GT AC
                         GCG CTGCGGGCA AG C  C
                         ||| |||||||||| || | |
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                              CGC  GACGCCCGT TC G  G
                              __   AG       C T TG II
GAM497 S100B          TGGCGGGCTGCACGGTGCACGC    7873          __ _  A GTCAC
                              TGGCGGGCTGC GG GCA GC
                              IIIIIIIIII II III II
                              ACCGCCCGACG CC CGT CG
                                 TG  A   G  IIICA
GAM497 S100B          TGGCGGGCTGCACGGTGCACGC    7873          __ _  AGIII
                              TGGCGGGCTGC GG GCA
                              IIIIIIIIII II III
                              ACCGCCCGACG CC CGT
                                 TG  A   GCGII
GAM497 SOD3           GGGCTGCGGGGAGACTTCA     7871        CAA  GTCII
                              GGGCTGCGGG  GC
                              IIIIIIIII  II
                              CCCGACGCCC  TG
                                 CTC  AAGTI
GAM497 SOD3           GGGCTGCGGGGAGACTTCA     7871 TG   CTGC  A__  TCA
                              GCGGG  GGGC  AGCG
                              IIIII  IIII  IIII
                              CGCCC  TCTG  TCGT
                              A_   C___  AAG   CII
GAM497 SPG7           GGGCGGTCGTGCAAGCGTC     7870    TG_ G     II
                              GGGC  CG GCAAGCGT
                              IIII  II IIIIIIII
                              CCCG  GC CGTTCGCA
                                CCA  A     GI
GAM497 TEM7           GGGATACAGGCAAGCGTCAC     7872  C              I
                              GG TGCGGGCAAGCGTCA
                              II IIIIIIIIIIIIIII
                              CC ATGTCCGTTCGCAGT
                                 T        I
GAM497 TEM7           GGGATACAGGCAAGCGTCAC     7872 TGGCGGGC
                                 TGCGGGCAAGCGTCA
                              IIIIIIIIIIIIIII
                                 ATGTCCGTTCGCAGT
                                 _____
GAM497 TNFRSF11A       GGCGGGCTGCTGAGCATCCGT    7864 G    _    AGCGI
                              CGGGCTGC GGGCA
                              IIIIIIII IIIII
                              GCCCGACG CTCGT
                                _   A  AGGCI
GAM497 TNFRSF11A       GGCGGGCTGCTGAGCATCCGT    7864 TG     _  AG  CAC
                              GCGGGCTGC GGGCA CGT
                              IIIIIIIII IIIII III
                              CGCCCGACG CTCGT GCA
                                __    A  AG  CII
GAM498 ADPRT          CACCGGGTGTGACTCGGCTAC     7881 TCACA     _ __  ACTA
                              GGGTGTGACT GGC CC
                              IIIIIIIIII III II
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                          CCCACACTGA CCG  GG
                        TGG__        G  AT  IIIA
GAM498 ENC1             TCACAGGGTGAGAATGGTCAAGTA  7888       T  C   CCCACTAI
                         TCACAGGGTG GA TGG
                         ||||||||| || |||
                         AGTGTCCCAC CT ACC
                            T  T  AGTTCATI
GAM498 FEN1             CACAGAGGAGGGATGACTGGCC   7878 TCAC___   T      CACTA
                          AGGG GTGACTGGCC
                          |||| ||||||||||
                          TCCC TACTGACCGG
                         TGTCTCC   _      AIIIA
GAM498 GNA15            TCCCAGGGTGTGCGTCACCCAC   7886 A      ACTG    TA
                         TC CAGGGTGTG  GCCCAC
                         || |||||||||  ||||||
                         AG GTCCCACAC  TGGGTG
                           G     GCAG    II
GAM498 ICA1            CAGTGTGAGAACACTGGCCCAC   7883 TCACAGG  T ___
                        GTG GA  CTGGCCCACTA
                        ||| ||  ||||||||||
                        CAC CT  GACCGGGTGGT
                       A_____  T TGT
GAM498 POU2AF1         CAGAGGGTGTGAGTGACCC   7879 TCAC     C    ACT
                         AGGGTGTGA TGGCCC
                         ||||||||| ||||||
                         TCCCACACT ACTGGG
                       TC__     C   AII
GAM498 PRX            CAGAGGGCAAGGCTGGCCCAC   7882 TCAC    TGA      TA
                       AGGGTG CTGGCCCAC
                       |||||| |||||||||
                       TCCCGT GACCGGGTG
                       TC__  TCC      CI
GAM498 RASSF1        TCTCAGGGCAGCCCTGGCCCACTA  7889 A    _ GA        I
                       TC CAGGGT GT CTGGCCCACTA
                       || |||||| || ||||||||||
                       AG GTCCCG CG GACCGGGTGAT
                        A    T G_       I
GAM498 SFTPA2        TCACAGGGT-TGGCTTGGGCACCAC  7885     G  A __ _ TAI
                       TCACAGGGT TG CT GGC CCAC
                       ||||||||| || || ||| ||||
                       AGTGTCCCA AC GA CCG GGTG
                        _ C AC  T   III
GAM498 SH3BP2        TCACAGG--GTCACTGCCCCTCT  7887     GTG  G  A A
                       TCACAGGGT  ACTG CCC CT
                       |||||||||  |||| ||| ||
                       AGTGTCCCA  TGAC GGG GA
                           G__  G A I
GAM498 SLC14A2       CAGGGTGTG-GTGGCACAC       7884 TCACAG    AC  C
                       GGTGTG  TGGC CAC
                       |||||| |||| |||
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                           CCACAC  ACCG GTG
                           _____      C_  T
GAM498  SYN3      CAGAGGGTGTGA-T-GCCCA    7880 TCAC      CTG   C
                           AGGGTGTGA  GCCCA
                           ||||||||| |||||
                           TCCCACACT CGGGT
                           TC__      A__   A
GAM499  CELL      TCAC-TGTGGGCAGCGCCA    7895  C     CA_ TCGA
                           TCAC TGTGGGCA  CCA
                           |||| |||||||| |||
                           AGTG ACACCCGT GGT
                            _      CGC  IIIA
GAM499  CELL      TCAC-TGTGGGCAGCGCCA    7895  C     CACCII
                           TCAC TGTGGGCA
                           |||| ||||||||
                           AGTG ACACCCGT
                            _      CGCGGT
GAM499  CFTR      CAGCTGTGGGCAACAAC-TCGA    7892 AC      _ CCA  I
                           CTGTGGGCA CA  TCG
                           |||||||||| ||  |||
                           GACACCCGT GT  AGC
                           TC      T TG_  I
GAM499  CFTR      CAGCTGTGGGCAACAAC-TCGA    7892 TCAC      _ CCA   GA
                           CTGTGGGCA CA  TCGA
                           |||||||||| ||  ||||
                           GACACCCGT GT  AGCT
                           TC__      T TG_  AI
GAM499  SELE      CCTGTGGGCATTCAACATC    7894        __ C  III
                           CCTGTGGGCA CA CAT
                           |||||||||| || |||
                           GGACACCCGT GT GTA
                            AA  T  GII
GAM499  SELE      CCTGTGGGCATTCAACATC    7894 TCACCT    __ C  GAG
                           GTGGGCA CA CATC
                           ||||||| || ||||
                           CACCCGT GT GTAG
                           _____      AA  T  ACA
GAM499  SLC19A1      CACCTGTGGGCAAGGCACTAGCG    7893 ACC      ___ CATCI
                           TGTGGGCA CAC
                           |||||||| |||
                           ACACCCGT GTG
                            ___      TCC  ATCGI
GAM499  SLC19A1      CACCTGTGGGCAAGGCACTAGCG    7893 TC      ___ CAT AGAI
                           ACCTGTGGGCA CAC  CG
                           ||||||||||| ||| ||
                           TGGACACCCGT GTG  GC
                            __      TCC  ATC GIII
GAM500  ABCD4      CATGCTTGTGCTTTCTGGGTT    7899    AG ___      III
                           CATGCT GT  TTCTGGGT
                           |||||| ||  ||||||||
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                    GTACGA CA  AAGACCCA
                     AA CGA      AII
GAM500 ABCD4        CATGCTTTGTGCTTTCTGGGTT   7899 TGGCA_   AGGT      CT
                     TGCT   TTCTGGGTT
                     ||||   |||||||||
                     ACGA   AAGACCCAA
                     CGAAAC  ____       AA
GAM500 BLTR2        GGCATGGTGCTAGGTTCCAGG   7904  ___        TGIII
                     GGCA  TGCTAGGTTTC
                     ||||  ||||||||||
                     CCGT  ACGATCCAAGG
                      ACC         TCCII
GAM500 BLTR2        GGCATGGTGCTAGGTTCCAGG   7904 ___ CA      T  TTCT
                     TGG  TGCTAGGTTTC GGG
                     |||  |||||||||||| |||
                     ACC  ACGATCCAAGG CCT
                     CGT  __        T  IIIT
GAM500 CD1C         GGC-TCCTGGGTTGCTGGGTTCT   7907 _ ATG A  T     I
                      GC  CT GGTT CTGGGTTC
                      ||  || |||| |||||||||
                      CG  GA CCAA GACCCAAG
                      C AG_ C  C      I
GAM500 CD1C         GGC-TCCTGGGTTGCTGGGTTCT   7907 TGGCATG A   T
                        CT GGTT CTGGGTTCT
                        || |||| |||||||||
                        GA CCAA GACCCAAGA
                     CGAG___  C   C
GAM500 ERBB2        GGCAGTACTAGGTTTCAGGG   7903   _        T II
                     GGCA TGCTAGGTTTC GG
                     |||| |||||||||| ||
                     CCGT ATGATCCAAAG CC
                        C     T CI
GAM500 ERBB2        GGCAGTACTAGGTTTCAGGG   7903 TG _      T TTC
                      GCA TGCTAGGTTTC GGG
                      ||| |||||||||| |||
                      CGT ATGATCCAAAG CCC
                      __  C      T TII
GAM500 HPS4         GCATGCTAG--AGCTGGTGTTCT   7902 _     TTT  _ I
                     CATGCTAGG CTGG GTTC
                     ||||||||| |||| ||||
                     GTACGATCT GACC CAAG
                       C   C__ A  I
GAM500 HPS4         GCATGCTAG--AGCTGGTGTTCT   7902 TGGC    TTT  _
                      ATGCTAGG CTGG GTTCT
                      |||||||| |||| |||||
                      TACGATCT GACC CAAGA
                      ____      C__ A
GAM500 MARS         CTAGGGTTGCTCTGGGTTCT   7900  T___       III
                      CTAGG  TTCTGGGTTC
                      |||||  ||||||||||
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                          GATCC   GAGACCCAAG
                           CAAC        AII
GAM500 MMP19         TGGCATG---GGA--CTGGGTTCT  7908      CTA TTT
                     TGGCATG GG CTGGGTTC
                     |||||| || ||||||||
                     ACCGTAC CC GACCCAAG
                          ___  T__
GAM500 MMP19         TGGCATG---GGA--CTGGGTTCT  7908 _    CTA TTT
                      GGCATG GG CTGGGTT
                      |||||| || |||||||
                      CCGTAC CC GACCCAA
                      A    ___ T__
GAM500 PON2        CATGCCATACATTTCTGGGT     7898       G__       III
                    CATGCTA GTTTCTGGG
                    ||||||| |||||||||
                    GTACGGT TAAAGACCC
                          ATG        AII
GAM500 PON2        CATGCCATACATTTCTGGGT     7898 T G   TAG        C
                     G CATGC GTTTCTGGGTT
                     | ||||| ||||||||||||
                     C GTATG TAAAGACCCAG
                      _ G    ___         T
GAM500 SLC10A1      GGCAGATTCGGTTTCTGGTTTC  7906   TGCTA      GTTI
                     GCA   GGTTTCTGG
                     |||   ||||||||||
                     CGT   CCAAAGACC
                      CTAAG       AAAI
GAM500 SLC10A1      GGCAGATTCGGTTTCTGGTTTC  7906 TG  TGCTA      G  T
                      GCA   GGTTTCTGG TTC
                      |||   |||||||||| |||
                      CGT   CCAAAGACC AAG
                      __  CTAAG       A  T
GAM500 SLC39A4      GGCTT-CTGGGTTTCTGGG     7905  ATG A      I
                      GGC  CT GGTTTCTGG
                      |||  || |||||||||
                      CCG  GA CCAAAGACC
                       AA_  C        C
GAM500 SLC39A4      GGCTT-CTGGGTTTCTGGG     7905 TG  ATG A        T
                      GC  CT GGTTTCTGGGT
                      ||  || |||||||||||
                      CG  GA CCAAAGACCCG
                      __  AA_ C         I
GAM500 THBD      GCATACTCGGATTGCTGGGTTCT  7901 C    A T _     I
                  ATGCT GG TT CTGGGTTC
                  ||||| || || |||||||||
                  TATGA CC AA GACCCAAG
                   _   G  T  C        I
GAM500 THBD      GCATACTCGGATTGCTGGGTTCT  7901 TGGC    A T _      I
                  ATGCT GG TT CTGGGTTCT
                  ||||| || || |||||||||
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                        TATGA CC AA GACCCAAGA
                 ____       G T C      G
GAM501 AK1       TGGGAATACAGGCACATGCCACC  7916      ___ _      TTTTAl
                 TGGGAATAC  CATA GCCACC
                 |||||||||  |||| ||||||
                 ACCCTTATG  GTGT CGGTGG
                    TCC   A     lllATT
GAM501 ARSD      TGGGATTAAAGGCATGAGCCACCTT 7915    A C___ _      TTAll
                 TGGGA TA   CAT AGCCACCTT
                 ||||| ||   ||| |||||||||
                 ACCCT AT   GTA TCGGTGGAA
                    A TTCC  C      lllAT
GAM501 DACH      AATAACACATAGCCACCCTT    7911 TGGGAAT _
                   AC CATAGCCACCTTTT
                   || ||||||||||||||
                   TG GTATCGGTGGGAAG
                 _____ T
GAM501 DEDD      GGGAATACCACTTCCACTTTCTTTT 7912 TG      AG  C  All
                 GGAATACCAT CCAC TTTT
                 |||||||||| |||| ||||
                 CCTTATGGTG GGTG AAGA
                  __       AA  A  AAA
GAM501 IDH3B     TGGCAAGTAGCATAGCCACC   7914  G _ C      TTTT
                 TGG AA TA CATAGCCACC
                 ||| || || |||||||||||
                 ACC TT AT GTATCGGTGG
                    G C C      lllA
GAM501 TCF3      TGGGAGGGTCAGAGCCACCTT   7917  ATAC T     TTA
                 TGGGA  CA AGCCACCTT
                 |||||  || |||||||||
                 ACCCT  GT TCGGTGGAA
                    CCCA  C      lll
GAM501 TIC       GGGAA-ACTGTCGCCACCTTTTA 7913 T    ACCATA
                 GGGAAT   GCCACCTTTTA
                 ||||||   |||||||||||
                 CCTTTG   CGGTGGAAAAT
                  _     ACAG__
GAM502 CAPN9     AGTGG-ATGGAAAAGAAAGTG   7920 TTA  CAA      TT
                  GTGG  GGAAGAAAGTG
                  ||||  |||||||||||
                  TACC  TTTTCTTTCAC
                 ACC    ___      TT
GAM502 HBD       TTA-TGTCA--GAAGAAAGTGT  7923 TTA  GCAA       T
                  GTG   GGAAGAAAGTGT
                  |||   |||||||||||
                  TAC   TCTTCTTTCACA
                 AA_ AG__       l
GAM502 SCGB2A2   GTGGCAAGGATCAAGGAAG    7921 TTAGTG    ___ A  GTT
                 GCAAGGA AG AAGT
                 |||||||  || ||||
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                         CGTTCCT   TC TTCG
                  _____         AGT  C   GCI
GAM502 ZNFN2A1        TGGTAATGAAAGAAAGTGGTC    7922 TTAGTGGCAA        T
                         GGAAGAAAGTG TC
                         |||||||||| ||
                         CTTTCTTTCAC AG
                  TTA_____           C
GAM503 APBA2          AACAGTAATAATAGCATCTA-AAT  7927 TA    _       CAATI
                         ACAGTA TAATAGCATTTA
                         |||||| |||||||||||
                         TGTCAT ATTATCGTAGAT
                         __   T      TTATI
GAM503 ATP6V1C1      AACAGTATAAATG--TTTACA    7929 TA     TAGCA    A
                         ACAGTATAA   TTTACA
                         |||||||||   ||||||
                         TGTCATATT   AAATGT
                         __      TAC__   G
GAM503 BCRP2         TATAAAACCAGCATTTACAAT    7951 TAACAGTATAA
                         TAGCATTTACAAT
                         |||||||||||||
                         GTCGTAAATGTTA
                  TG_____
GAM503 BRCA1         TAACAGCACAA---CATTTACAA  7949       ATA
                         TAACAGTATA  GCATTTACAA
                         |||||||||| ||||||||||
                         ATTGTCGTGT  TGTAAATGTT

                         ___
GAM503 CASP3         AACAGTATAA-AACA-TTACTAT  7931 TA     T   T AAT
                         ACAGTATAA AGCATT AC
                         ||||||||| |||||| ||
                         TGTCATATT TTGTAA TG
                         __    _   _ ATA
GAM503 CCNT2         AAAAGTGAATACATAGCATTTCAAAT 7926 TAAC__    A    A TII
                         AGTATA TAGCATTT CAA
                         |||||| |||||||| |||
                         TTATGT ATCGTAAA GTT
                  TTTCAC    _     _  TAA
GAM503 DISC1         ACAGTATAATATCACACTTACA   7932 TAAC        __       AT
                         AGTATAATA GCATTTACA
                         ||||||||| |||||||||
                         TCATATTAT TGTGAATGT
                         ____      AG      AA
GAM503 DKK1          TAAAAGTTTCATTGCATTTACA   7947  C ATA A     AT
                         TAA AGT  AT GCATTTACA
                         ||| |||  || |||||||||
                         ATT TCA  TA CGTAAATGT
                         T  AAG A      II
GAM503 DSCR5         TAACAATACTTGAACATTTACAAT  7950        AAT       I
                         TAACAGTAT AGCATTTACAAT
                         ||||||||| ||||||||||||
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                        ATTGTTATG  TTGTAAATGTTA
                           AAC            I
GAM503 FPRL1        TAACAGTATATAAACATAAACA   7948        AT   TT  AT
                   TAACAGTATA  AGCAT  ACA
                   |||||||||| |||||  |||
                   ATTGTCATAT  TTGTA  TGT
                       AT    TT  II
GAM503 GM2A        ACATTGTAATAGCATCTTTAAT   7939 TAACAGTA        ACAAT
                       TAATAGCATTT
                       |||||||||||
                       ATTATCGTAGA
                   TAAC____        AATTA
GAM503 KLK3        ACAGTATAACAGCTCTTTA     7934 TAAC      A_  CAA
                     AGTATAATAGC  TTTA
                     |||||||||| ||||
                     TCATATTGTCG  AAAT
                   ____         AG   AAI
GAM503 MEN1        ACAATATAG--GCATTTACAA    7937 TAAC    ATA
                     AGTATA  GCATTTACAA
                     ||||||  ||||||||||
                     TTATAT  CGTAAATGTT
                   ____        C__
GAM503 MYB        TAACCATA-AATGAGCATTTACAAT 7943   A  TAAT       I
                     TAAC GTA   AGCATTTACAAT
                     |||| |||   |||||||||||
                     ATTG TAT   TCGTAAATGTTA
                      G   TTAC           I
GAM503 NAB1        TAACAGTATAAAAGTTGTTTAC   7945        T CA_   AAT
                     TAACAGTATAA AG  TTTAC
                     |||||||||| || |||||
                     ATTGTCATATT TC  AAATG
                       T AAC    III
GAM503 PEX1        ACATAATTATAGCATTTACCAAT   7935 TAACAGTATA       AATI
                       ATAGCATTTAC
                       |||||||||||
                       TATCGTAAATG
                   TATTAA____        GTTA
GAM503 PLGL        ACAGTATAACAACGATTACA     7936 TAAC      AT   A
                     AGTATAATAGC  TTACA
                     |||||||||| |||||
                     TCATATTGTTG  AATGT
                   ____         CT   A
GAM503 PLGL        TAACAACGATTACATAGCATTTACA 7941   TATA___      ATII
                     TAACAG     ATAGCATTTACA
                     ||||||     ||||||||||||
                     ATTGTT     TATCGTAAATGT
                      GCTAATG          IIIT
GAM503 PRSS16       TAACATTCAAAATACCAATATTTACAAT7942    GTAT_  G  ___      III
                     TAACA    AATA CA  TTTACAAT
                     |||||    |||| ||  ||||||||
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                    ATTGT    TTAT GT  AAATGTTA
                    AAGTT    G  TAT       III
GAM503  SCML2       AATATTTTATTGGCATTTACAA    7930 TAACAGTATAATA
                            GCATTTACAAT
                            IIIIIIIIII
                            CGTAAATGTTG
                    TATAAAATAAC__
GAM503  SELE        AGT-TGACAGCATTTACAA    7940 TAACAGTATA
                            ATAGCATTTACA
                            IIIIIIIIIII
                            TGTCGTAAATGT
                    C_____
GAM503  SON         ACAGTATAAAAGCGTTATTTA    7933 TAAC    T  ATTTACAAT
                            AGTATAA AGC
                            IIIIIIII III
                            TCATATT TCG
                    ____      T  CAATAAATT
GAM503  TAF5        TAA-ATTAAAATAGCATTT    7946 TAACAG  T    ACA
                            TA AATAGCATTT
                            II IIIIIIIIII
                            AT TTATCGTAAA
                    ATTTA_ T       III
GAM503  TM4SF6      ACAGTATTACTTCATTTACAAT    7938 TAAC    A  AG
                            AGTAT AT  CATTTACAAT
                            IIIII II  IIIIIIIIII
                            TCATA TG  GTAAATGTTA
                    ____      A  AA
GAM503  TSG         TAAAA-TATGGTAAGCATTTAC    7944 TAAC    AAT_      AAT
                            AGTAT  AGCATTTAC
                            IIIII  IIIIIIIII
                            TTATA  TCGTAAATG
                    ATT_  CCAT       III
GAM503  UBE2A       AACATTAGACAAACATTTACAA    7928 TAAC_ T  T     TI
                            AG ATAA AGCATTTACAA
                            II IIII IIIIIIIIII
                            TC TGTT TTGTAAATGTT
                    TGTAA _ _        CI
GAM504  ADARB1      GACACACACGG--AACACAAT    7986 TG     AGT_ CACCATC
                            ACACACAC  CAC
                            IIIIIIII  III
                            TGTGTGTG  GTG
                        __    CCTT  TTACIII
GAM504  ADRB3       GACACACACACACACAC    7983 TG     GT _ CATC
                            ACACACACA CAC CAC
                            IIIIIIIII III III
                            TGTGTGTGT GTG GTG
                        __    GT  T  TIII
GAM504  ADRB3       ACACACACACACACACACCAT    7966 TG     GT _ CA
                            ACACACACA CAC CACCAT
                            IIIIIIIII III IIIIII
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                            TGTGTGTGT GTG GTGGTA
                            __        __ T   CA
GAM504 AMPD3       ACACACACACACAACTAACA   7980 TG      GT  C  CATCA
                            ACACACACA CAC AC
                            ||||||||| ||| ||
                            TGTGTGTGT GTG TG
                            __        __ T ATTGT
GAM504 AOAH       TGACACACACA--CCCCACCCTC   7991        G A   A A
                            TGACACACACA TC CCACC TC
                            ||||||||||| || ||||| ||
                            ACTGTGTGTGT GG GGTGG AG
                                     _ _    G I
GAM504 BCL7A       ACACACACACACACACACAT   7963 TG      GT _  _ CA
                            ACACACACA CAC CAC CAT
                            ||||||||| ||| ||| |||
                            TGTGTGTGT GTG GTG GTA
                            __        __ T  T  TG
GAM504 CHC1L       GACAAAGACCACTCACCACCATC   7981 T____  A  ACAG     AI
                            GAC CAC   TCACCACCATC
                            ||| |||   ||||||||||
                            CTG GTG   AGTGGTGGTAG
                            TGTTT _  ____         GI
GAM504 DCX       ACACACACACACACATGCACCA   7958 TG__     GT    ATCA
                            ACACACACA CACCACC
                            ||||||||| |||||||
                            TGTGTGTGT GTGGTGG
                            TGTG      AC    IIIA
GAM504 DMC1       ACACACACACACACAAACAT   7976 TG__      T CCACCATC
                            ACACACACAG CA
                            |||||||||| ||
                            TGTGTGTGTT GT
                            TGTG       T ATGIIIAC
GAM504 EPHB3       ACACACACACACACACTCACACATC 7957 TG     GT _ _ AII
                            ACACACACA CAC CAC CATC
                            ||||||||| ||| ||| ||||
                            TGTGTGTGT GTG GTG GTAG
                            __        GT A T GGI
GAM504 EPHB3       ACACACACACTCACACATCCCATC   7961 TGAC    G  _  _    AI
                            ACACACA TCAC CA  CCATC
                            ||||||| |||| ||  |||||
                            TGTGTGT AGTG GT GGTAG
                            ____     G  T AG   AG
GAM504 FAT2       ACACACACAGCCACAAACCACTCA   7965 TGAC       C_  CAI
                            ACACACAGTCAC ACCAT
                            |||||||||||| |||||
                            TGTGTGTCGGTG TGGTG
                            ____        TT  AGT
GAM504 FLT1       ACACACACAGTTACACCAC      7956 TGAC      __  CATC
                            ACACACAGT CACCAC
                            ||||||||| ||||||
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                        TGTGTGTCA GTGGTG
                          ____      AT    ACII
GAM504  FXYD6         ACACACACACACACACA-CATCA   7967 TG       GT _ C
                        ACACACACA CAC CAC ATCA
                        ||||||||| ||| ||| ||||
                        TGTGTGTGT GTG GTG TAGT
                          __        __ T _
GAM504  GRM4          GACACACACAGAGGCCACCA      7984 TG       TCA   TC
                        ACACACACAG  CCACCA
                        |||||||||  ||||||
                        TGTGTGTGTC GGTGGT
                          __        TCC   CI
GAM504  GSTM5         ACACACACACACACACCCATC     7977 TG      GT CA   A
                        ACACACACA CAC CCATC
                        ||||||||| ||| |||||
                        TGTGTGTGT GTG GGTAG
                          __         __ TG   A
GAM504  HMGB2         ACACACACATTCCACACGCATCA   7969 TGAC     G AC _   I
                        ACACACA TC CAC CATCA
                        ||||||| || ||| |||||
                        TGTGTGT AG GTG GTAGT
                          ____      A GT  C   A
GAM504  HSPA4         ACACACACACACACACACCA      7964 TG       GT _   C
                        ACACACACA CAC CACCAT
                        ||||||||| ||| ||||||
                        TGTGTGTGT GTG GTGGTA
                          __        __ T    C
GAM504  IL21R         ACACACACAGACACTGTAAACATCA 7960 TGAC     T CAC___   II
                        ACACACAG CAC     CATCA
                        |||||||| |||     |||||
                        TGTGTGTC GTG     GTAGT
                          ____       T  ACATTT   CC
GAM504  IL21R         GACACACACACACACAC         7983 TG       GT _ CATC
                        ACACACACA CAC CAC
                        ||||||||| ||| |||
                        TGTGTGTGT GTG GTG
                          __        GT  T  TIII
GAM504  JUND          ACACACACACACACAACCA       7970 TG      GT C  TC
                        ACACACACA CAC ACCA
                        ||||||||| ||| ||||
                        TGTGTGTGT GTG TGGT
                          __        __ T  CC
GAM504  KCNN4         GACACACACAGACA-CACGAT     7985 TG       T C CATC
                        ACACACACAG CAC AC
                        |||||||||| ||| ||
                        TGTGTGTGTC GTG TG
                          __         T _ CTAC
GAM504  KCNN4         TGACACACACCTCTACTCACCAC   7987         AG _ _   CAI
                        TGACACACAC TC AC CACCAT
                        |||||||||| || || ||||||
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                        ACTGTGTGTG  AG TG GTGGTG
                            G_  A A    III
GAM504 MAX          ACACACACACTCACTCACTCACTCA 7962 TG    A  G   _  _  CAII
                        ACACAC CA TCAC CAC CAT
                        IIIIII II IIII III III
                        TGTGTG GT AGTG GTG GTG
                        TG    A G   A  A AIII
GAM504 MEF2A        ACACACACACTCACACCCA      7973 TGAC    G   CA   C
                        ACACACA TCAC  CCAT
                        IIIIIIII IIII  IIII
                        TGTGTGT AGTG  GGTG
                        ____      G   TG   T
GAM504 MPP2        TGACACACACACACACAC      7989       GT  _  CATC
                        TGACACACACA  CAC CAC
                        IIIIIIIIIII III III
                        ACTGTGTGTGT GTG GTG
                            GT  T  IIIA
GAM504 NOS1        ACACACACAGGCACGCACAACCA 7968 TGAC    T  _  C   I
                        ACACACAG CAC CAC ATCA
                        IIIIIIII III III IIII
                        TGTGTGTC GTG GTG TGGT
                        ____       C  C  T   T
GAM504 PFKFB2       GAAACACACAGTTACACCACC   7982 TGAC     __       ATCA
                        ACACACAGT CACCACC
                        IIIIIIIII IIIIIII
                        TGTGTGTCA GTGGTGG
                        TT__     AT     CIII
GAM504 PITX1        ACACACACA-CCACCCGCGCCATC 7959 TG     AGT  A___   AI
                        ACACACAC CACC  CCATC
                        IIIIIIII IIII  IIIII
                        TGTGTGTG GTGG  GGTAG
                        __     ___  GCGC   GG
GAM504 PKD1        ACACACACACACA-CACAGTCA    7979 TG____       ACCATCA
                        ACACACACAGTCACC
                        IIIIIIIIIIIIIII
                        TGTGTGTGTCAGTGG
                        TGTGTG        IIIACTA
GAM504 PTGFRN        ACCCATCACATTTACCACCATC   7954 TGACA _ GTC     A
                        CA CACA  ACCACCATC
                        II IIII  IIIIIIIII
                        GT GTGT  TGGTGGTAG
                        G____  A  AAA      C
GAM504 SFN          ACACACACACCCATCTCCA    7972 TG    A_  A  CCATC
                        ACACACAC GTC CCA
                        IIIIIIII III III
                        TGTGTGTG TAG GGT
                        __      GG  A  CGIII
GAM504 SFN          ACACACACACACACACCCATC    7977 TG    GT CA  A
                        ACACACACA CAC CCATC
                        IIIIIIIII III IIIII
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                          TGTGTGTGT GTG GGTAG
                          __      __ TG   A
GAM504 SLC25A1       TGTCACACACAG--ACCAC      7990 TGA      TC   CAT
                          CACACACAG ACCAC
                          |||||||| |||||
                          GTGTGTGTC TGGTG
                          ACA       __  |||
GAM504 SLC30A3       ACACACACAGACAAAACCA      7975 TGAC    T CC   C
                          ACACACAG CA ACCAT
                          |||||||| || |||||
                          TGTGTGTC GT TGGTG
                          ___        T TT   T
GAM504 SYNGR1       TGTCAC-CAGAAGTCACCACCTTCA 7988 TGA  A C_      A  |
                          CAC CA AGTCACCACC TCA
                          ||| || |||||||||| |||
                          GTG GT TCAGTGGTGG AGT
                          ACA _ CT      A  |
GAM504 TCF15        ACACACACACCCTGTCACCAACA   7955 TG      A__    C TCA|
                          ACACACAC  GTCACCA CA
                          ||||||||  ||||||| ||
                          TGTGTGTG  CAGTGGT GT
                          __       GGA    T CA||
GAM504 USF2         ACACACACACACACCCCCA       7971 TG      GT  A  TC
                          ACACACACA CACC CCA
                          ||||||||| |||| |||
                          TGTGTGTGT GTGG GGT
                          __       __ G  TT
GAM504 WSX1         ACACACACACTCTCTGCCA       7974 TG      AG A_  CCATC
                          ACACACAC TC CCA
                          |||||||| || |||
                          TGTGTGTG AG GGT
                          __       AG AC  TT|||
GAM504 WT1          ACACACACACACACGACCATC     7978 TG      GT  C   A
                          ACACACACA CAC ACCATC
                          ||||||||| ||| ||||||
                          TGTGTGTGT GTG TGGTAG
                          __       __ C   A
GAM505 ATSV         CAGGCATGGGATTGGGGTCTCT    7995 CAG   T    C|
                          GTGG ATTGGGGTC
                          |||| |||||||||
                          TACC TAACCCCAG
                          G__      C    AG
GAM505 ATSV         CAGGCATGGGATTGGGGTCTCT    7995 TGGCAG   T    C C
                          GTGG ATTGGGGTC CT
                          |||| ||||||||| ||
                          TACC TAACCCCAG GA
                          CG___     C    A C
GAM505 B4GALT1      GGCAG-TGGT-TTGGGGTCC      8010      G  A   |
                          GGCAG TGGT TTGGGGT
                          ||||| |||| |||||||
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                      CCGTC ACCA AACCCCA
                      _   _        G
GAM505 B4GALT1        GGCAG-TGGT-TTGGGGTCC    8010 TG   G   A        C
                      GCAG TGGT TTGGGGTCC
                      |||| |||| |||||||||
                      CGTC ACCA AACCCCAGG
                      __   _   _        C
GAM505 BMP1           GCAGGACGCA--GGGGTCCCTC   8001    TG  TT       I
                      GCAGG GTA GGGGTCCC
                      ||||| ||| |||||||||
                      CGTCC CGT CCCCAGGG
                            TG  __      A
GAM505 BMP1           GCAGGACGCA--GGGGTCCCTC   8001 TGGC TG  TT
                      AGG GTA GGGGTCCCT
                      ||| ||| |||||||||
                      TCC CGT CCCCAGGGA
                      ____     TG  __
GAM505 CYP1A2         GGCAGGTGGATAACTTGGGGTC   8006        TA___     III
                      GGCAGGTGG   TTGGGGT
                      |||||||||   |||||||
                      CCGTCCACC   AACCCCA
                      TATTG    GII
GAM505 CYP1A2         GGCAGGTGGATAACTTGGGGTC   8006 TG    TA___     CCTC
                      GCAGGTGG   TTGGGGTC
                      ||||||||   |||||||||
                      CGTCCACC   AACCCCAG
                      __       TATTG    TIII
GAM505 DLG5           GGCAGGTGGGA--GGAGTCCC   8012 _      TATT     I
                      GCAGGTGG   GGGGTCC
                      ||||||||   |||||||
                      CGTCCACC   CCTCAGG
                      C       CT__     I
GAM505 DLG5           GGCAGGTGGGA--GGAGTCCC   8012 TG     TATT
                      GCAGGTGG   GGGGTCCCT
                      ||||||||   |||||||||
                      CGTCCACC   CCTCAGGGG
                      __       CT__
GAM505 DNASE1L1       TGGCAGGTGGCATGAGTGCAGGGCCCCT8023              CIII
                      TGGCAGGTGGTAT   TGGGGTCCCT
                      |||||||||||||   ||||||||||
                      ACCGTCCACCGTA   GTCCCGGGGA
                      CTCAC       IIIC
GAM505 DNASE1L1       TGGCAGGTGGCATGAGTGCAGGGCCCCT8023 __  __  GTAT     I
                      GGCA GGTG  TGGGGTCCC
                      |||| |||| |||||||||
                      CCGT TCAC  GTCCCGGGG
                      CA  AC   ____      I
GAM505 EGLN2          TGGCCTCACCACTG-CCACTGCTG   8019 A   AG__ T       II
                      TG CCTCA  TG CCACTGCTG
                      || ||||| || |||||||||
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                        AC GGAGT   AC GGTGACGAC
                          C   GGTG _      II
GAM505 FADD             GCAGGTGGTCTGTGGCTCACTC   8002      A  _  G C I
                          CAGGTGGT TTG GG TC CT
                          IIIIIIII III II II II
                          GTCCACCA GAC CC AG GA
                            _   A G T I
GAM505 FADD             GCAGGTGGTCTGTGGCTCACTC   8002 TGGC    A  _  G C
                           AGGTGGT TTG GG TC CTC
                           IIIIIII III II II III
                           TCCACCA GAC CC AG GAG
                           ____     _ A G T
GAM505 FGFR1            GCAGTGTGGGGTTTGGGGTCCC   7999 CA__ T  A      I
                            GG GGT TTGGGGTCC
                            II III IIIIIIIII
                            CC CCA AACCCCAGG
                           CACA _  _      I
GAM505 FGFR1            GCAGTGTGGGGTTTGGGGTCCC   7999 TGGCA T  A      TC
                            GG GGT TTGGGGTCCC
                            II III IIIIIIIIII
                            CC CCA AACCCCAGGG
                           TCACA _  _        TG
GAM505 GALNS           GGCAGGTGGAATTGTCAGTCCC   8008 GC    TAT__ G  I
                            AGGTGG   TG GGTCC
                            IIIIII   II IIIII
                            TCCACC   AC TCAGG
                            __    TTAAC G  I
GAM505 GALNS           GGCAGGTGGAATTGTCAGTCCC   8008 TG    TAT__ G   CI
                            GCAGGTGG   TG GGTCCCT
                            IIIIIIII   II IIIIIII
                            CGTCCACC   AC TCAGGGG
                            __     TTAAC G   II
GAM505 GRB7            CAGGTGGTAGGAGGGTGTCCC   7996    TT_ _  III
                            CAGGTGGTA GGG GTCC
                            IIIIIIIII III IIII
                            GTCCACCAT CCC CAGG
                             CCT  A  GII
GAM505 GRB7            CAGGTGGTAGGAGGGTGTCCC   7996 TGGCAG   TT_ _  TC
                             GTGGTA GGG GTCCC
                             IIIIII III IIIII
                             CACCAT CCC CAGGG
                             _____   CCT  A  CT
GAM505 ITGA7          GGCAGGTCCT--TGGGGTCC   8011    GGTA   I
                            GGCAGGT TTGGGGT
                            IIIIIII IIIIIII
                            CCGTCCA AACCCCA
                             GG__   G
GAM505 ITGA7          GGCAGGTCCT--TGGGGTCC   8011 TG    GGTA    C
                            GCAGGT TTGGGGTCC
                            IIIIII IIIIIIIII
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                          CGTCCA  AACCCCAGG
                      __    GG__        A
GAM505 KCNQ1          CATGGGGTATTGGGGCCTCT    7998 CA  T        CI
                      GG GGTATTGGGGTC
                      || ||||||||||||
                      CC CCATAACCCCGG
                      A_ _          AG
GAM505 KCNQ1          CATGGGGTATTGGGGCCTCT    7998 TGGCA  T        C
                      GG GGTATTGGGGTC CT
                      || |||||||||||| ||
                      CC CCATAACCCCGG GA
                      _____ _          A
GAM505 KLK3         GCAGGTGGTAAGCTTGGGG       8000        ___    III
                      GCAGGTGGTA  TTGGG
                      |||||||||| |||||
                      CGTCCACCAT  AACCC
                        TCG    CII
GAM505 KLK3         GCAGGTGGTAAGCTTGGGG       8000 TGGC     ___     CCCT
                      AGGTGGTA  TTGGGGT
                      |||||||| |||||||
                      TCCACCAT  AACCCCG
                      ____      TCG    AIII
GAM505 LENG4       CAGGCGCCAGTGGGGTCCC        7997     G  T     II
                      CAGGTG TA TGGGGTCC
                      |||||| || |||||||||
                      GTCCGC GT ACCCCAGG
                        G  C      GI
GAM505 LENG4       CAGGCGCCAGTGGGGTCCC        7997 TGGCAG  G  T
                      GTG TA TGGGGTCCCT
                      ||| || |||||||||||
                      CGC GT ACCCCAGGGG
                      _____    G  C
GAM505 MNT       TGGCAGGTGGCTGTGCTGGGGT       8021        A___     CCCTC
                      TGGCAGGTGGT  TTGGGGT
                      |||||||||| |||||||
                      ACCGTCCACCG  GACCCCA
                        ACAC      IIICT
GAM505 MNT       TGGCAGGTGGCTGTGCTGGGGT       8021         A___     III
                      TGGCAGGTGGT  TTGGG
                      |||||||||| ||||||
                      ACCGTCCACCG  GACCCC
                        ACAC     AII
GAM505 MYBPC2      TGGGAGGTTGGGGATTGGGGTC     8020  C __ T      CCTC
                      TGG AGGT GG ATTGGGGTC
                      ||| |||| || ||||||||||
                      ACC TCCA CC TAACCCCAG
                        C  AC C      IIIC
GAM505 MYBPC2      TGGGAGGTTGGGGATTGGGGTC     8020 __ CA T T      I
                      GG  GG GG ATTGGGGT
                      ||  || || |||||||
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                        CC  CC CC TAACCCCA
                        CT  AA _  _      I
GAM505 NPM3             GGCAGGTGGGAAGGGAGGCCC   8013 TG     TATT_     TC
                        GCAGGTGG   GGGGTCCC
                        ||||||||   ||||||||
                        CGTCCACC   CTCCGGGG
                        __    CTTCC    II
GAM505 NPM3             GGCAGGTGGGAAGGGAGGCCC   8013       TATT_    CI
                        GCAGGTGG   GGGGTC
                        ||||||||   ||||||
                        CGTCCACC   CTCCGG
                        CTTCC     II
GAM505 OCLN             GGCAGCACGGATGGGGGTCCCT   8015   _  T T     I
                        GCAG GTGG AT GGGGTCCC
                        |||| |||| || |||||||||
                        CGTC TGCC TA CCCCAGGG
                        G  _  C     I
GAM505 OCLN             GGCAGCACGGATGGGGGTCCCT   8015 T_   GG  T T     C
                        GGCA  TGG AT GGGGTCCCT
                        ||||  ||| || ||||||||||
                        TCGT  GCC TA CCCCAGGGA
                        CG  __ _ C     C
GAM505 PCTK3            GGAAGCTGGTATTGGGATC     8009  C G        II
                        GG AG TGGTATTGGGGT
                        || || |||||||||||||
                        CC TC ACCATAACCCTA
                        T  G     GI
GAM505 PCTK3            GGAAGCTGGTATTGGGATC     8009 TGGC  G        CCT
                        AG TGGTATTGGGGTC
                        || |||||||||||||
                        TC ACCATAACCCTAG
                        CT__  G       TII
GAM505 PDPK1           TGGCAGGTGGTCTGGAAGCGTCCC  8025          A  ___   TCI
                        TGGCAGGTGGT TTGGG  GTCCC
                        ||||||||||| |||||  |||||
                        ACCGTCCACCA GACCT  CAGGG
                        _  TCG    III
GAM505 PDPK1           TGGCAGGTGGTCTGGAAGCGTCCC  8025 GG      A  ___   I
                        CAGGTGGT TTGGG  GTCC
                        |||||||| |||||  ||||
                        GTCCACCA GACCT  CAGG
                        __    _  TCG  I
GAM505 PFKM            GGCTGG-GGTATCTGGGGTCCC   8007  A T  _     I
                        GC GG GGTAT TGGGGTCC
                        || || ||||| ||||||||
                        CG CC CCATA ACCCCAGG
                        A _  G     I
GAM505 PFKM            GGCTGG-GGTATCTGGGGTCCC   8007 TG A T  _       C
                        GC GG GGTAT TGGGGTCCCT
                        || || ||||| ||||||||||
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                                    CG CC CCATA ACCCCAGGGG
                                    __  A  _     G       I
GAM505 PML          GGCAGGTGGAGGGTGGGGGACCCT 8004 GC     TATT__   T  I
                              AGGTGG    GGGG CCC
                              |||||||   |||| |||
                              TCCACC    CCCC GGG
                              __    TCCCAC   T   I
GAM505 PML          GGCAGGTGGAGGGTGGGGGACCCT 8004 TG      TATT__   T  CI
                              GCAGGTGG    GGGG CCCT
                              ||||||||    |||| ||||
                              CGTCCACC    CCCC GGGA
                              __       TCCCAC   T   TI
GAM505 PML          TGGCAGGTGGGATGGATGGGG   8024        TAT___    TCCCTC
                              TGGCAGGTGG    TGGGG
                              ||||||||||    |||||
                              ACCGTCCACC    ACCCC
                              CTACCT    IIICTC
GAM505 PML          TGGCAGGTGGGATGGATGGGG   8024        TAT___    III
                              TGGCAGGTGG    TGGG
                              ||||||||||    ||||
                              ACCGTCCACC    ACCC
                              CTACCT    CII
GAM505 PRKR          GGCAGGTGGATTACTTGAGGTC   8005        TA___     III
                              GGCAGGTGG    TTGGGGT
                              |||||||||    |||||||
                              CCGTCCACC    AACTCCA
                              TAATG    GII
GAM505 PRKR          GGCAGGTGGATTACTTGAGGTC   8005 TG     TA___     CCTC
                              GCAGGTGG    TTGGGGTC
                              ||||||||    ||||||||
                              CGTCCACC    AACTCCAG
                              __       TAATG     TIII
GAM505 RS1           GGTGGTGTGTGAGGGGGTCCCT   8017 ___   _ ATT      IIIA
                              GGTG GT  GGGGTCCC
                              |||| ||  ||||||||
                              CCAC CA  CCCCAGGG
                              CCA  A CTC     AIII
GAM505 RS1           GGTGGTGTGTGAGGGGGTCCCT   8017 TGGCAG  GTATT      C
                              GTG    GGGGTCCCT
                              |||    ||||||||||
                              CAC    CCCCAGGGA
                              A_____    ACTC_      T
GAM505 RS1           GTGGTCATTTGGGGTCCCT    8018   A__       III
                              GTGGT  TTGGGGTCCC
                              |||||  ||||||||||
                              CACCA  AACCCCAGGG
                              GTA      AII
GAM505 SCT           GGCAGGTGGTGAGGGGGTTCCT   8016        ATT   _ CI
                              GCAGGTGGT  GGGGT CC
                              |||||||||  ||||| ||
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                    CGTCCACCA  CCCCA GG
                       CTC    A II
GAM505 SCT          GGCAGGTGGTGAGGGGGTTCCT    8016 TG      ATT    C  C
                       GCAGGTGGT  GGGGT CCT
                       |||||||||  ||||| |||
                       CGTCCACCA  CCCCA GGA
                          __    CTC    A  A
GAM505 TGFB1        GGGAGGCGGTCT-GGGGTCCC     8014 GC_    A      I
                         AGGTGGT TTGGGGTCC
                         ||||||| |||||||||
                         TCCGCCA GACCCCAGG
                         CCC     _     I
GAM505 TGFB1        GGGAGGCGGTCT-GGGGTCCC     8014 T  C      A
                         GG AGGTGGT TTGGGGTCCCT
                         || ||||||| |||||||||||
                         CC TCCGCCA GACCCCAGGGG
                            _   _    _
GAM505 THRA        TGGCAGGTGGGAGGGCTGGGG      8022      TA___     TCCCTC
                       TGGCAGGTGG  TTGGGG
                       ||||||||||  ||||||
                       ACCGTCCACC  GACCCC
                          CTCCC      IIICTC
GAM505 THRA        TGGCAGGTGGGAGGGCTGGGG      8022      TA___    III
                       TGGCAGGTGG  TTGGG
                       ||||||||||  |||||
                       ACCGTCCACC  GACCC
                          CTCCC    CII
GAM505 TIMM44      GCAGGTGGTGTTGCGGTGCCTC     8003      A  G  C  I
                       CAGGTGGT TTG GGT CCT
                       |||||||| ||| ||| |||
                       GTCCACCA AAC CCA GGA
                          C  G  C  I
GAM505 TIMM44      GCAGGTGGTGTTGCGGTGCCTC     8003 TGGC    A  G  C
                       AGGTGGT TTG GGT CCTC
                       ||||||| ||| ||| ||||
                       TCCACCA AAC CCA GGAG
                       ____    C  G  C
GAM505 TNXB        ACCACAAATGCAGCCACTGCTG     7994 TGACCT     __      I
                       CAAGTGT CCACTGCTG
                       ||||||| |||||||||
                       GTTTACG GGTGACGAC
                    GT____    TC     A
GAM506 ATP7B       CAGACAAGGCCGCGTGCTGCA-GGGC 8035 GC  _     _ AT__   GII
                       AGA AAGGCCGCG GC   GGGCG
                       ||| ||||||||| ||   |||||
                       TCT TTCCGGCGC CG   CCCGT
                       __  G     A ACGT   III
GAM506 B3GAT1      AGAAAAGAACAGGCATGGGC      8030 GCA    GC C      G
                       GAAAG  CG GGCATGGGC
                       |||||  || |||||||||
```

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                              TTTTC  GT CCGTACCCG
                   ___        TT _      G
GAM506 BARHL1      CAGAAAGGCGGGCGGAAGGGGC  8036 GC     C_   CAT   GG
                       AGAAAGGC GCGG  GGGC
                       |||||||| |||| ||||
                       TCTTTCCG CGCC  CCCG
                        __      CC  TTC  GI
GAM506 C1orf6      GAGAGGCAGGAGGCATGGC    8041 GCAGAA  CGC_     G
                            AGGC   GGCATGGGC
                            ||||   |||||||||
                            TCCG   CCGTACCCG
                       _____  TCCT     G
GAM506 COL1A1      GCAGAAAGG--GCAGCATTGG    8048      CC     _ GCG
                       GCAGAAAGG GCGGCAT GG
                       ||||||||| ||||||| ||
                       CGTCTTTCC CGTCGTA CC
                        __      A |||
GAM506 DUSP7       GCAGAAAGG-AGCGTCCTGG     8047      CC GCA  GCG
                       GCAGAAAGG GCG  TGG
                       ||||||||| |||  |||
                       CGTCTTTCC CGC  ACC
                        T_ AGG  |||
GAM506 DVL1        CAGGAAGGCCGCGATGTGTGCG  8040 GC A     CA G  G
                        AG AAGGCCGCGG  TG GCG
                        || |||||||||| || |||
                        TC TTCCGGCGCT AC CGC
                       __  C     AC A  G
GAM506 EVX1        AGAAAGGCCGGGTGCCTGGGAGG  8028 GCAG    CG_ A  C I
                        AAAGGCCG  GC TGGG GG
                        ||||||||  || |||| ||
                        TTTCCGGC  CG ACCC CC
                       ____      CCA G  T C
GAM506 FANCC       AGGAAGGAAGGGGCATGGGC     8033 GCAGA  CCGC
                         AAGG   GGCATGGGCG
                         ||||   ||||||||||
                         TTCC   CCGTACCCGT
                       C____    TTCC
GAM506 GPC1        GCAGAAAGGCAGGCGAGGC     8046      CGC  AT  G
                       GCAGAAAGG  GGC GGGC
                       |||||||||  ||| ||||
                       CGTCTTTCCG  CCG TCCG
                        T__ C_  I
GAM506 HR          GAAAGGCCGAGG---GGCCGG    8043 GCAGAA     C CAT G
                       AGGCCG GG  GG C
                       |||||| || || |
                       TCCGGC CC  CC G
                       _____   T ___ G
GAM506 HRB         GGCCGCGGCGCCAAGGGAGG     8050 GCAGAAAG  C CAT__ G
                        GCCG GG   GG CG
                        |||| ||    || ||
```

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                          CGGT CC    CC GC
                       CG_____   T CTCCT  G
GAM506  HUNK          CAGAAAGGCTGGGGC-TGAGC    8038 GC      CGC  A    G
                       AGAAAGGC  GGC TGGGC
                       ||||||||  ||| |||||
                       TCTTTCCG  CCG ACTCG
                          __     ACC  _   G
GAM506  IKBKB         GCAGAAAGGACCACAG-ATGG    8045       _   C   GCG
                       GCAGAAAGG CCGCGG ATGG
                       ||||||||| |||||| ||||
                       CGTCTTCC GGTGTC TACC
                          T   _  |||
GAM506  KCNAB2        GCAGAAAGGGGCCCTCG--ATGGGC 8044       __  G_ GC    GGI
                       GCAGAAA GGCC CG ATGGGC
                       ||||||| |||| || ||||||
                       CGTCTTT CCGG GC TACCCG
                          CC   GA __    |||
GAM506  MAP3K9        AGAAAGGCC-CTGCA-GGGC    8031 GCAG    GCG  T
                       AAAGGCC  GCA GGGC
                       |||||||  ||| ||||
                       TTTCCGG  CGT CCCG
                       ____     GA_  _
GAM506  MCM5          GCAGAAAGGAGGGTGCCTGGG    8049       CCGCG A  CGG
                       GCAGAAAGG   GC TGGG
                       |||||||||   || ||||
                       CGTCTTTCC   CG ACCC
                          TCCCA G   |||
GAM506  NR1I2         CAGTAAAGCAGGGGCATGGGC    8039 GC A   CGC     GG
                       AG AAGGC  GGCATGGGC
                       || |||||  |||||||||
                       TC TTTCG  CCGTACCCG
                       __  A  TCC       GI
GAM506  POU2AF1       AGGCCACCAGGGCATGGGC     8034 GCAGAAAGG  C
                       CCG GGCATGGGCG
                       ||| |||||||||
                       GGT CCGTACCCGT
                       _____  C
GAM506  RNH           CAGAAAGGCCAC--CATGGGC    8037 GC       GG
                       AGAAAGGCCGC CATGGGCG
                       ||||||||||| |||||||||
                       TCTTTCCGGTG GTACCCGT
                          __      __
GAM506  SRP46         GAAAGGCCGGGCGGAGAGGCGG   8042 GCAGAA    C AT__
                       AGGCCG GGC  GGGCGG
                       |||||| |||  ||||||
                       TCCGGC CCG  TCCGCC
                       _____    _  CCTC
GAM506  UBQLN2        AGAAAGGCCTGGGCGTAGGC    8032 GCAG     GC A   G
                       AAAGGCC  GGC TGGGC
                       ||||||||  ||| |||||
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                    TTTCCGG  CCG ATCCG
                    ____      AC  C   G
GAM506 WHSC1        AGAAAGGC--CGGCCTGAGGACGG  8029 GCAG     GC  AT__
                    AAAGGCC GGC  GGGCGG
                    ||||||| |||  ||||||
                    TTTCCGG CCG   CCTGCC
                    ____        __  GACT
GAM507 ATP1B2       GGAAAAGGATGTGAGGCTCAGAC   8062 TGGC  TT  T_      TI
                    AAAG  TGT GGCTCAGAC
                    |||| ||| |||||||||
                    TTTC  ACA  CCGAGTCTG
                    CT__   CT  CT       TI
GAM507 BNC          TGGTAACAGGTTGTTGGCT        8064   CAA_ T       CAGAC
                    TGG   AG TTGTTGGCT
                    |||   || |||||||||
                    ACC   TC AACAACCGA
                    ATTG  C       IIITC
GAM507 CIAS1        AAAGTTCTCCTGTTGGCTC        8053 TGGCAAAG      A  C
                    TTTGTTGGCTC GA
                    ||||||||||| ||
                    GGACAACCGAG CT
                    AAGA____        _  A
GAM507 COL10A1      GGGAAGGTTTGTTGG-TCTGA      8063 T C A      C A  C
                    GG AA GTTTGTTGG TC GA
                    || || |||||||| || ||
                    CC TT CAAACAACC AG CT
                    _ _  C     _  A A
GAM507 CREBL2       CACAGTGTGTTCTGGCTCAGA      8056 TGGCAAA  G      CT
                    GTTT TTGGCTCAGA
                    |||| |||||||||
                    CAAA GACCGAGTCT
                    TCACA__  _      CG
GAM507 CRH          TGGCATTCTCT-TTGGCTCAGAC    8070    AAG  G       T
                    TGGCA  TTT TTGGCTCAGAC
                    |||||  ||| ||||||||||
                    ACCGT  GAG AACCGAGTCTG
                    AA_  A        I
GAM507 FMO1         TGGGAAAGAGGTATGATGGCTCAGA  8065   C  TT___  T      CTII
                    TGG AAAG   TG TGGCTCAGA
                    ||| ||||    || |||||||||
                    ACC TTTC   AC ACCGAGTCT
                    C   TCCAT T       IIIT
GAM507 HR           TGGCACTGTGGTTGTTGGCT       8066   AA __       CAGAC
                    TGGCA GT TTGTTGGCT
                    ||||| || |||||||||
                    ACCGT CA AACAACCGA
                    GA CC       IIITC
GAM507 LMO2         GGGAAGGTCTATTTTGGCTCAGGCT  8058 T C A    __       ACTII
                    GG AA GTTTGT TGGCTCAG
                    || || |||||| ||||||||
```

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                        CC TT CAGATA  ACCGAGTC
                        _ _ C    AA      CGAAI
GAM507 MCL1         CAAAGTTTGTTTGTTGCTGAAACT  8055 TGGCAAA      G  C   I
                        GTTTGTTG CT AGACT
                        |||||||| || |||||
                        CAAACAAC GA TTTGA
                    TCAAA__    _ C   C
GAM507 MN1         TGGCAAAGTGTTGATGACTCA   8067      _ T    GACT
                        TGGCAAAGT TTG TGGCTCA
                        |||||||| ||| |||||||
                        ACCGTTCA AAC ACTGAGT
                          C  T    IIIT
GAM507 NR2F2        GCAAAGTTTTGTCGATGGCT      8057 TGGC    _ ___     CAGAC
                        AAAGTTT GT  TGGCT
                        ||||||| ||  |||||
                        TTTCAAA CA  ACCGA
                        ____    A GCT   ACIII
GAM507 PTHLH       AAAGTGTGAATGGCTCAGA      8054 TGGCAAA TTGT     C
                        GT  TGGCTCAGA
                        ||  |||||||||
                        CA  ACCGAGTCT
                        A_____ CTT_      T
GAM507 RFC2        GGGACAGTCATGTTGGCTCAGCCT  8060 T  AA _       A I
                        GGCA GTT TGTTGGCTCAG CT
                        |||| ||| ||||||||||| ||
                        CTGT CAG ACAACCGAGTC GG
                        C __ T    _ A
GAM507 SIAT8E       GGCAAAGTTTCTGGTTGGC      8061 TG      ___     TCAGAC
                        GCAAAGTTT GTTGGC
                        ||||||||| ||||||
                        CGTTTCAAA CAACCG
                        __     GAC    CIIITC
GAM507 SLC16A2       TGGCAA-GTTACTGTTGGCTC    8068    A __      AGAC
                        TGGCAA GTT TGTTGGCTC
                        |||||| ||| |||||||||
                        ACCGTT CAA ACAACCGAG
                         _ TG    IIIT
GAM507 SORBS1       GGGACAGTCTTGGTAGCTCAGACT  8059 T  AAG  T       I
                        GGCA  TTTG TGGCTCAGACT
                        ||||  |||| |||||||||||
                        CTGT  GAAC ATCGAGTCTGA
                        C  CA_  C      C
GAM507 ZNF175       TGGCACAGTTTGTTGACTC       8069   A         AGAC
                        TGGCA AGTTTGTTGGCTC
                        ||||| |||||||||||||
                        ACCGT TCAAACAACTGAG
                          G      IIIT
GAM508 ALCAM        TGTGTGTCTATATGCATCTGTGA   8090 TGGCTGTG    __     C I
                        GTCTA TGCATCT TGA
                        ||||| ||||||| |||
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                        CAGAT  ACGTAGA ACT
                        A_____   AT    C  A
GAM508  ATF7            TGGCTGTGG---ATGCATC      8084       TCT     TC
                        TGGCTGTGG  ATGCATC
                        |||||||||  |||||||
                        ACCGACACC  TACGTAG
                                      II
GAM508  ATP10C          TGGCTGTGG--GATGCATATTCCTGA 8086       TCT    C__    I
                        TGGCTGTGG  ATGCAT  TCTGA
                        |||||||||  ||||||  |||||
                        ACCGACACC  TACGTA  GGACT
                              C__     TAA    I
GAM508  CELSR1          TGGCTGTGG-CTTTGTCCCTCTG     8088       T A  CA     A
                        TGGCTGTGG CT TG  TCTCTG
                        ||||||||| || ||  ||||||
                        ACCGACACC GA AC  GGAGAC
                             _  A  AG     I
GAM508  CIT             GCTGTGGTCTCTTCCAGCTCTG    8077 TGGC      ATG_ T    A
                        TGTGGTCT  CA CTCTG
                        ||||||||  || |||||
                        ACACCAGA  GT GAGAC
                          ____       GAAG  C    A
GAM508  CRAT            TGGCTGTGGT---GGCATC      8085       CTAT   TC
                        TGGCTGTGGT  GCATC
                        ||||||||||  |||||
                        ACCGACACCA  CGTAG
                               C___     II
GAM508  DLG5            GCTG-GGTC-A-GCATCTCTG    8078 TGGC T   TAT
                        TG GGTC  GCATCTCT
                        || ||||  ||||||||
                        AC CCAG  CGTAGAGA
                          ____ _  T__
GAM508  GABRE           TGGCTGTGGT-TTTG-AACACTGA 8089       CTAT_ TCT
                        TGGCTGTGGT   GCA  CTGA
                        ||||||||||   |||  ||||
                        ACCGACACCA   TGT  GACT
                              AAACT   ___
GAM508  GABRP           TGGCCGAGGAATGTGCATCTCTG   8087       T TCTA     AI
                        TGGCTG GG   TGCATCTCTG
                        |||||| ||   ||||||||||
                        ACCGGC CC   ACGTAGAGAC
                          T TTAC        II
GAM508  INHBC           GCTGTGGTCT---CAACTCTG     8079 TGGC      ATG T
                        TGTGGTCT  CA CTCT
                        ||||||||  || ||||
                        ACACCAGA  GT GAGA
                          ____       ___ T
GAM508  IRAK4           GGCTGTGGT-TAT-CATCT       8080 TG      C  G    CT
                        GCTGTGGT TAT CATCT
                        |||||||| ||| |||||
```

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                          CGACACCA ATA GTAGA
                          __     _  _   CI
GAM508  KRT16        GGCTGTGGTAGAGGCAGCTC    8081 TG     CTAT  T  TG
                     GCTGTGGT  GCA CTC
                     |||||||| ||| |||
                     CGACACCA  CGT GAG
                     __        TCTC  C  TI
GAM508  PCDHB11       GGCTGAGGGGAGTGCATCTCT   8082 TG  T TCTA      GA
                     GCTG GG  TGCATCTCT
                     |||| || |||||||||
                     CGAC CC  ACGTAGAGA
                     __  T CCTC         AI
GAM508  SLC7A7       CTGTGGTCTGATGCTCCTC     8074 TGGCTG   _ AT  G
                     TGGTCT ATGC  CTCT
                     |||||| |||| ||||
                     ACCAGA TACG  GAGG
                     _____     C  AG  A
GAM508  TRO          CTGTGGTCTCAGTCTGTATATCTGA 8073 _ G    A C   CTGAII
                     TGG CT TGGTCT TG ATCT
                     ||| || |||||| || ||||
                     ACC GA GTCAGA AT TAGA
                     A _    C A   CTTTAI
GAM508  UBQLN3       GCTGTGGTCCCGTCCTTCTCT   8076 TGGC     ATGCA_   GA
                     TGTGGTCT   TCTCT
                     ||||||||   |||||
                     ACACCAGG   AGAGA
                     ____       GCAGGA  AA
GAM508  VDR          GGCAGCGGTGGAGGCATCTCTG   8083 T_ T  TCTAT      A
                     GGC GTGG   GCATCTCTG
                     ||| ||||   |||||||||
                     TCG CACC   CGTAGAGAC
                     CG  C  TC___      C
GAM508  WFDC1        CTGTC-TCTAAGCATCTCTG    8075 TGGCTGTGG  T
                     TCTA GCATCTCTG
                     |||| |||||||||
                     AGAT CGTAGAGAC
                     AG_____    T
GAM509  ADRBK1       TGGGCGGGGGTACACTGATGG   8107 GAGA  AG___      I
                     GGCG  ACACTGATG
                     ||||  |||||||||
                     CCGC  TGTGACTAC
                     C___  CCCCA       I
GAM509  ADRBK1       TGGGCGGGGGTACACTGATGG   8107 TGAGA  AG___      CAC
                     GGCG   ACACTGATGG
                     ||||   ||||||||||
                     CCGC   TGTGACTACC
                     AC___  CCCCA       III
GAM509  AP2M1        GAGGGAGGAGACACTGATG     8096 GA  C__        II
                     GAGG  GAGACACTGAT
                     ||||  |||||||||||
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                              CTCC  CTCTGTGACTA
                              __    CTC        CI
GAM509 AP2M1          GAGGGAGGAGACACTGATG      8096 TGA  CG       GCA
                              GAGG AGACACTGATG
                              |||| ||||||||||
                              CTCC TCTGTGACTAC
                         TCC  __            AII
GAM509 AVP            GAGGCGAGACGCGGCCGCCAC    8102      ACT A  AI
                              AGGCGAGAC  G TGGC
                              ||||||||| | ||||
                              TCCGCTCTG  C GCCG
                              ___ _      GC
GAM509 AVP            GAGGCGAGACGCGGCCGCCAC    8102 TGAGAG    ACTGA  G
                              GCGAGAC    TG CAC
                              |||||||    || |||
                              CGCTCTG    GC GTG
                              _____        CGCCG G
GAM509 B3GNT3        TGACTGGC-AGACACTGA-GGC    8108  GA  G      T  A
                              TGA  GGC AGACACTGA GGC
                              |||  ||| |||||||||| |||
                              ACT  CCG TCTGTGACT CCG
                               GA  _      _ I
GAM509 B3GNT3        TGACTGGC-AGACACTGA-GGC    8108 _ GA  G     T I
                               GA  GGC AGACACTGA GG
                               ||  ||| |||||||||| ||
                               CT  CCG TCTGTGACT CC
                                A GA  _      _ I
GAM509 BTD           AGAGGA-AGACACTGAGGG       8093    C      TGI
                              AGAGG GAGACACTGA
                              ||||| ||||||||||
                              TCTCC TTCTGTGACT
                              _          CCC
GAM509 BTD           AGAGGA-AGACACTGAGGG       8093 TGAG  C      T  C
                              AGG GAGACACTGA GG
                              ||| |||||||||| ||
                              TCC TTCTGTGACT CC
                              ____ _        C T
GAM509 CYP2F1         TGAGCTGCAGGAGACACTG      8103   AG __      ATGGCA
                              TGAG GC GAGACACTG
                              |||| || |||||||||
                              ACTC CG CTCTGTGAC
                               GA TC        IIICAC
GAM509 CYP2F1         TGAGCTGCAGGAGACACTG      8103   AG __      III
                              TGAG GC GAGACACT
                              |||| || ||||||||
                              ACTC CG CTCTGTGA
                               GA TC      CII
GAM509 EIF1A         TGAAAAGAGCAGACACTGAT      8104   __ G      GGCA
                              TGAGA GGC AGACACTGAT
                              ||||| ||| ||||||||||
```

```
                              ACTTT  TCG TCTGTGACTA
                               TC   _          IIIC
GAM509  EIF1A          TGAAAAGAGCAGACACTGAT      8104   __  G      II
                              TGAGA  GGC AGACACTGA
                              |||||  ||| |||||||||
                              ACTTT  TCG TCTGTGACT
                               TC   _          AI
GAM509  FTSJ2          TGGGAGCCCAGACACTGAT      8105  A  GCG      GGCA
                              TG GAG  AGACACTGAT
                              || |||  ||||||||||
                              AC CTC  TCTGTGACTA
                               C  GGG          IIIC
GAM509  FTSJ2          TGGGAGCCCAGACACTGAT      8105  A  GCG      II
                              TG GAG  AGACACTGA
                              || |||  |||||||||
                              AC CTC  TCTGTGACT
                               C  GGG        AI
GAM509  GALR1          TGAGAGGCGA-AAACAGCTCGGC   8106        _ _  GA   AC
                              TGAGAGGCGAGA CA CT  TGGC
                              |||||||||||| || || ||||
                              ACTCTCCGCTTT GT GA  GCCG
                                     T  C  __     II
GAM509  GALR1          TGAGAGGCGA-AAACAGCTCGGC   8106        _ _  GATGGI
                              GAGAGGCGAGA CA CT
                              |||||||||| || ||
                              CTCTCCGCTTT GT GA
                                    T  C  GCCIII
GAM509  GRB10          GAGAGATTATACACTGATGGGAC   8098      CGAG      CAI
                              AGAGG   ACACTGATGG
                              |||||   ||||||||||
                              TCTCT   TGTGACTACC
                               AATA        CTI
GAM509  GRB10          GAGAGATTATACACTGATGGGAC   8098 T  GGCGAG      C  I
                              GAGA    ACACTGATGG AC
                              ||||    |||||||||| ||
                              CTCT    TGTGACTACC TG
                               T  AATA__        C  A
GAM509  INSM1          GAGGCGAGAC-CAGACCGCA      8099 _      ACT  G  I
                              AGGCGAGAC  GAT GC
                              |||||||||  ||| ||
                              TCCGCTCTG  CTG CG
                               C      GT_  G  I
GAM509  INSM1          GAGGCGAGAC-CAGACCGCA      8099 TGAGAG   ACT  G
                              GCGAGAC  GAT GCA
                              |||||||  ||| |||
                              CGCTCTG  CTG CGT
                              _____       GT_  G
GAM509  ITPR1          AGGAGATGACACTGATTGGC      8095  C  _     _ III
                              AGG GA GACACTGAT GG
                              ||| || |||||||||| ||
```

```
                    TCC CT CTGTGACTA CC
                     T  A      A GII
GAM509  ITPR1       AGGAGATGACACTGATTGGC    8095 TGAGAGGCGA     _  A
                       GACACTGAT GGC
                       |||||||||| |||
                       CTGTGACTA CCG
                     CTA_____      A  G
GAM509  MAGEB4      GAGTGG-GAGACACTGCTGGACAC  8097 AGA C     A _ I
                       GG GAGACACTG TGG CA
                       || ||||||||| ||| ||
                       CC CTCTGTGAC ACC GT
                     TCA _      G  T I
GAM509  MAGEB4      GAGTGG-GAGACACTGCTGGACAC  8097 TGAGA C     A _ I
                       GG GAGACACTG TGG CAC
                       || ||||||||| ||| |||
                       CC CTCTGTGAC ACC GTG
                     TCA__ _      G  T  G
GAM509  MAN2A1      GAGGCGAGACTC-GCCGGCA    8100 _      ACTGA  I
                       AGGCGAGAC   TGGC
                       |||||||||   ||||
                       TCCGCTCTG   GCCG
                     C     AGCG_  I
GAM509  MAN2A1      GAGGCGAGACTC-GCCGGCA    8100 TGAGAG    ACTGA
                       GCGAGAC   TGGCA
                       |||||||   |||||
                       CGCTCTG   GCCGT
                     _____    AGCG_
GAM509  PITX2       AGATGTCAGACACTGAGGACA   8094 GAGGCG     T I
                       AGACACTGA GGC
                       |||||||||| |||
                       TCTGTGACT CTG
                     CTACAG    C  I
GAM509  PITX2       AGATGTCAGACACTGAGGACA   8094 TGAGAGGCG    T  C
                       AGACACTGA GGCA
                       |||||||||| ||||
                       TCTGTGACT CTGT
                     TACAG____    C  A
GAM509  SUFU        GAGGCGA---ACTGATGGCAC   8101      GAC    I
                       GAGGCGA ACTGATGGC
                       |||||||  |||||||||
                       CTCCGCT TGACTACCG
                       ___      T
GAM509  SUFU        GAGGCGA---ACTGATGGCAC   8101 TGAGAG  GAC
                       GCGA ACTGATGGC
                       ||||  |||||||||
                       CGCT TGACTACCG
                     _____    _____
GAM510  AIM1        AAGAACCAAAATTACAGGCCT   8115 TATAAAGAAAG    _
                       AAAATTACAG CCT
                       |||||||||| |||
```

```
                          TTTTAATGTC GGA
                  TGG_____        C
GAM510 ATP8A2        TATAACAAATGGAAATTACAGACT  8135    A  AGA      C  I
                  TATAA GAA   AAATTACAG CT
                  ||||| |||  ||||||||| ||
                  ATATT TTT   TTTAATGTC GA
                   G   ACC         T  I
GAM510 BIG1          AAAGAAAAGAAAATGACAGC    8111 TATAAA      T    C
                     GAAAGAAAAT ACAGC
                     |||||||||| |||||
                     TTTTCTTTTA TGTCG
                   C_____        C   T
GAM510 CALB1         ATATA-AAAGAAAA-TACAGCCT   8124 TATAAA       T
                     GAAAGAAAAT ACAGCCT
                     |||||||||| |||||||
                     TTTTCTTTTA TGTCGGA
                   ATA___         _
GAM510 CD34          TAGAGAAAGAAAA-TACAG    8126 TATAA      T  C
                     AGAAAGAAAAT ACAG
                     |||||||||| ||||
                     TCTTTCTTTTA TGTC
                   C____       _  C
GAM510 CDY1          TATAAAGGAAAAGAAAATCA-AGC  8130     __       C  CTI
                     TATAAAG  AAAGAAAATTA AGC
                     |||||||  ||||||||||| |||
                     ATATTTC  TTTCTTTTAGT TCG
                   CT           _   |||
GAM510 CYP4F3        TATGAAAGAAAGAAACTT-CAG    8127  _       A  A  CCT
                     TAT AAAGAAAGAAA TT CAG
                     ||| |||||||||| || |||
                     ATA TTTCTTTCTTT AA GTC
                      C      G  _  |||
GAM510 DMD           TATAAAGGAAAAAGAAAATAAC    8129       ___       T AGCCT
                     TATAAAG  AAAGAAAAT AC
                     |||||||  |||||||| ||
                     ATATTTC  TTTCTTTTA TG
                      CTT       T |||TC
GAM510 DUSP4         AAAGAAAGAAAAAT-CAGC    8113 TATAAA      TTA
                     GAAAGAAAA  CAGC
                     |||||||||  ||||
                     CTTTCTTTT  GTCG
                     _____         TA_
GAM510 EYA4          AAAGAAAGAAAAATTGCATCC    8112 TATAAA      TTA_ G T
                     GAAAGAAAA  CA CC
                     |||||||||  || ||
                     CTTTCTTTT  GT GG
                     _____         TAAC  A  T
GAM510 FZD10         AAGAAAGAAAAACACAACC    8116 TATAAAGA      T
                     AAGAAAA TACAGCC
                     ||||||| ||||||
```

```
                         TTCTTTT GTGTTGG
                         ‾‾‾‾‾‾‾      T
GAM510 HEPH          ATAAAGAAAGAAATATCCAG    8122 TA      ATTA CC
                         TAAAGAAAGAAA   CAG
                         ||||||||||| |||
                         ATTTCTTTCTTT  GTC
                             __      ATAG  TI
GAM510 HHLA1        TAAAG---GAAAATTACAG      8125 TATAAAGAAA
                             GAAAATTACAG
                             ||||||||||
                             CTTTTAATGTC
                         TTC‾‾‾‾‾‾‾
GAM510 HLF          AAGAAAGAAAGAAACAACC      8118 TATA      ATT A
                         AAGAAAGAAA  AC GCC
                         ||||||||||  || |||
                         TTCTTTCTTT  TG CGG
                         ‾‾‾‾        GT_ G
GAM510 IL11         TATATAGAAAGAAAAACACA     8132  A      T  GCC
                         TATA AGAAAGAAAA TACA
                         |||| |||||||||| ||||
                         ATAT TCTTTCTTTT GTGT
                            A      T   III
GAM510 LEF1         AAAGAAAGAAAAATGAAGC      8114 TATAAA     TTAC  C
                             GAAAGAAAA  AGC
                             |||||||||  |||
                             CTTTCTTTT  TCG
                         ‾‾‾‾‾‾        TACT  T
GAM510 LYPLA1       ATAAAGCAA-AAAATTACA      8121 TA   AA        C
                         TAAAG AGAAAATTACAG
                         ||||| ||||||||||||
                         ATTTC TTTTTAATGTT
                            __   G_       I
GAM510 MAP2         TATAAAGAATGAATATAACA     8131      A  A T GCC
                         TATAAAGAA GAA AT ACA
                         ||||||||| ||| || |||
                         ATATTTCTT CTT TA TGT
                            A   A T III
GAM510 MEN1         ATATAGAAAGAAACTCCTACA    8120 TATAA      AT__   CCT
                             AGAAAGAAA  TACAG
                             |||||||||  |||||
                             TCTTTCTTT  ATGTT
                         ATA__       GAGG   III
GAM510 MEN1         ATAAAGAAAGGTGAGTACAG     8123 TA     AAAAT   CC
                             TAAAGAAAG   TACAG
                             ||||||||   |||||
                             ATTTCTTTC  ATGTC
                             __     CACTC   TI
GAM510 OGT          TATAAAGAAAAAAAAATCCAG    8134          TTA CCT
                         TATAAAGAAAGAAAA CAG
                         ||||||||||||| |||
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                              ATATTTCTTTTTTTT  GTC
                                     TAG    III
GAM510  RGR            TAAAAAGTCAAAAAATTACAG    8133 TAT  AA       CCT
                           AAAG  AGAAAATTACAG
                           IIII  IIIIIIIIIII
                           TTTC  TTTTTTAATGTC
                           ATT   AG         III
GAM510  TFCP2          TATATAAGAAA-AAAATTACAG   8128  _      A    CCT
                           TATA AAGAAAGAAA TTACAG
                           IIII IIIIIIIII IIIIII
                           ATAT TTCTTTTTT AATGTC
                               A       _    III
GAM510  TYRP1          ATAAAGTGAAAGAAAA-TACAG   8119 TATAAA     T  CCT
                             GAAAGAAAAT ACAG
                             IIIIIIIIII IIII
                             CTTTCTTTTA TGTC
                           ATTTCA         _  AII
GAM510  ZIC1           AAGAAAGAAAGAAAAAGCC    8117 TATA     TTAC
                            AAGAAAGAAAA  AGCC
                            IIIIIIIIIII  IIII
                            TTCTTTCTTTT  TCGG
                            ____        ____
GAM511  FAAH           CCATGCAGGACATTTCCTT     8143 T _ A      II
                            CC TG AG ACATTTCCT
                            II II II IIIIIIIII
                            GG AC TC TGTAAAGGA
                             T  G  C      AI
GAM511  FAAH           CCATGCAGGACATTTCCTT     8143 TGAGACCTTG A
                               AG ACATTTCCTT
                               II IIIIIIIIII
                               TC TGTAAAGGAA
                           G_____  C
GAM511  GABRE          AGAACTTTGGACAACATTTCC   8141  C __ G     III
                           AGA CTT GA AACATTTC
                           III III II IIIIIIII
                           TCT GAA CT TTGTAAAG
                            T  AC G      GII
GAM511  GABRE          AGAACTTTGGACAACATTTCC   8141 TGA  C _ G      TTC
                           GAC TTG A AACATTTCC
                           III III I IIIIIIIII
                           TTG AAC T TTGTAAAGG
                           ___    A  C G     CGI
GAM511  GPC5           AGACATTCAGA-CATTTCCTTC  8142 _  C G A     I
                            GAC TT AGA CATTTCCTT
                            III II III IIIIIIIII
                            CTG AA TCT GTAAAGGAA
                             T  T  G  _      I
GAM511  GPC5           AGACATTCAGA-CATTTCCTTC  8142 TGAG  C G  A
                            AC TT AGA CATTTCCTTC
                            II II III IIIIIIIIII
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                               TG AA TCT GTAAAGGAAG
                               ____  T G  _
GAM511 PINX1          TGAGAGCCACGATTGAGAACATT  8144   _ ____        TCCTTCI
                     TGAGA CC   TTGAGAACATT
                     ||||| ||  ||||||||||||
                     ACTCT GG   AACTCTTGTAA
                          C TGCT       IIICTTC
GAM511 PINX1          TGAGAGCCACGATTGAGAACATT  8144   _ ____        IIIA
                     TGAGA CC   TTGAGAACAT
                     ||||| ||  |||||||||
                     ACTCT GG   AACTCTTGTA
                          C TGCT       AIII
GAM511 PKD2L1        TGAATCCT-GAGTTCATTTCCTT  8148   A  T  AA      C
                     TGAG CCT GAG  CATTTCCTT
                     |||| ||| |||  |||||||||
                     ACTT GGA CTC  GTAAAGGAA
                       A  _   AA      I
GAM511 PKD2L1        TGAATCCT-GAGTTCATTTCCTT  8148 _  A  T  AA      I
                      GAG CCT GAG  CATTTCCT
                      ||| ||| |||  ||||||||
                      CTT GGA CTC  GTAAAGGA
                       A  A  _  AA      I
GAM511 RNGTT         ACCTTGAGAA-TTTTCCCTC    8139 _      CA      I
                      CCTTGAGAA TTTCCTT
                      ||||||||| |||||||
                      GGAACTCTT AAAGGGA
                           T   A_     I
GAM511 RNGTT         ACCTTGAGAA-TTTTCCCTC    8139 TGAGACCT    CA
                         TGAGAA TTTCCTT
                         |||||| |||||||
                         ACTCTT AAGGGAG
                      _____   AA
GAM511 ST7         TGAGACCTTGATATAATTT     8147       GAACATTII
                     TGAGACCTTGA
                     |||||||||||
                     ACTCTGGAACT
                       ATATTAAAI
GAM511 ST7         TGAGACCTTGATATAATTT     8147       GAACATTTCCTT
                     TGAGACCTTGA
                     |||||||||||
                     ACTCTGGAACT
                       ATATTAAAIIIC
GAM511 TEM7R         TGAGACATCAGAGAACATTT    8146    CTT_      CCTT
                     TGAGAC  GAGAACATTT
                     ||||||  ||||||||||
                     ACTCTG  CTCTTGTAAA
                        TAGT      IIIC
GAM511 TEM7R         TGAGACATCAGAGAACATTT    8146    CTT_      II
                     TGAGAC  GAGAACATT
                     ||||||  |||||||||
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                              ACTCTG   CTCTTGTAA
                               TAGT       AI
GAM511 TGFBI          TGAGACACATTTGACAGAACATTTC 8145    C___  __      CTTCII
                          TGAGAC  TTGA GAACATTTC
                          |||||| |||| |||||||||
                          ACTCTG  AACT CTTGTAAAG
                           TGTA    GT      IIICTT
GAM511 TGFBI          TGAGACACATTTGACAGAACATTTC 8145 GA____   CTTG      I
                             GAC   AGAACATTT
                             |||   |||||||||
                             CTG   TCTTGTAAA
                          TGTAAA   ____       I
GAM511 UBE4A            ACCTTTA--ACATTTCCTTC    8140    GAG        I
                         ACCTT  AACATTTCCT
                         |||||  ||||||||||
                         TGGAA  TTGTAAAGGA
                           A__      A
GAM511 ZNF264          ACCTTGA-AACATTTCCCTTC    8138     A    I
                          CCTTGAGA CATTTCCTT
                          |||||||| |||||||||
                          GGAACTTT GTAAAGGGA
                              _       A
GAM511 ZNF264          ACCTTGA-AACATTTCCCTTC    8138 TGAGACCT   A
                          TGAGA CATTTCCTT
                          ||||| |||||||||
                          ACTTT GTAAAGGGA

                       _____   _
GAM512 ACAD8           TGAATAGCA-CTCCTGGACCAC    8160   A  T  _    CA
                        TGAA AGC GCTC TGGACCAC
                        |||| ||| |||| ||||||||
                        ACTT TCG TGAG ACCTGGTG
                          A   _   G    II
GAM512 GABRB1         AAGAGCTGATAACCTGGACCAC    8151 TGAAA   C___     CAI
                         AGCTG   TCTGGACCAC
                         |||||   ||||||||||
                         TCGAC   GGACCTGGTG
                         C____   TATT     CCI
GAM512 HOXD4          GAAAAGCTGCTCTATGTCACCA    8157 TG        GAC  I
                         AAAAGCTGCTCTG  CACCA
                         ||||||||||||| |||||
                         TTTTCGACGAGAT  GTGGT
                           __       ACA   C
GAM512 LEF1           GAAAAGCTGCTCAGCTGCCCCAC   8154 TG        ___ GA  CAI
                         AAAAGCTGCTC  TG CCAC
                         ||||||||||| || ||||
                         TTTTCGACGAG  AC GGTG
                           __        TCG GG  TII
GAM512 LNK           TGTAAAGCTGCTGTAAACCA    8161 A     C   CCA
                        TG AAAGCTGCT TGGACCA
                        || ||||||||| |||||||
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                              AC TTTCGACGA ATTTGGT
                               A        C      III
GAM512  NCOA3          GAAAAGCTGTGGTGCACTACC    8155 TG      CTC G  C  A
                          AAAAGCTG  TG AC ACC
                          |||||||| || || |||
                          TTTTCGAC  AC TG TGG
                            __       ACC G  A  G
GAM512  P2RY2          GAACAGTTGACTCTGGACCAC    8153 TGAAA C  _       CA
                            AG TG CTCTGGACCAC
                            || || |||||||||||
                            TC AC GAGACCTGGTG
                          TTG__  A  T       TI
GAM512  PIP5K1B         AAAAGCTGCTTAGTAGCAACA    8152 TGAA     C  ACCACCA
                            AAGCTGCT TGG
                            |||||||| |||
                            TTCGACGA ATC
                          ____       _  ATCGTTG
GAM512  PRKG1          TGAAAGGCTTTGCTTCAGGACCACCA 8158    A  __  _T       III
                          TGAAA GCT  GCT C GGACCACCA
                          ||||| |||  ||| | |||||||||
                          ACTTT CGA  CGA G CCTGGTGGT
                            C  AA  A T       III
GAM512  PYGB           GAAAAGCAG----GGACCACCA    8156 TG    TGCTCT
                           AAAAGC   GGACCACC
                           ||||||   ||||||||
                           TTTTCG   CCTGGTGG
                          __      TC____
GAM512  REQ            TGAAAAGCTCCTTGTGGAC      8159     G C_   CACC
                          TGAAAAGCT CT TGGAC
                          ||||||||| || |||||
                          ACTTTTCGA GA  ACCTG
                            G  AC   IIIA
GAM513  AGRN           ACAAAGAAGATCCTGGTGTCC    8168 TGAC     C  A_ _  T
                          AAAGAAG TTC GT TCTCC
                          ||||||| ||| || |||||
                          TTTCTTC AGG  CA AGGGG
                          ____      T  AC C   I
GAM513  ATP8A2         TGACAAAGAA--TTCAATT      8184         GC    CTC
                          TGACAAAGAA TTCAGTT
                          |||||||||| |||||||
                          ACTGTTTCTT AAGTTAA
                              __       III
GAM513  BCAT1          ACAAAGAAGGTACACTTCT      8167 TGAC    CTT G  CC
                          AAAGAAG  CA TTCT
                          |||||||  || ||||
                          TTTCTTC  GT AAGA
                          ____       CAT G  TA
GAM513  CLECSF5        AAAGAAGC-TCAGTT-TCC      8164 TGACAAAG   T   CT
                          AAGCT CAGTT C
                          ||||| ||||| |
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                               TTCGA GTCAA  G
                               _____    _       AG
GAM513 EYA1           GACAAAGAAACAGCAGAATCTC   8179 TG      TT  T_   CT
                          ACAAAGAAGC  CAG  TCTC
                          |||||||||| ||| ||||
                          TGTTTCTTTG  GTC  AGAG
                               __       TC  TT   TI
GAM513 FBXL7          CACAGAA---TCAGTTCTCCT    8174 TGACAAAGA  CT
                             AG  TCAGTTCTC
                             || |||||||||
                             TC  AGTCAAGAG
                          _____  TT
GAM513 FER           GACAAAGAAGATACTTGAG       8177 TG      ___  C  TTCTCC
                          ACAAAGAAG  CTT AG
                          ||||||||| ||| ||
                          TGTTTCTTC  GAA TC
                               __       TAT  C  TIIITC
GAM513 GALNT1        CATAGAAGGTACAGTTCTCC      8172 TGACAA    CTT
                             AGAAG  CAGTTCTCC
                             ||||| |||||||||
                             TCTTC  GTCAAGAGG
                          _____  CAT
GAM513 GPR85         AACAA-CTTCCCAGTTCTCCT     8165 TGACAAAGAAGC
                               TTCAGTTCTCC
                               |||||||||||
                               GGGTCAAGAGG
                     GAA_____
GAM513 KMO           TGACAAAGAGGAGTTTCAG       8180       __  C   TTCTCC
                          TGACAAAGA AG TTCAG
                          ||||||||| || |||||
                          ACTGTTTCT TC AAGTC
                             CC  A   IIITCC
GAM513 LFG           CAAAGAAGC--CATTTCTC       8170 TGACAA    TCAG
                             AGAAGCT  TTCTC
                             |||||||  |||||
                             TCTTCGG  AAGAG
                          _____    TA__
GAM513 MEST          TGACAAAGAGGACTCAGCTCT     8185      A_  T    CCT
                          TGACAAAGA GCT CAGTTCT
                          ||||||||| ||| |||||||
                          ACTGTTTCT TGA GTCGAGA
                             CC  _    III
GAM513 NAV2          CACAGCAACTTGAGTTCTCCT     8176 TGACAA A   C
                             AG AGCTT AGTTCTCCT
                             || ||||| |||||||||
                             TC TTGAA TCAAGAGGA
                          _____  G  C
GAM513 NUP155        TGA-AAAGAAGCTGCTTGCTGTTCTCC8183  C     TCA____   TII
                          TGA AAAGAAGCT    GTTCTCC
                          ||| |||||||||    |||||||
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                         ACT TTTCTTCGA     CAAGAGG
                         _         CGAACGA      III
GAM513 NXF2              GACAAAGAAGACATCGGAGGGCTCCT 8178 TG      _ T __ TT   II
                         ACAAAGAAG C TC  AG  CTCCT
                         ||||||||| | || || |||||
                         TGTTTCTTC G AG  TC  GAGGA
                         __        T T CC CC   AI
GAM513 OLR1             TGACAAAGAATAGCTTAAATTC   8181       __   C   TCCT
                        TGACAAAGA  AGCTT AGTTC
                        ||||||||| ||||| |||||
                        ACTGTTTCT TCGAA TTAAG
                          TA   T    IIIT
GAM513 PCDHB16          CACAGAAGCTTCATGTATCC   8171 TGACAA      _ _
                         AGAAGCTTCA GT TCTCC
                         |||||||||| || |||||
                         TCTTCGAAGT CA AGGGG
                        _____       A T
GAM513 SAS             CACAGAAGCTTCCCATATCCT   8175 TGACAA      A___   CT
                        AGAAGCTTC  GTTCTC
                        |||||||||  |||||
                        TCTTCGAAG  TAGGAG
                        _____      GGTA   AA
GAM513 SHMT1           AGAAGCTAATTCAGTTCTCCT   8169 TGACAAAGAAGC
                               TTCAGTTCTCCT
                               ||||||||||||
                               AAGTCAAGAGGA
                        ATT_____
GAM513 SMARCA3         CAAAGAAGC--AAGCTGTCCT   8173 TGACAA    TTCA_
                        AGAAGC   GTTCTCC
                        ||||||   |||||||
                        TCTTCG   CAGGAGG
                        _____     TTCGA
GAM513 TIM3            TGAAAAATATAGCTTCAGTT   8182  C  GA_     CTCC
                        TGA AAA  AGCTTCAGTT
                        ||| |||  ||||||||||
                        ACT TTT  TCGAAGTCAA
                         T  ATA      IIIT
GAM513 TLL1            TGAAAGAGACCTTTCAGTTCTC   8186 TG C   AG __    CT
                        A AAAGA  CT TCAGTTCTC
                        | ||||| ||  ||||||||||
                        A TTTCT  GG  AGTCAAGAG
                        __ C   CT AA      II
GAM513 TXK            ACACAACAGTCTTCAGTTCTTCT   8166 TG   AGAAG     C I
                        ACAA    CTTCAGTTCT CT
                        ||||    |||||||||| ||
                        TGTT    GAAGTCAAGA GA
                        __   GTCA_       A C
GAM514 AIRE          TCTCAGCTCACTGCAACCTC   8194      G  A   GGC
                      TCTCAGCTCA TG AACCTC
                      |||||||||| || ||||||
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                      AGAGTCGAGT AC TTGGAG
                          G  G    III
GAM514 AIRE           TCTCAGCTCACTGCAACCTC    8194      G  A   I
                          CTCAGCTCA TG AACCT
                          |||||||||| || |||||
                          GAGTCGAGT AC TTGGA
                              G  G    I
GAM514 CARKL          TCTCAGCTCACTGCAACCTCTGCC  8202      G  A    G I
                          CTCAGCTCA TG AACCTC GC
                          |||||||||| || |||||| ||
                          GAGTCGAGT AC TTGGAG CG
                              G  G    A I
GAM514 CARKL          TCTCAGCTCACTGCAACCTCTGCC  8202      G  A    G I
                          TCTCAGCTCA TG AACCTC GCC
                          |||||||||| || |||||| |||
                          AGAGTCGAGT AC TTGGAG CGG
                              G  G    A I
GAM514 CKAP1          AGC-CA-TGAAACCTCTGC     8189   CA       GGI
                          AGCT GTGAAACCTC
                          |||| ||||||||||
                          TCGG TACTTTGGAG
                          __       ACG
GAM514 CPT2           TCTCAGCTCACTGCAACCTC    8194      G  A   GGC
                          TCTCAGCTCA TG AACCTC
                          |||||||||| || ||||||
                          AGAGTCGAGT AC TTGGAG
                              G  G    III
GAM514 CPT2           TCTCAGCTCACTGCAACCTC    8194      G  A   I
                          CTCAGCTCA TG AACCT
                          |||||||||| || |||||
                          GAGTCGAGT AC TTGGA
                              G  G    I
GAM514 CYP4F3         TCTCGGCTCACTGAAACCTC     8195   A   G    GGC
                          TCTC GCTCA TGAAACCTC
                          |||| ||||| |||||||||
                          AGAG CGAGT ACTTTGGAG
                             C    G     III
GAM514 CYP4F3         TCTCGGCTCACTGAAACCTC     8195   A   G    I
                          CTC GCTCA TGAAACCT
                          ||| ||||| ||||||||
                          GAG CGAGT ACTTTGGA
                             C    G     I
GAM514 DDOST          TCTCAGCTCACTGCAAGCTCTGCC  8204      G  AAAC  G I
                          TCTCAGCTCA TG   CTC GCC
                          |||||||||| ||   ||| |||
                          AGAGTCGAGT AC   GAG CGG
                              G  GTTC  A I
GAM514 DDOST          TCTCAGCTCACTGCAAGCTCTGCC  8204      G  AAAC  G I
                          CTCAGCTCA TG   CTC GC
                          |||||||||| ||   ||| ||
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                           GAGTCGAGT AC   GAG CG
                               G GTTC  A I
GAM514 DGKI         TCTCAGCTCACTGCCAGCTCCGCC  8206       G AAAC  G I
                        TCTCAGCTCA TG   CTC GCC
                        ||||||||| ||   ||| |||
                        AGAGTCGAGT AC   GAG CGG
                               G GGTC  G I
GAM514 DGKI         TCTCAGCTCACTGCCAGCTCCGCC  8206       G AAAC  G I
                         CTCAGCTCA TG   CTC GC
                         ||||||||| ||   ||| ||
                         GAGTCGAGT AC   GAG CG
                               G GGTC  G I
GAM514 DSCAM          TCAGCTCAGTGGGCCCCCGGC    8192        AAA    I
                          CAGCTCAGTG  CCTCGG
                          ||||||||||  ||||||
                          GTCGAGTCAC  GGGGCC
                               CCG    I
GAM514 DSCAM          TCAGCTCAGTGGGCCCCCGGC    8192 TCTC      AAA     C
                           AGCTCAGTG  CCTCGGC
                           |||||||||  |||||||
                           TCGAGTCAC  GGGGCCG
                    ____        CCG     T
GAM514 FGFR1        TCTCAGCTCACTGCAACCTCTGCC  8202      G A   G I
                        TCTCAGCTCA TG AACCTC GCC
                        |||||||||| || |||||| |||
                        AGAGTCGAGT AC TTGGAG CGG
                               G G   A I
GAM514 FGFR1        TCTCAGCTCACTGCAACCTCTGCC  8202      G A   G I
                         CTCAGCTCA TG AACCTC GC
                         ||||||||| || |||||| ||
                         GAGTCGAGT AC TTGGAG CG
                               G G   A I
GAM514 GALNT7       TCTCAGCTCACTGCAACCTCTGCC  8202       G A   G I
                         CTCAGCTCA TG AACCTC GC
                         ||||||||| || |||||| ||
                         GAGTCGAGT AC TTGGAG CG
                               G G   A I
GAM514 GALNT7       TCTCAGCTCACTGCAACCTCTGCC  8202       G A   G I
                        TCTCAGCTCA TG AACCTC GCC
                        |||||||||| || |||||| |||
                        AGAGTCGAGT AC TTGGAG CGG
                               G G   A I
GAM514 HIP1         TCTCAGCTCACTGCAACCTCTGCC  8202     G A   G I
                        TCTCAGCTCA TG AACCTC GCC
                        |||||||||| || |||||| |||
                        AGAGTCGAGT AC TTGGAG CGG
                               G G   A I
GAM514 HIP1         TCTCAGCTCACTGCAACCTCTGCC  8202     G A   G I
                         CTCAGCTCA TG AACCTC GC
                         ||||||||| || |||||| ||
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                          GAGTCGAGT AC TTGGAG CG
                             G  G    A I
GAM514  IRAK4        TCTCAGCTCACTGCAACCTC    8194      G  A    GGC
                        TCTCAGCTCA TG AACCTC
                        |||||||||| || ||||||
                        AGAGTCGAGT AC TTGGAG
                             G  G    III
GAM514  IRAK4        TCTCAGCTCACTGCAACCTC    8194      G  A    I
                        CTCAGCTCA TG AACCT
                        ||||||||| || |||||
                        GAGTCGAGT AC TTGGA
                             G  G    I
GAM514  IRS1        CAGCTCAGTCGCAGAGACCGCGGC  8190 AGCT  ____  A  T  I
                         CAGT   GA ACC CGG
                         ||||   || ||| |||
                         GTCA   CT TGG GCC
                         ____   GCGT C  C  I
GAM514  IRS1        CAGCTCAGTCGCAGAGACCGCGGC  8190 T   C  A _  A  T  CI
                         CTCAG TC GT GA ACC CGGC
                         ||||| || || || ||| ||||
                         GAGTC AG CG CT TGG GCCG
                         _   _ _  T  C  C   CG
GAM514  KAI1        TCTCAGCTCACTGCAACCTCCGC   8197      G  A    G CI
                        TCTCAGCTCA TG AACCTC GC
                        |||||||||| || |||||| ||
                        AGAGTCGAGT AC TTGGAG CG
                             G  G    G II
GAM514  KAI1        TCTCAGCTCACTGCAACCTCCGC   8197      G  A    GGI
                        CTCAGCTCA TG AACCTC
                        ||||||||| || ||||||
                        GAGTCGAGT AC TTGGAG
                             G  G    GCI
GAM514  MAFF        TCTCAGCTCACTACAACCTCTGCC  8200       G  A   G I
                        TCTCAGCTCA TG AACCTC GCC
                        |||||||||| || |||||| |||
                        AGAGTCGAGT AT TTGGAG CGG
                             G  G    A I
GAM514  MAFF        TCTCAGCTCACTACAACCTCTGCC  8200       G  A   G I
                        CTCAGCTCA TG AACCTC GC
                        ||||||||| || |||||| ||
                        GAGTCGAGT AT TTGGAG CG
                             G  G    A I
GAM514  MOG         TCTCAGCTCACTGCAACCTCTGCC  8202       G  A   G I
                        TCTCAGCTCA TG AACCTC GCC
                        |||||||||| || |||||| |||
                        AGAGTCGAGT AC TTGGAG CGG
                             G  G    A I
GAM514  MOG         TCTCAGCTCACTGCAACCTCTGCC  8202       G  A   G I
                        CTCAGCTCA TG AACCTC GC
                        ||||||||| || |||||| ||
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                        GAGTCGAGT AC TTGGAG CG
                              G  G    A I
GAM514 NPHS1            TCTCAGCTCACTGCAACCTCCGCC  8201        G  A    G I
                        TCTCAGCTCA TG AACCTC GCC
                        |||||||||| || |||||| |||
                        AGAGTCGAGT AC TTGGAG CGG
                              G  G    G I
GAM514 NPHS1            TCTCAGCTCACTGCAACCTCCGCC  8201        G  A    G I
                         CTCAGCTCA TG AACCTC GC
                         ||||||||| || |||||| ||
                        GAGTCGAGT AC TTGGAG CG
                              G  G    G I
GAM514 PA2G4           TCTCAGCTCACTGCAACCTC    8194        G  A    GGC
                        TCTCAGCTCA TG AACCTC
                        |||||||||| || ||||||
                        AGAGTCGAGT AC TTGGAG
                              G  G    III
GAM514 PA2G4           TCTCAGCTCACTGCAACCTC    8194       G  A    I
                         CTCAGCTCA TG AACCT
                         ||||||||| || |||||
                        GAGTCGAGT AC TTGGA
                              G  G    I
GAM514 PCSK1          GCTCAGTGAAGCGCTTCGG     8191       ACCTCGIII
                        GCTCAGTGAA
                        ||||||||||
                        CGAGTCACTT
                          CGCGAAGCC
GAM514 PLA2G2D       TCTGGGCTCACTGAAACCTCTGCC 8209  CA  G      G I
                        TCT  GCTCA TGAAACCTC GCC
                        |||  ||||| |||||||||| |||
                        AGA  CGAGT ACTTTGGAG CGG
                           CC  G    A I
GAM514 PLA2G2D       TCTGGGCTCACTGAAACCTCTGCC 8209 CTCA  G      G I
                          GCTCA TGAAACCTC GC
                          ||||| |||||||||| ||
                          CGAGT ACTTTGGAG CG
                        GACC  G    A I
GAM514 POLH            TCTCAGCTCAATGCAACCTCCGCC  8198          A  G I
                        TCTCAGCTCAGTG AACCTC GCC
                        ||||||||||||| |||||| |||
                        AGAGTCGAGTTAC TTGGAG CGG
                              G   G I
GAM514 POLH            TCTCAGCTCAATGCAACCTCCGCC  8198          A  G I
                         CTCAGCTCAGTG AACCTC GC
                         |||||||||||| |||||| ||
                        GAGTCGAGTTAC TTGGAG CG
                              G   G I
GAM514 POLH            TCTCAGCTCACCCCAACCTCTGCC  8199        GTGA   G I
                        TCTCAGCTCA   AACCTC GCC
                        ||||||||||   |||||| |||
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                         AGAGTCGAGT   TTGGAG CGG
                             GGGG    A  I
GAM514  POLH             TCTCAGCTCACCCCAACCTCTGCC  8199       GTGA    G  I
                         CTCAGCTCA   AACCTC GC
                         IIIIIIIII   IIIIII II
                         GAGTCGAGT   TTGGAG CG
                             GGGG    A  I
GAM514  PSMD5            TCTCAGCTCACTGCAACCTCTGCC  8202       G A    G  I
                         TCTCAGCTCA TG AACCTC GCC
                         IIIIIIIIII II IIIIII III
                         AGAGTCGAGT AC TTGGAG CGG
                               G G    A  I
GAM514  PSMD5            TCTCAGCTCACTGCAACCTCTGCC  8202       G A    G  I
                         CTCAGCTCA TG AACCTC GC
                         IIIIIIIII II IIIIII II
                         GAGTCGAGT AC TTGGAG CG
                               G G    A  I
GAM514  SLC19A1          TCACAGGGCCCTGCAAACCTCGGCC  8193  T __   A  G        II
                         TC CA  GCTC GT AAACCTCGGCC
                         II II  IIII II IIIIIIIIIII
                         AG GT  CGGG CG TTTGGAGCCGG
                          T  CC   A  _        II
GAM514  SLC19A1          TCACAGGGCCCTGCAAACCTCGGCC  8193 CTCA_  A  G       I
                              GCTC GT AAACCTCGGC
                              IIII II IIIIIIIIII
                              CGGG CG TTTGGAGCCG
                          TGTCC   A  _       I
GAM514  SUDD             TCTCAGCTCACTGCAACCTCTGCC  8202       G A    G  I
                         TCTCAGCTCA TG AACCTC GCC
                         IIIIIIIIII II IIIIII III
                         AGAGTCGAGT AC TTGGAG CGG
                               G G    A  I
GAM514  SUDD             TCTCAGCTCACTGCAACCTCTGCC  8202       G A    G  I
                         CTCAGCTCA TG AACCTC GC
                         IIIIIIIII II IIIIII II
                         GAGTCGAGT AC TTGGAG CG
                               G G    A  I
GAM514  SWAP70           TCTCAGCTCGCTGCAACCTCCGCC  8207       A GA_    G  I
                         TCTCAGCTC GT  AACCTC GCC
                         IIIIIIIII II  IIIIII III
                         AGAGTCGAG CG  TTGGAG CGG
                           _ ACG    G  I
GAM514  SWAP70           TCTCAGCTCGCTGCAACCTCCGCC  8207       A GA_    G  I
                         CTCAGCTC GT  AACCTC GC
                         IIIIIIII II  IIIIII II
                         GAGTCGAG CG  TTGGAG CG
                           _ ACG    G  I
GAM514  TADA2L           TCTCAGCTCGCTGCAACCTCTGCC  8208       A GA_    G  I
                         TCTCAGCTC GT  AACCTC GCC
                         IIIIIIIII II  IIIIII III
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                              AGAGTCGAG CG  TTGGAG CGG
                               _ ACG     A  I
GAM514  TADA2L        TCTCAGCTCGCTGCAACCTCTGCC  8208      A GA_    G I
                         CTCAGCTC GT  AACCTC GC
                         IIIIIIII II  IIIIII II
                         GAGTCGAG CG  TTGGAG CG
                               _ ACG     A  I
GAM514  TPMT          TCTCAGCTCACTGCAACCTCCGCC  8201       G A    G I
                         TCTCAGCTCA TG AACCTC GCC
                         IIIIIIIIII II IIIIII III
                         AGAGTCGAGT AC TTGGAG CGG
                              G G     G I
GAM514  TPMT          TCTCAGCTCACTGCAACCTCCGCC  8201       G A    G I
                         CTCAGCTCA TG AACCTC GC
                         IIIIIIIII II IIIIII II
                         GAGTCGAGT AC TTGGAG CG
                              G G     G I
GAM514  TRIM14        TCTCAGCTCACTGCAATCTCCGCC  8205      G AAAC  G I
                         TCTCAGCTCA TG   CTC GCC
                         IIIIIIIIII II   III III
                         AGAGTCGAGT AC   GAG CGG
                              G GTTA G  I
GAM514  TRIM14        TCTCAGCTCACTGCAATCTCCGCC  8205      G AAAC  G I
                         CTCAGCTCA TG   CTC GC
                         IIIIIIIII II   III II
                         GAGTCGAGT AC   GAG CG
                              G GTTA G  I
GAM514  TSHR          TCTCAGCTC--TG-CACCTCGG    8196      A GAA     C
                         TCTCAGCTC GT  ACCTCGG
                         IIIIIIIII II  IIIIIII
                         AGAGTCGAG CG  TGGAGCC
                               A ___     I
GAM514  TSHR          TCTCAGCTC--TG-CACCTCGG    8196 _     A GAA
                         CTCAGCTC GT  ACCTCG
                         IIIIIIII II  IIIIII
                         GAGTCGAG CG  TGGAGC
                               A    A ___
GAM514  UBE2G2        TCTCAGCTCACTGCAAGCTCCGCC  8203       G AAAC  G I
                         TCTCAGCTCA TG   CTC GCC
                         IIIIIIIIII II   III III
                         AGAGTCGAGT AC   GAG CGG
                              G GTTC  G I
GAM514  UBE2G2        TCTCAGCTCACTGCAAGCTCCGCC  8203       G AAAC  G I
                         CTCAGCTCA TG   CTC GC
                         IIIIIIIII II   III II
                         GAGTCGAGT AC   GAG CG
                              G GTTC  G I
GAM514  UPK1B         TCTCAGCTCACTGCAACCTC      8194      G A   I
                         CTCAGCTCA TG AACCT
                         IIIIIIIII II IIIII
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                        GAGTCGAGT AC TTGGA
                           G G    I
GAM514  UPK1B        TCTCAGCTCACTGCAACCTC      8194        G A    GGC
                        TCTCAGCTCA TG AACCTC
                        |||||||||| || ||||||
                        AGAGTCGAGT AC TTGGAG
                           G G    III
GAM514  VDR          TCTCAGCTCACTGCAACCTC      8194        G A    GGC
                        TCTCAGCTCA TG AACCTC
                        |||||||||| || ||||||
                        AGAGTCGAGT AC TTGGAG
                           G G    III
GAM514  VDR          TCTCAGCTCACTGCAACCTC      8194      G A    I
                        CTCAGCTCA TG AACCT
                        ||||||||| || |||||
                        GAGTCGAGT AC TTGGA
                           G G    I
GAM514  XRCC2        TCTCAGCTCACTGCAACCTC      8194        G A    GGC
                        TCTCAGCTCA TG AACCTC
                        |||||||||| || ||||||
                        AGAGTCGAGT AC TTGGAG
                           G G    III
GAM514  XRCC2        TCTCAGCTCACTGCAACCTC      8194      G A    I
                        CTCAGCTCA TG AACCT
                        ||||||||| || |||||
                        GAGTCGAGT AC TTGGA
                           G G    I
GAM514  ZNF14        TCTCAGCTCACTGCAACCTC      8194      G A    GGC
                        TCTCAGCTCA TG AACCTC
                        |||||||||| || ||||||
                        AGAGTCGAGT AC TTGGAG
                           G G    III
GAM514  ZNF14        TCTCAGCTCACTGCAACCTC      8194      G A    I
                        CTCAGCTCA TG AACCT
                        ||||||||| || |||||
                        GAGTCGAGT AC TTGGA
                           G G    I
GAM514  ZNF264       TCTCAGCTCACTGCAACCTCCGCC  8201        G A    G I
                        TCTCAGCTCA TG AACCTC GCC
                        |||||||||| || |||||| |||
                        AGAGTCGAGT AC TTGGAG CGG
                           G G    G I
GAM514  ZNF264       TCTCAGCTCACTGCAACCTCCGCC  8201        G A    G I
                        CTCAGCTCA TG AACCTC GC
                        ||||||||| || |||||| ||
                        GAGTCGAGT AC TTGGAG CG
                           G G    G I
GAM515  CLCN7        CTGTGAGGGCTAAGCAGGG       8215  T      __    III
                        CT TGAGGGCTA CAGG
                        || |||||||||| ||||
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                              GA ACTCCCGAT GTCC
                               C     TC  CII
GAM515 CYP8B1         CCAGACTTTGAAG---ACAGG    8214          TACI
                         CCAGACTTTGAGGGC
                         |||||||||||||
                         GGTCTGAAACTTCTG
                                 TCCI
GAM515 CYP8B1         CCAGACTTTGAAG---ACAGG    8214 GTCC      GCT
                          AGACTTTGAGG  ACAG
                          ||||||||||| ||||
                          TCTGAAACTTC  TGTC

                          ___        __
GAM515 HAP1          CCAGACTTTG-GGGTTTCTGG    8213 _      A CTACAGI
                          CAGACTTTG GGG
                          ||||||||| |||
                          GTCTGAAAC CCC
                          G    _   AAAGACI
GAM515 HAP1          CCAGACTTTG-GGGTTTCTGG    8213 GTCC     A CTACA
                          AGACTTTG GGG   GG
                          |||||||| |||   ||
                          TCTGAAAC CCC   CC
                          ____      _   AAAGA
GAM515 PYGO2         GTCCAGACTTTCAGG---ACAG    8216      G   TACAGG
                        GTCCAGACTTT AGGGC
                        ||||||||||| |||||
                        CAGGTCTGAAA TCCTG
                             G    TCIIIG
GAM515 PYGO2         GTCCAGACTTTCAGG---ACAG    8216      G   TAI
                        GTCCAGACTTT AGGGC
                        ||||||||||| |||||
                        CAGGTCTGAAA TCCTG
                             G    TCI
GAM515 TCP10         CCAAATATTGAGGGCTACA     8212    CT        II
                       CCAGA TTGAGGGCTAC
                       ||||| ||||||||||
                       GGTTT AACTCCCGATG
                         AT       TI
GAM515 TCP10         CCAAATATTGAGGGCTACA     8212 GTCC CT        G
                        AGA TTGAGGGCTACAG
                        ||| |||||||||||||
                        TTT AACTCCCGATGTT
                        ____  AT       A
GAM515 UBE2V1        TCCGGTACTTTGAGGTCTACA    8217 CCAG    G   I
                        ACTTTGAGG CTAC
                        ||||||||| ||||
                        TGAAACTCC GATG
                        GCCA     A  I
GAM515 UBE2V1        TCCGGTACTTTGAGGTCTACA    8217 GT AG_     G   GG
                         CC ACTTTGAGG CTACAG
                         || ||||||||| ||||||
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                            GG  TGAAACTCC GATGTT
                            __  CCA      A     II
GAM516 ADD3        TGTGAATAAA---ATTCCAAATGAAT 8235      GCAA  __    I
                            TGTGAATAAAG  TCCA TGAAT
                            ||||||||||  |||| |||||
                            ACACTTATTTT  AGGT ACTTA
                                A___  TT   I
GAM516 ADD3        TGTGAATAAA---ATTCCAAATGAAT 8235 _     GCAA  __    I
                            GTGAATAAAG  TCCA TGAA
                            |||||||||  |||| ||||
                            CACTTATTTT  AGGT ACTT
                              A    A___  TT   I
GAM516 APPL       AAGAAAAGCATATCCATGAAT    8220 AT    _       I
                            AAAGGCA ATCCATGAA
                            ||||||| |||||||||
                            TTTTCGT TAGGTACTT
                                C_     A     I
GAM516 APPL       AAGAAAAGCATATCCATGAAT    8220 TGTGAATA    _
                            AAGGCA ATCCATGAAT
                            |||||| ||||||||||
                            TTTCGT TAGGTACTTA
                            _____       A
GAM516 ARHGEF6    TGTGAACTGAAGGCAATC--TGAA 8232    A_    CA   T
                            TGTGAAT AAGGCAATC TGAA
                            ||||||| ||||||||| ||||
                            ACACTTG TTCCGTTAG ACTT
                                AC        __   I
GAM516 ARHGEF6    TGTGAACTGAAGGCAATC--TGAA 8232 _   A_    CA   I
                            GTGAAT AAGGCAATC TGA
                            |||||| ||||||||| |||
                            CACTTG TTCCGTTAG ACT
                            A   AC        __   I
GAM516 B4GALT5    GTGGATACAATCAATCCATG    8227 A AAGG      I
                            TG ATA   CAATCCAT
                            || |||   |||||||||
                            AC TAT   GTTAGGTA
                             C  GTTA      I
GAM516 B4GALT5    GTGGATACAATCAATCCATG    8227 TG A AAGG     AA
                            TG ATA   CAATCCATG
                            || |||   |||||||||
                            AC TAT   GTTAGGTAC
                            __  C  GTTA     AI
GAM516 IL2RB      ATAAAGGCAA--CAGGAAT      8223      CCATGAAI
                            ATAAAGGCAAT
                            |||||||||||
                            TATTTCCGTTG
                              TCCTTAII
GAM516 IL2RB      ATAAAGGCAA--CAGGAAT      8223 TGTGAATAA  C   A
                            AGG AATCC TGA
                            ||| ||||| |||
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                              TCC TTAGG ACT
                           CCGTTG___  _   _
GAM516 KIF3C               GTGAATAAAGG--ATCTAT      8225        CA  CAI
                           GTGAATAAAGG ATC
                           IIIIIIIIII III
                           CACTTATTTCC TAG
                              __   ATA
GAM516 KIF3C               GTGAATAAAGG--ATCTAT      8225 TG      CA  C GA
                           TGAATAAAGG ATC AT
                           IIIIIIIIII III II
                           ACTTATTTCC TAG TA
                              __     __  A AI
GAM516 KIT                 ATAAAGGCAACATACCTGAAT     8222        ___  A   III
                           ATAAAGGCAAT  CC TGAA
                           IIIIIIIIII  II IIII
                           TATTTCCGTTG  GG ACTT
                              TAT _  AII
GAM516 NCOA6IP             GTGAATAAAGG-AAGACATG      8226 _      C  TC  I
                           TGAATAAAGG AA  CAT
                           IIIIIIIIII II III
                           ACTTATTTCC TT GTA
                           C      _ CT  I
GAM516 NCOA6IP             GTGAATAAAGG-AAGACATG      8226 TG     C  TC  AA
                           TGAATAAAGG AA  CATG
                           IIIIIIIIII II IIII
                           ACTTATTTCC TT GTAC
                              __       _ CT  GI
GAM516 ODC1                GTGAATAAA---AATCCAT      8224        GGC
                           GTGAATAAA AATCCA
                           IIIIIIIII  IIIIII
                           CACTTATTT TTAGGT
                                ___
GAM516 ODC1                GTGAATAAA---AATCCAT       8224 TG     GGC
                           TGAATAAA AATCCATG
                           IIIIIIII IIIIIIII
                           ACTTATTT TTAGGTAT
                                __      __
GAM516 PACE4               TGAATAAAGGGAAAACATG       8230        C  TC  II
                           TGAATAAAGG AA  CAT
                           IIIIIIIIII II III
                           ACTTATTTCC TT GTA
                              C  TT  CI
GAM516 PACE4               TGAATAAAGGGAAAACATG       8230 TGTG    C  TC  AA
                           AATAAAGG AA  CATG
                           IIIIIIII II IIII
                           TTATTTCC TT GTAC
                           ____      C  TT  CA
GAM516 PARK2               TGAACTGAAATCCAATCCATG     8228   __  GG      III
                           TGAAT AAA CAATCCAT
                           IIIII III IIIIIIII
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                          ACTTG TTT GTTAGGTA
                          AC  AG     CII
GAM516 PARK2        TGAACTGAAATCCAATCCATG    8228 TG_   TAAAGG      AAT
                          TGAA    CAATCCATG
                          ||||   |||||||||
                          ACTT    GTTAGGTAC
                          TTG TAG___       AGI
GAM516 PRKY       AATAATGCCAGTTCCATGAAT    8221 ATAAAG AA__      I
                          GC   TCCATGAA
                          ||   ||||||||
                          CG   AGGTACTT
                          ATTA__ GTCA     I
GAM516 PSCDBP       TGTGAATAAAGATCACTCCA     8234         _ A  TGAA
                          TGTGAATAAAGG CA TCCA
                          ||||||||||| || ||||
                          ACACTTATTTCT GT AGGT
                            A  G   IIIT
GAM516 PSCDBP       TGTGAATAAAGATCACTCCA     8234         _ A  II
                          TGTGAATAAAGG CA TCC
                          ||||||||||| || |||
                          ACACTTATTTCT GT AGG
                            A  G   TI
GAM516 TMP21       TGAAAGAGGGCAATCCAAATGAA   8229 TGAATAAA      TI
                          GGCAATCCA
                          |||||||||
                          CCGTTAGGT
                          CTC_____         TT
GAM516 TMP21       TGAAAGAGGGCAATCCAAATGAA   8229 TGTGAATAAA       __ TI
                          GGCAATCCA TGAA
                          ||||||||| ||||
                          CCGTTAGGT ACTT
                          TTTCTC____       TT  CA
GAM516 TOX        TGTACAAAG-CAATCCATG      8231 TGAATA         I
                          AAGGCAATCCAT
                          ||||||||||||
                          TTTCGTTAGGTA
                          ACATG_         C
GAM516 TOX        TGTACAAAG-CAATCCATG      8231 TGTGAATA        A
                          AAGGCAATCCATG
                          |||||||||||||
                          TTTCGTTAGGTAC
                          ATG_____         C
GAM516 TRIM       TGTGAATAAGAGGTAAGCCA     8233        _ C T TGAA
                          TGTGAATAA AGG AA CCA
                          ||||||||| ||| || |||
                          ACACTTATT TCC TT GGT
                            C A C  IIIT
GAM516 TRIM       TGTGAATAAGAGGTAAGCCA     8233        _ C T II
                          TGTGAATAA AGG AA CC
                          ||||||||| ||| || ||
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                      ACACTTATT TCC TT GG
                        C   A  C  TI
GAM517 AGTR1          CCGGCAGAGCTGCTAGCGGCGC   8244 CG      __      AGI
                        GCAGAGC  CTGGTGG
                        ||||||| |||||||
                        CGTCTCG GATCGCC
                        __    AC      GCI
GAM517 AGTR1          CCGGCAGAGCTGCTAGCGGCGC   8244 TCACCG    __     A T
                        GCAGAGC  CTGGTGG GC
                        ||||||| ||||||| ||
                        CGTCTCG GATCGCC CG
                        _____      AC    G C
GAM517 ARHGEF7         CCGGCAGAG--GGGCGGAG     8246       CCT    I
                        CCGGCAGAG  GGTGGA
                        ||||||||| ||||||
                        GGCCGTCTC  CCGCCT
                            C__      C
GAM517 ARHGEF7         CCGGCAGAG--GGGCGGAG     8246 TCACCG    CCT
                        GCAGAG  GGTGGAG
                        |||||| |||||||
                        CGTCTC  CCGCCTC
                             _____    C__
GAM517 BAG1           CGGCAGAG-CTGGTGGCGC      8249     C   AGI
                        CGGCAGAGC TGGTGG
                        ||||||||| ||||||
                        GCCGTCTCG ACCACC
                           _    GCG
GAM517 BAG1           CGGCAGAG-CTGGTGGCGC      8249 TCACCGGC   C    A
                        AGAGC TGGTGG G
                        ||||| |||||| |
                        TCTCG ACCACC C
                        _____   _    G
GAM517 CCT3          ACCGGCAGAACCTTCTGGAG      8239        GG   I
                        CCGGCAGAGCCT TGGA
                        |||||||||||| ||||
                        GGCCGTCTTGGA ACCT
                           AG    I
GAM517 CCT3          ACCGGCAGAACCTTCTGGAG      8239 TCAC       GG   C
                        CGGCAGAGCCT TGGAG
                        |||||||||||| |||||
                        GCCGTCTTGGA ACCTC
                            ____      AG    T
GAM517 DLEC1        CACC--CAG---CTGGTGGAG      8242 A__    AGAGCC
                        CCGGC    TGGTGG
                        |||||    ||||||
                        GGTCG    ACCACC
                        GTG    _____
GAM517 DLEC1        CACC--CAG---CTGGTGGAG      8242 TCA   AGAGCC
                        CCGGC    TGGTGGA
                        |||||    |||||||
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                              GGTCG    ACCACCT
                              TG_      _____
GAM517 GALC          CCGGCGTCACCTGGTGGAGC    8247   AGA       I
                              CGGC  GCCTGGTGGAG
                              ||||  ||||||||||
                              GCCG  TGGACCACCTC
                               CAG        I
GAM517 GALC          CCGGCGTCACCTGGTGGAGC    8247 TCACCG AGA
                               GC  GCCTGGTGGAGC
                               ||  ||||||||||||
                               CG  TGGACCACCTCG
                              _____  CAG
GAM517 HCS           ACCAGGCAGGGCCTGGTGG      8238  _    A     II
                              ACC GGCAG GCCTGGTG
                              ||| ||||| ||||||||
                              TGG CCGTC CGGACCAC
                               T   C     CI
GAM517 HCS           ACCAGGCAGGGCCTGGTGG      8238 TCACC   A      AGC
                              GGCAG GCCTGGTGG
                              ||||| |||||||||
                              CCGTC CGGACCACC
                              GT___  C    GAI
GAM517 MYBL2         CCGGCAGAGCCCGGAGCGGGAGC  8245 CGG     T___   I
                              CAGAGCCTGG  GGAG
                              ||||||||||  ||||
                              GTCTCGGGCC  CCTC
                              ___     TCGC  I
GAM517 MYBL2         CCGGCAGAGCCCGGAGCGGGAGC  8245 TCACCG     T___   I
                              GCAGAGCCTGG  GGAGCT
                              |||||||||||  ||||||
                              CGTCTCGGGCC  CCTCGG
                              _____     TCGC   C
GAM517 PAX2          GCAGCAGCCTGGTGG-GCT      8250  _     A II
                              GCAG AGCCTGGTGG GC
                              |||| |||||||||| ||
                              CGTC TCGGACCACC CG
                               G       _ AI
GAM517 SH3GL1        GCAGAGCCTGGGGTCCGGAGCT   8251         ____   IIIA
                              GCAGAGCCTGG  TGGAGC
                              |||||||||||  ||||||
                              CGTCTCGGACC  GCCTCG
                               CCAG    AIII
GAM517 SIGLEC11      CCAGCAGGAAGCCTGGTGGAG    8243   __         III
                              CCGGCAG AGCCTGGTGGA
                              ||||||| |||||||||||
                              GGTCGTC TCGGACCACCT
                               CT       CII
GAM517 SIGLEC11      CCAGCAGGAAGCCTGGTGGAG    8243 TCACCG __         CT
                              GCAG AGCCTGGTGGAG
                              |||| ||||||||||||
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```
                      CGTC  TCGGACCACCTC
                      _____      CT        CC
GAM517 SMP1           CACAGG--GAGCCTGGTGG      8241  C CA       I
                         CAC GG  GAGCCTGGTG
                         ||| ||  ||||||||||
                         GTG CC  CTCGGACCAC
                          T  __        C
GAM517 SMP1           CACAGG--GAGCCTGGTGG      8241 TCAC  CA        AG
                           CGG  GAGCCTGGTGG
                           |||  ||||||||||
                           GTC  CTCGGACCACC
                          T___  C_       GI
GAM517 STK4           TCACC--CAAAGCCTGGGTGGAGCT 8253    GG       _   I
                         TCACC CAGAGCCTGG TGGAGCT
                         ||||| |||||||||| |||||||
                         AGTGG GTTTCGGACC ACCTCGA
                           __          C   I
GAM517 STK4           TCACC--CAAAGCCTGGGTGGAGCT 8253 _  GG       _   I
                          CACC CAGAGCCTGG TGGAGC
                          |||| |||||||||| ||||||
                          GTGG GTTTCGGACC ACCTCG
                          A   __          C   I
GAM517 TEAD3          CGGCTGAGCCTGGTCCGAGCT     8248 G A      G_  I
                            GC GAGCCTGGT GAGC
                            || |||||||| ||||
                            CG CTCGGACCA CTCG
                            _  A        GG  I
GAM517 TEAD3          CGGCTGAGCCTGGTCCGAGCT     8248 TCACCGGCA      G_
                             GAGCCTGGT GAGCT
                             ||||||||| |||||
                             CTCGGACCA CTCGA
                          A_____         GG
GAM517 TNFAIP2        GCAGAGCCTTAGGGGGAGC      8252       __ T  III
                         GCAGAGCCT GG GGAG
                         ||||||||| || ||||
                         CGTCTCGGA CC CCTC
                          AT  C   GII
GAM517 TNP1           CACCAGGGCAGAGCCCGCTGG     8240   __        G III
                         CACC GGCAGAGCCTG TG
                         |||| |||||||||||| ||
                         GTGG CCGTCTCGGGC AC
                          TC         G CII
GAM517 TNP1           CACCAGGGCAGAGCCCGCTGG     8240 TC __       G AGCT
                          ACC GGCAGAGCCTG TGG
                          ||| |||||||||||| |||
                          TGG CCGTCTCGGGC ACC
                          __ TC        G CIII
GAM518 CHST5          TCCTGGTAGGCAGCAACAAT      8268 CAGC TA      GGC
                         TCC AG AGCAACAAT
                         ||| || |||||||||
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                         AGG   TC TCGTTGTTA
                        ACCA  CG        III
GAM518 CHST5        TCCTGGTAGGCAGCAACAAT      8268 CCCAGC TA       I
                        AG AGCAACAA
                        II IIIIIIII
                        TC TCGTTGTT
                       GGACCA CG       I
GAM518 DNASE1      GCAG-AA--AACAATGGCT      8264    TAAGC
                       GCAG    AACAATGGC
                       IIII   IIIIIIIII
                       CGTC   TTGTTACCG
                         TT___
GAM518 ITGA1       CAGCATTAACAGCAACAAT       8257    GTA__      III
                       CAGCA   AGCAACAA
                       IIIII   IIIIIIII
                       GTCGT   TCGTTGTT
                         AATTG    AII
GAM518 ITGA1       CAGCATTAACAGCAACAAT      8257 TCCCAGCAGTA      GGC
                        AGCAACAAT
                        IIIIIIIII
                        TCGTTGTTA
                      GTAATTG____      GGC
GAM518 LAIR1       TCCCAGCAGT--GCAGC-CTGGC  8270      A_ AACAATI
                       TCCCAGCAGT AGC
                       IIIIIIIIII III
                       AGGGTCGTCA TCG
                         CG GACCGII
GAM518 LAIR1       TCCCAGCAGT--GCAGC-CTGGC  8270      AA ACAA
                       TCCCAGCAGT GCA  TGGC
                       IIIIIIIIII III  IIII
                       AGGGTCGTCA CGT  ACCG
                         __ CGG_
GAM518 LENG4        CCCAGCAGTGGGAAACACTGGC   8262      AAGC  A  I
                       CCAGCAGT   AACA TGG
                       IIIIIIII   IIII III
                       GGTCGTCA   TTGT ACC
                         CCCT  G  I
GAM518 LENG4        CCCAGCAGTGGGAAACACTGGC  8262 TC      AAGC  A
                       CCAGCAGT   AACA TGGCT
                       IIIIIIII   IIII IIIII
                       GGTCGTCA   TTGT ACCGG
                         __     CCCT  G
GAM518 MASP1       TCCCAGCAGTCAGC-ACAA      8267     A A TGG
                       TCCCAGCAGT AGCA CAA
                       IIIIIIIIII IIII III
                       AGGGTCGTCA TCGT GTT
                         G _ III
GAM518 MASP1       TCCCAGCAGTCAGC-ACAA      8267     A  ACAI
                       TCCCAGCAGT AGCA
                       IIIIIIIIII IIII
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                           AGGGTCGTCA TCGT
                             G   GTTI
GAM518 MOX2              AGCAGTAAGCAGGAACTGG    8256        ACAATGII
                          AGCAGTAAGCA
                          IIIIIIIIII
                          TCGTCATTCGT
                            CCTTGACC
GAM518 MYCN             TCCCAGCAGAACCCCACACTGG  8269        TAAGCA  A  CT
                          TCCCAGCAG    ACA TGG
                          IIIIIIIII    III III
                          AGGGTCGTC    TGT ACC
                            TTGGGG  G  II
GAM518 MYCN             TCCCAGCAGAACCCCACACTGG  8269      TA  AA ATGI
                          CCCAGCAG AGC CA
                          IIIIIIII III II
                          GGGTCGTC TTG GT
                            __  GG GTGA
GAM518 PCTP             TCCTAATAGTAAGCAAGCAAAGG 8266   C C      _ T CTI
                          TCC AG AGTAAGCAA CAA GG
                          III II IIIIIIIII III II
                          AGG TT TCATTCGTT GTT CC
                           A  A      C T III
GAM518 PCTP             TCCTAATAGTAAGCAAGCAAAGG 8266 CCCAGC      _ TI
                              AGTAAGCAA CAA
                              IIIIIIIII III
                              TCATTCGTT GTT
                          ATTA__       C TC
GAM518 PDCL             CCAGGTCAGTAAGCATCAA     8258  __        ACAIII
                          CCAG CAGTAAGCA
                          IIII IIIIIIIII
                          GGTC GTCATTCGT
                           CA       AGTTI
GAM518 PDCL             CCAGGTCAGTAAGCATCAA     8258 TCCCAG    A GGC
                          CAGTAAGCA CAAT
                          IIIIIIIII IIII
                          GTCATTCGT GTTG
                          TCCA__       A GII
GAM518 POLG             CCCAACA---AGCAACAATG    8261      GTA    I
                          CCCAGCA AGCAACAA
                          IIIIIII IIIIIIII
                          GGGTTGT TCGTTGTT
                              ___        A
GAM518 POLG             CCCAACA---AGCAACAATG    8261 TC   GTA      G
                           CCAGCA AGCAACAATG
                           IIIIII IIIIIIIIII
                           GGTTGT TCGTTGTTAC
                           __  ___      G
GAM518 PPP1CB           TCCCAGCAG-CGGGAACAAGGGCT 8271       AAGC  T  I
                          TCCCAGCAGT  AACAA GGCT
                          IIIIIIIIII  IIIII IIII
```

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                          AGGGTCGTCG   TTGTT CCGA
                               CCC_    C   I
GAM518  PPP1CB         TCCCAGCAG-CGGGAACAAGGGCT  8271 _      AAGC   T  I
                          CCCAGCAGT   AACAA GGC
                          |||||||||   ||||| |||
                          GGGTCGTCG   TTGTT CCG
                               A    CCC_   C  I
GAM518  SOX11          CCAGCAGTAAGTAA-AATGG     8260 _      CAACAATGI
                          CAGCAGTAAG
                          ||||||||||
                          GTCGTCATTC
                            G      ATTTTACII
GAM518  SOX11          CCAGCAGTAAGTAA-AATGG     8260 TCCC    C  C   C
                            AGCAGTAAG AA AATGG
                            ||||||||| || |||||
                            TCGTCATTC TT TTACC
                          ____         A  _  T
GAM518  SQSTM1         TCCCAGCAGGAAGCCCACAACACTGGC8265    T  A_  ___  TIII
                          TCCCAGCAG AAGC ACAA TGGC
                          ||||||||| |||| |||| ||||
                          AGGGTCGTC TTCG TGTT ACCG
                               C  GG  GTG  IIIT
GAM518  SQSTM1         TCCCAGCAGGAAGCCCACAACACTGGC8265 CC   C_  AA   A  I
                            CAG AGT GCAACA TGG
                            ||| ||| |||||| |||
                            GTC TCG TGTTGT ACC
                          C_  CT  GG   G  I
GAM518  UBE2L3         CCAGCAGATCTTCTACAATGGCT   8259 C   TAAGCA_     I
                            AGCAG    ACAATGGC
                            |||||    ||||||||
                            TCGTC    TGTTACCG
                          _   TAGAAGA    I
GAM518  UBE2L3         CCAGCAGATCTTCTACAATGGCT   8259 TCCC   TAAGCA_      I
                            AGCAG    ACAATGGCT
                            |||||    |||||||||
                            TCGTC    TGTTACCGA
                          ____      TAGAAGA      C
GAM518  WHSC1          CCCAGCAGT---CAACA--GGCT   8263 _      AAG   AT
                            CCAGCAGT  CAACA  GG
                            ||||||||  |||||  ||
                            GGTCGTCA  GTTGT  CC
                               G    ___    __
GAM518  WHSC1          CCCAGCAGT---CAACA--GGCT   8263 TC      AAG   AT
                            CCAGCAGT  CAACA  GG
                            ||||||||  |||||  ||
                            GGTCGTCA  GTTGT  CC
                               __    ___    __
GAM519  CUBN          GGTTTGGTGAAAAACCATACA     8277 ____    GCTA      I
                            GGTGG  AAAACCATGC
                            |||||  ||||||||||
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                      CCACT  TTTTGGTATG
                      CAAA      ____         I
GAM519 CUBN           GGTTTGGTGAAAAACCATACA    8277 TAG    GCTA
                      GGTGG  AAAACCATGCA
                      |||||  ||||||||||
                      CCACT  TTTTGGTATGT
                      AAA       ____
GAM519 ERBB2IP        TGGTCCAAATAACCATGCA    8282 G    _      II
                      TGG CTAAA AACCATGC
                      ||| ||||| ||||||||
                      ACC GGTTT TTGGTACG
                      A   A    TI
GAM519 ERBB2IP        TGGTCCAAATAACCATGCA    8282 TAGGGTGGGCTAAA
                      AACCATGC
                      ||||||||
                      TTGGTACG
                      GTTTA_____
GAM519 FOSB           GGGTGGGAGAGCCAAAACCATG  8276 ____  T    A    III
                      GGG GGGCTAAAA CCAT
                      ||| |||||||||| ||||
                      CCC CTCGGTTTT GGTA
                      CCCA  T      _   CII
GAM519 FOSB           GGGTGGGAGAGCCAAAACCATG  8276 TA  T    A    CAI
                      GGG GGGCTAAAA CCATG
                      ||| |||||||||| |||||
                      CCC CTCGGTTTT GGTAC
                      CA  T      _   CAI
GAM519 GPC4           AGGGTGGGCTAGCTAACC-TGC  8275        AA_ ATGI
                      GGGTGGGCTA  AACC
                      ||||||||||  ||||
                      CCCACCCGAT  TTGG
                      CGA   ACII
GAM519 GPC4           AGGGTGGGCTAGCTAACC-TGC  8275 TA     AA_  A A
                      GGGTGGGCTA  AACC TGC
                      ||||||||||  |||| |||
                      CCCACCCGAT  TTGG ACG
                      __      CGA  _  G
GAM519 HNF3G          AGGGTGGGCTTCAGAGAAAACCA  8274       A_____    IIIT
                      AGGGTGGGCT    AAAACC
                      ||||||||||    ||||||
                      TCCCACCCGA    TTTTGG
                      AGTCTC    TIII
GAM519 HNF3G          AGGGTGGGCTTCAGAGAAAACCA  8274 TA    A_____    TGCAI
                      GGGTGGGCT    AAAACCA
                      |||||||||    |||||||
                      CCCACCCGA    TTTTGGT
                      __      AGTCTC    TIIIA
GAM519 HNF3G          GGTGGCCATCAAACCATGCA   8278 GTG  A_     I
                      GGCTA  AAACCATGC
                      |||||  |||||||||
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                                CCGGT TTTGGTACG
                          CA_     AG        I
GAM519  HNF3G         GGTGGCCATCAAACCATGCA    8278 TAGGGTG   A_
                          GGCTA AAACCATGCA
                          ||||| ||||||||||
                          CCGGT TTTGGTACGT
                          _____      AG
GAM519  MAX           TAGGGTGGGCAGGACACTATG    8281        TAAAA C  CA
                          TAGGGTGGGC   AC ATG
                          ||||||||||   || |||
                          ATCCCACCCG   TG TAC
                           TCCTG A  II
GAM519  MAX           TAGGGTGGGCAGGACACTATG    8281        TAAAA CATI
                          AGGGTGGGC    AC
                          |||||||||    ||
                          TCCCACCCG    TG
                           TCCTG ATAI
GAM519  PXN           TAGGGTGGGTCACTATAAAC     8279        ___  A  CATGCA
                          TAGGGTGGG  CTA AAAC
                          |||||||||  ||| ||||
                          ATCCCACCC  GAT TTTG
                           AGT  A   IIIACG
GAM519  PXN           TAGGGTGGGTCACTATAAAC     8279        CTAAAAAIII
                          TAGGGTGGG
                          |||||||||
                          ATCCCACCC
                          AGTGATATTT
GAM519  TMPRSS3       TAGGGTGGGCCCTAATCCA      8280        AA A  TGC
                          TAGGGTGGGCT AA CCA
                          ||||||||||| || |||
                          ATCCCACCCGG TT GGT
                           GA  A   III
GAM519  TMPRSS3       TAGGGTGGGCCCTAATCCA      8280        AA A II
                          TAGGGTGGGCT AA CC
                          ||||||||||| || ||
                          ATCCCACCCGG TT GG
                           GA  A  TI
GAM520  CACNA1C       GGGCCGGCGGCTGGCCGGGA     8296        AT__   III
                          GGGCCGGCGG  TCGGG
                          ||||||||||  |||||
                          CCCGGCCGCC  GGCCC
                           GACC    TII
GAM520  CACNA1C       GGGCCGGCGGCTGGCCGGGA     8296 TGAGAAG   C GA   G
                          GGCCGG G TTCGG
                          |||||| | |||||
                          CCGGCC C GAGCC
                          CGCCGA_   _TC   I
GAM520  CD44          GGGCCGGCGGAGGACGGGA      8295        TT_  II
                          GGGCCGGCGGA CGGG
                          |||||||||| ||||
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                        CCCGGCCGCCT  GCCC
                           CCT   TI
GAM520  CSH2          GAGAAGGGCCTGGAGGATT      8289        _  C   II
                          GAGAAGGGCC GG GGAT
                          ||||||||| || |||||
                          CTCTTCCCGG CC CCTA
                              A  T   AI
GAM520  CSH2          GAGAAGGGCCTGGAGGATT      8289 TG      _  C    CGGG
                           AGAAGGGCC GG GGATT
                           ||||||||| || |||||
                           TCTTCCCGG CC CCTAA
                           __        A  T   TIII
GAM520  CYP4A11         GAGAAGGGCAGGCAGACTGGGG    8293       C     C I
                          AGAAGGGC GGCGGATT GG
                          |||||||| ||||||| ||
                          TCTTCCCG CCGTCTGA CC
                             T    C I
GAM520  CYP4A11         GAGAAGGGCAGGCAGACTGGGG    8293 TG    C     C A
                          AGAAGGGC GGCGGATT GGG
                          |||||||| ||||||| |||
                          TCTTCCCG CCGTCTGA CCC
                          __      T    C  C
GAM520  ETS2          AGGGCCGGCGCTTGGTCGGGA    8285        GAT__   III
                          AGGGCCGGCG   TCGGG
                          ||||||||||   |||||
                          TCCCGGCCGC   AGCCC
                            GAACC    TII
GAM520  FAAH        GAGAAGGGCTG--TGATTCTGGA    8294        CGGCG   _  I
                          GAGAAGGGC   GATTC GG
                          |||||||||   ||||| ||
                          CTCTTCCCG   CTAAG CC
                           ACA__   A  T
GAM520  FAAH        GAGAAGGGCTG--TGATTCTGGA    8294 TG      CGGCG    G
                          AGAAGGGC   GATTC GGA
                          ||||||||   ||||| |||
                          TCTTCCCG   CTAAG CCT
                          __      ACA__   A
GAM520  LMO1       GAGAAGGGC--GCCGACTCGGG    8292 _      CG G    I
                          AGAAGGGC GC GATTCGG
                          |||||||| || |||||||
                          TCTTCCCG CG CTGAGCC
                             C    __ G    I
GAM520  LMO1       GAGAAGGGC--GCCGACTCGGG    8292 TG     CG G
                          AGAAGGGC GC GATTCGGG
                          |||||||| || |||||||
                          TCTTCCCG CG CTGAGCCC
                          __      __ G
GAM520  MBTPS1     AGGGCCGGCGGGCCCGGGA    8287        AT   II
                          AGGGCCGGCGG TCGGG
                          |||||||||| |||||
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                            TCCCGGCCGCC GGCCC
                               CG    TI
GAM520 MEF2D        TGAGAAGGGAAGGC-CATTC     8297      CC  GG   GGG
                            TGAGAAGGG GGC ATTC
                            |||||||| ||| ||||
                            ACTCTTCCC CCG TAAG
                               TT  G_    III
GAM520 MEF2D        TGAGAAGGGAAGGC-CATTC     8297 _     CC  GGATTI
                            GAGAAGGG GGC
                            |||||||| |||
                            CTCTTCCC CCG
                            A     TT  GTAAII
GAM520 NR3C1        TGAGAAGGGTGGTCAGAAT-GGGA 8299      CC _  TTC  I
                            TGAGAAGGG GG CGGA  GGGA
                            ||||||||| || |||| ||||
                            ACTCTTCCC CC GTCT  CCCT
                               A_  A  TA_  I
GAM520 NR3C1        TGAGAAGGGTGGTCAGAAT-GGGA 8299 _    CC _  TTC  I
                            GAGAAGGG GG CGGA  GGG
                            |||||||| || |||| |||
                            CTCTTCCC CC GTCT  CCC
                            A    A_ A  TA_  I
GAM520 PTGS1        TGAGAAGGGCAG--GGATCCAGG  8298     C C     A
                            TGAGAAGGGC GG GGATTCGGG
                            ||||||||||| || |||||||||
                            ACTCTTCCCG TC CCTAGGTCC
                               _ _        I
GAM520 PTGS1        TGAGAAGGGCAG--GGATCCAGG  8298 _   C C    I
                            GAGAAGGGC GG GGATTCGG
                            ||||||||| || |||||||||
                            CTCTTCCCG TC CCTAGGTC
                            A     _ _    I
GAM520 RET         AGGGCCGGCGG-GTCTGGA      8286      A TC  I
                            AGGGCCGGCGG T GGG
                            |||||||||| | |||
                            TCCCGGCCGCC A CCT
                               C GA  I
GAM520 SMARCA5      GAGAAGGG-CGGAGGGTTGGGG   8291 _     C C A C  I
                            AGAAGGGC GG GG TT GG
                            |||||||| || || || ||
                            TCTTCCCG CC CC AA CC
                            C    _ T C C I
GAM520 SMARCA5      GAGAAGGG-CGGAGGGTTGGGG   8291 TG    C C A C  A
                            AGAAGGGC GG GG TT GGG
                            |||||||| || || || |||
                            TCTTCCCG CC CC AA CCC
                            __     _ T C C  C
GAM520 SOX12       GAAGGGCCGGTGCGCTCAGGGA   8288 A      CGGA   I
                            AGGGCCGG  TTCGGG
                            |||||||   ||||||
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                         TCCCGGCC   GAGTCC
                         _     ACGC      C
GAM520  SOX12            GAAGGGCCGGTGCGCTCAGGGA  8288 TGAGAA       CGGA      A
                         GGGCCGG   TTCGGG
                         |||||||   ||||||
                         CCCGGCC   GAGTCC
                         _____       ACGC     C
GAM520  TPM4             GAGAAGGGCC--AGGATTC     8290          GC    I
                         GAGAAGGGCCG GGATT
                         ||||||||||| |||||
                         CTCTTCCCGGT CCTAA
                                  __     G
GAM520  TPM4             GAGAAGGGCC--AGGATTC     8290 TG       GC    GG
                         AGAAGGGCCG GGATTC
                         |||||||||| ||||||
                         TCTTCCCGGT CCTAAG
                                  __     __    AI
GAM521  COL1A1          GAGGGTTTCAGAGGAG-AGA     8306 G       _   AGCAI
                        AGGGTTTCAG GGA
                        |||||||||| |||
                        TCCCAAAGTC CCT
                               _      T  CTCTI
GAM521  COL1A1          GAGGGTTTCAGAGGAG-AGA     8306 TG       A C  AA
                        AGGGTTTCAGGG AG AGA
                        |||||||||||| || |||
                        TCCCAAAGTCTC TC TCT
                                __        C _  CI
GAM521  CYP1B1          TGAGGGTTTCTGATTAAAGCAGTAA 8313         AGG__     AAAAII
                        TGAGGGTTTC   GAAGCAG
                        ||||||||||   |||||||
                        ACTCCCAAAG   TTTCGTC
                             ACTAA      ATTIII
GAM521  CYP1B1          TGAGGGTTTCTGATTAAAGCAGTAA 8313 A     AGG__     AAI
                        GGGTTTC   GAAGCAG
                        ||||||||   |||||||
                        CCCAAAG   TTTCGTC
                             _    ACTAA     AII
GAM521  FE65L2          GAGGGTTTCAGCCGGAAGGCATCAAGAAAA8304 __   T     CAI
                        GAGGGT TCAGGGAAG
                        |||||| ||||||||||
                        CTTCCG AGTTCTTTT
                             GC    T     III
GAM521  FE65L2          GAGGGTTTCAGCCGGAAGGCATCAAGAAAA8304 TG       __   _ GA AIIIC
                        AGGGTTTCAG GGAAG CA AA
                        |||||||||| ||||| || ||
                        TCCCAAAGTC CCTTC GT TT
                             __       GG   C AG CTTTT
GAM521  FLG            TGATGGTTTCTG-GAAGCAGA     8317 G   AG     AA
                        TGA GGTTTC GGAAGCAGA
                        ||| |||||| ||||||||||
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```
                        ACT CCAAAG  CCTTCGTCT
                         A    A_      II
GAM521  FLG            TGATGGTTTCTG-GAAGCAGA    8317 _  G    AG      I
                        GA GGTTTC  GGAAGCAG
                        II IIIIII  IIIIIIII
                        CT CCAAAG  CCTTCGTC
                         A  A  A_     I
GAM521  GABRB2         TGAGGGTTTCACTGAAG-AGA    8316       GG   C AA
                        TGAGGGTTTCA GAAG AGA
                        IIIIIIIIII IIII III
                        ACTCCCAAAGT CTTC TCT
                              GA    _  II
GAM521  GABRB2         TGAGGGTTTCACTGAAG-AGA    8316 _       GG   C I
                        GAGGGTTTCA GAAG AG
                        IIIIIIIIII IIII II
                        CTCCCAAAGT CTTC TC
                         A   GA    _  I
GAM521  GATA2          GGGTTGAAGGGTTAGCAGAAAA   8308 G  TC   A_      I
                        GTT AGGG AGCAGAAA
                        III IIII IIIIIIII
                        CAA TCCC TCGTCTTT
                         _  CT   AA      I
GAM521  GATA2          GGGTTGAAGGGTTAGCAGAAAA   8308 T__    TCAGGGA
                         GAGGGTT    AGCAGAAAA
                         IIIIIII    IIIIIIIII
                         TTCCCAA    TCGTCTTTT
                        AAC      _____
GAM521  KLK13         TGAGATGTTTCAGGGATGCA     8311     _     A GAAA
                        TGAGG GTTTCAGGGA GCA
                        IIIII IIIIIIIIII III
                        ACTCT CAAAGTCCCT CGT
                          A      A  IIIA
GAM521  KLK13         TGAGATGTTTCAGGGATGCA     8311     _      A II
                        TGAGG GTTTCAGGGA GC
                        IIIII IIIIIIIIII II
                        ACTCT CAAAGTCCCT CG
                          A      A TI
GAM521  LOXL2         GAGGGTTTCATTGGAAG-AGA    8303       G_   C I
                        AGGGTTTCA GGAAG AG
                        IIIIIIIII IIIII II
                        TCCCAAAGT CCTTC TC
                           AA    _  I
GAM521  LOXL2         GAGGGTTTCATTGGAAG-AGA    8303 TG     G_   C AA
                        AGGGTTTCA GGAAG AGA
                        IIIIIIIII IIIII III
                        TCCCAAAGT CCTTC TCT
                          __      AA   _  CI
GAM521  MRPL49        TGAGGGTTTCCATGGAAGC      8312        AG_   AGAAA
                        TGAGGGTTTC  GGAAGC
                        IIIIIIIII  IIIIII
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                        ACTCCCAAAG  CCTTCG
                           GTA     IIIAA
GAM521 MRPL49           TGAGGGTTTCCATGGAAGC     8312        AG_     II
                        TGAGGGTTTC  GGAAG
                        IIIIIIIIII  IIIII
                        ACTCCCAAAG  CCTTC
                           GTA    GI
GAM521 MVK             TGGGAGCTTCAGGGAAGCAG     8315  A          AAA
                        TG GGGTTTCAGGGAAGCAG
                        II IIIIIIIIIIIIIIII
                        AC CTCGAAGTCCCTTCGTC
                          C          III
GAM521 MVK             TGGGAGCTTCAGGGAAGCAG     8315 GA           I
                          GGGTTTCAGGGAAGCA
                          IIIIIIIIIIIIIIII
                          CTCGAAGTCCCTTCGT
                          CC          I
GAM521 PTP4A2           GTTTCAC---AGCAGAAAA     8310      GGGA
                        GTTTCA  AGCAGAAA
                        IIIIII  IIIIIIII
                        CAAAGT  TCGTCTTT
                            G___
GAM521 PTPRF           TGAGGGTTT----GAAGCAGAA   8318      CAGG
                        TGAGGGTTT  GAAGCAGAA
                        IIIIIIIII  IIIIIIIII
                        ACTCCCAAA  CTTCGTCTT

                            ____
GAM521 PTPRF           TGAGGGTTT----GAAGCAGAA   8318 _     CAGG
                        GAGGGTTT  GAAGCAGA
                        IIIIIIII  IIIIIIII
                        CTCCCAAA  CTTCGTCT
                          A       ____
GAM521 RBP5           TGAAGGTTTCAGGAGAATGCAG    8314            _ _ AAAA
                        TGAGGGTTTCAGG GAA GCAG
                        IIIIIIIIIII III IIII
                        ACTTCCAAAGTCC CTT CGTC
                            T  A   IIIA
GAM521 RBP5           TGAAGGTTTCAGGAGAATGCAG    8314 GA         _ _ I
                          GGGTTTCAGG GAA GCA
                          IIIIIIIIII III III
                          TCCAAAGTCC CTT CGT
                            __      T  A  I
GAM521 RFX5          AGGGTGAGAGGGAAGCAGGAA      8302  TTC        AAI
                        GGGT AGGGAAGCAG
                        IIII IIIIIIIIII
                        CCCA TCCCTTCGTC
                          CTC       CTI
GAM521 RFX5          AGGGTGAGAGGGAAGCAGGAA      8302 TGAG TTC        AAAA
                        GGT AGGGAAGCAG
                        III IIIIIIIIII
```

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                                          CCA    TCCCTTCGTC
                                          ____    CTC        CTTA
GAM521 SCA2              GAGGGGT-CAGACGGAAGCAGAA 8305 A    TCAG        I
                                GGGTT  GGAAGCAGA
                                |||||  |||||||||
                                CCCAG  CCTTCGTCT
                                  C    TCTG        I
GAM521 SCA2              GAGGGGT-CAGACGGAAGCAGAA 8305 TG   TT  __        AA
                                AGGG  TCAG  GGAAGCAGAA
                                ||||  ||||  ||||||||||
                                TCCC  AGTC  CCTTCGTCTT
                                __    C_   TG     GI
GAM521 SIGLEC5            GGCTGTCAGGGAAG--GAAA     8309 G   _      C  I
                                GGTT  TCAGGGAAG AGA
                                ||||  ||||||||| |||
                                CCGA  AGTCCCTTC TTT
                                  _    C       C I
GAM521 SIGLEC5            GGCTGTCAGGGAAG--GAAA     8309 TGAGGGTT      CA
                                    TCAGGGAAG  GAA
                                    ||||||||| |||
                                    AGTCCCTTC  CTT
                          AC_____         __
GAM521 THPO             GGGTTTCAGGAGAAAGTAGGAAA  8307 G      _   CAGAAAI
                                TTTCAGG GAAG
                                ||||||| ||||
                                AAAGTCC CTTT
                                  _     T   CATCCTI
GAM521 THPO             GGGTTTCAGGAGAAAGTAGGAAA  8307 TGAGGG     _   CA__   AI
                                TTTCAGG GAAG    GAAA
                                ||||||| ||||    ||||
                                AAAGTCC CTTT    CTTT
                                _____        T   CATC    AG
GAM522 ADAM19            AGGATGGGAGGAGGCCCCA       8322    TGTAT      II
                                AGGGT   GAGGCCCC
                                |||||   ||||||||
                                TCCTA   CTCCGGGG
                                  CCCTC     TI
GAM522 ADAM19            AGGATGGGAGGAGGCCCCA       8322 TGAA  TTGTAT      T
                                GGG   GAGGCCCCA
                                |||   |||||||||
                                CCC   CTCCGGGGT
                                TA__  TC____       C
GAM522 CD209L           GAAGAGGTTGTATGGAGCCTCCAT 8323 AA      AG  _  I
                                GGGTTGTATG GCC CCA
                                |||||||||| ||| |||
                                TCCAACATAC CGG GGT
                                  C_     CT A  I
GAM522 CD209L           GAAGAGGTTGTATGGAGCCTCCAT 8323 TG  _    AG  _  CI
                                AAG GGTTGTATG GCC CCAT
                                ||| ||||||||| ||| ||||
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                           TTC CCAACATAC  CGG GGTA
                           __    T       CT  A   CI
GAM522  CDKN2D            GGGTCTCGTCTGAGGCCCCA   8326    GTA__        III
                           GGGTT    TGAGGCCCC
                           |||||    |||||||||
                           CCCAG    ACTCCGGGG
                            AGCAG         TII
GAM522  CDKN2D            GGGTCTCGTCTGAGGCCCCA   8326 TGAAGGG  A      T
                            TTGT TGAGGCCCCA
                            |||| |||||||||||
                            AGCA ACTCCGGGGT
                           G_____    G       C
GAM522  CNP              GGGTTCTGGCTGTGGCCCCATC   8327 ____       ATGA     I
                           GGTTGT  GGCCCCAT
                           ||||||  ||||||||
                           CCGACA  CCGGGGTA
                           AAGA       ____     I
GAM522  CNP              GGGTTCTGGCTGTGGCCCCATC   8327 TGAAG    ATGA
                           GGTTGT  GGCCCCATC
                           ||||||  |||||||||
                           CCGACA  CCGGGGTAG
                           AGA__      ____
GAM522  GABRA2           AAGGGTTGTA-CAGGATCCCCAT   8321 A       G  __   I
                           GGGTTGTAT AGG  CCCCA
                           ||||||||| |||  |||||
                           CCCAACATG TCC  GGGGT
                           _       _ TA   I
GAM522  GABRA2           AAGGGTTGTA-CAGGATCCCCAT   8321 TGAA      G  __   C
                           GGGTTGTAT AGG  CCCCAT
                           ||||||||| |||  ||||||
                           CCCAACATG TCC  GGGGTA
                           ____       _ TA   A
GAM522  GRIA1            TGAAGGGTTTGGGATGGGGC     8331      GT__ A CCCAT
                           TGAAGGGTT   ATG GGC
                           |||||||||   ||| |||
                           ACTTCCCAA   TAC CCG
                            ACCC  C  IIICT
GAM522  GRIA1            TGAAGGGTTTGGGATGGGGC     8331      GT__ A III
                           TGAAGGGTT   ATG GG
                           |||||||||   ||| ||
                           ACTTCCCAA   TAC CC
                            ACCC  C  GII
GAM522  MAP1B            GAAGGGTTG-ATCAGGACC      8325      T G _I
                           GAAGGGTTG AT AGG CC
                           ||||||||| || ||| ||
                           CTTCCCAAC TA TCC GG
                            _  G  T  I
GAM522  MAP1B            GAAGGGTTG-ATCAGGACC      8325 TG     T G _ CCA
                           AAGGGTTG AT AGG CC
                           |||||||| || ||| ||
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                        TTCCCAAC TA TCC GG
                        __        _ G  T  TII
GAM522 NR1D1       GAAGGGTTGGACGTTGAGGC      8324        TA___     III
                        GAAGGGTTG   TGAGG
                        IIIIIIIII   IIIII
                        CTTCCCAAC   ACTCC
                          CTGCA    GII
GAM522 NR1D1       GAAGGGTTGGACGTTGAGGC      8324 TG     TA___     CCCAT
                        AAGGGTTG   TGAGGC
                        IIIIIIII   IIIIII
                        TTCCCAAC   ACTCCG
                        __       CTGCA   TIIIC
GAM522 OTP       TGCAGGGTTGTA-GATGTCC       8332  A      T GG_ CCAT
                        TG AGGGTTGTA GA   CC
                        II IIIIIIIII II   II
                        AC TCCCAACAT CT   GG
                         G       _ ACA  IIIC
GAM522 OTP       TGCAGGGTTGTA-GATGTCC       8332 _A      T GGCCI
                         G AGGGTTGTA GA
                         I IIIIIIIII II
                         C TCCCAACAT CT
                        A G       _ ACAGI
GAM522 PBX3      GGTTTGTATGAGTTCGCAT        8328  G      GCCCCAII
                        GG TTGTATGAG
                        II IIIIIIIII
                        CC AACATACTC
                          A       AAGCGTAI
GAM522 PBX3      GGTTTGTATGAGTTCGCAT        8328 TGAA_  _     CCCCAT
                        GGGTT GTATGAGG
                        IIIII IIIIIIII
                        CTCAA CGTACTCC
                        ACATA   G    IIICTA
GAM522 RAB1A       TGAAGGGTTGTCGCCCGCCCCAT 8334        ATGAG   CI
                        TGAAGGGTTGT   GCCCCAT
                        IIIIIIIIIII   IIIIIII
                        ACTTCCCAACA   CGGGGTA
                          GCGGG     II
GAM522 RAB1A       TGAAGGGTTGTCGCCCGCCCCAT 8334        ATGAG   I
                        GAAGGGTTGT   GCCCCA
                        IIIIIIIIII   IIIIII
                        CTTCCCAACA   CGGGGT
                          GCGGG     I
GAM522 SDPR      TGAGGGTGTAGGATGAGGCCC      8330  A  T ___    CATC
                        TGA GGGT GTA   TGAGGCCC
                        III IIII III   IIIIIIII
                        ACT CCCA CAT   ACTCCGGG
                        _  _ CCT    IIIC
GAM522 SDPR      TGAGGGTGTAGGATGAGGCCC      8330 GA  T ___    I
                        AGGGT GTA   TGAGGCC
                        IIIII III   IIIIIII
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                              TCCCA CAT  ACTCCGG
                              __   _   CCT     I
GAM522  TAL1         GGCTGAATTAGGGCCCCATC    8329    T GA_      II
                              GGTTG AT  GGCCCCAT
                              ||||| || |||||||||
                              CCGAC TA  CCGGGGTA
                               T ATC      GI
GAM522  TAL1         GGCTGAATTAGGGCCCCATC    8329 TGAAGGGTTGTATGA
                                  GGCCCCAT
                                  ||||||||
                                  CCGGGGTA
                    TTAATC_____
GAM522  XRCC3        TGAGGGG--GTCTGAGGCCCCA   8333  A_   GTA      T
                          TGA GGGTT  TGAGGCCCCA
                          ||| ||||| ||||||||||
                          ACT CCCAG  ACTCCGGGGT
                           CC     ___      I
GAM522  XRCC3        TGAGGGG--GTCTGAGGCCCCA   8333 _ A_   GTA      I
                           GA GGGTT  TGAGGCCCC
                           || ||||| |||||||||
                           CT CCCAG  ACTCCGGGG
                          A CC     ___      I
GAM523  AR          TGGCTGGCA-CAGAGTAGT      8343 A  A      CTC
                          TG CTGGTA CAGAGTAGT
                          || |||||| |||||||||
                          AC GACCGT GTCTCATCA
                           C    _      III
GAM523  CYP1A2       CTGGCAACAGAGTAAGACTC     8338 TGACTG       _T G
                          GTAACAGAGTA G CTC
                          ||||||||||| | |||
                          CGTTGTCTCAT C GAG
                          _____      T T  A
GAM523  EGFL4        TGCCTG---ACAGAGTAGGTACTCGA 8341 TGA  GTA       T__  I
                          CTG  ACAGAGTAG  CTCGA
                          ||| ||||||||| |||||
                          GAC  TGTCTCATC  GAGCT
                          ACG   ___        CAT  I
GAM523  FGA          TGACGTGTAACAGAG-AGT      8342  TG    T CTC
                          TGAC  GTAACAGAG AGT
                          |||| ||||||||| |||
                          ACTG  CATTGTCTC TCA
                           CA      _   III
GAM523  GALNT7       CTGGATAACAGAGTA-TCT      8337 TGACT       G  C
                          GGTAACAGAGTA TCT
                          |||||||||||| |||
                          CTATTGTCTCAT AGA
                          _____        A
GAM523  NDUFB3       TGACTGAGGTAACAGA-TACTGTAGA 8339   __      ____     TCTCGAII
                          TGACT GGTAACAGA  GTAG
                          ||||| |||||||||  ||||
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                    ACTGA CCATTGTCT  CATC
                    CT      ATGA  TIIIAGCT
GAM523 RFP          TGACTGGTAAGGGATCTAGT    8340      CA G_  CTCG
                    TGACTGGTAA GA TAGT
                    |||||||||| || ||||
                    ACTGACCATT CT ATCA
                         CC AG   IIIA
GAM524 ASNS         TCAGC-AAGT-CACTTGATG    8350 TGTCACCTAAATG
                              CACTTGATG
                              |||||||||
                              GTGAACTAC
                    TCGTTCA_____
GAM524 GOLGA5         TGTCACCTAACATACA---GATGGT 8352        _  CTT
                     TGTCACCTAA ATGCA  GATGGT
                     |||||||||| ||||| ||||||
                     ACAGTGGATT TATGT  CTACCA
                          G   ___
GAM524 MRE11A       TGTCAGA-AAATGCACTCGAT    8353    CCT       GG
                    TGTCA AAATGCACTTGAT
                    ||||| |||||||||||||
                    ACAGT TTTACGTGAGCTA
                     CT_           II
GAM524 MTCP1        GTCACCTAAGGGAACCTGA    8348 TG    ATGC    TGG
                     TCACCTAA  ACTTGA
                     ||||||||  ||||||
                     AGTGGATT  TGGACT
                      __    CCCT   TII
GAM524 MYB        TCAACTAAATGCACTTGGTG    8349 TGTCAC      A G
                    CTAAATGCACTTG TG
                    ||||||||||||| ||
                    GATTTACGTGAAC AC
                    TT____         C G
GAM524 NARS         ACCTTAATATCACTTGATG    8346 TGTCACCTA  _    G
                       AATG CACTTGATG
                       |||| |||||||||
                       TTAT GTGAACTAC
                     A_____  A    A
GAM524 RGS9         TGTCACCCAAATGCACTT--TGGT 8354          GA
                    TGTCACCTAAATGCACTT TGGT
                    |||||||||||||||||| ||||
                    ACAGTGGGTTTACGTGAA ACCA
                           __
GAM524 TCEB1L        GTCACCTAAAGTTAACTTG    8347 TG   TGC_ ATGG
                     TCACCTAAA ACTTG
                     ||||||||| |||||
                     AGTGGATTT TGAAC
                      __    CAAT  CIII
GAM524 TMOD         TGTCACACATTTTAAATGCACTTGA 8351    C_____        TGGTII
                    TGTCAC  TAAATGCACTTGA
                    ||||||  ||||||||||||
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                        ACAGTG     ATTTACGTGAACT
                        TGTAAA         IIITGG
GAM525  ABCB9           AAGGGGAGAGGCCTAGTCTC      8357 TGGAA      A     A AT
                        GGGGAG CTTAGT TC
                        IIIIII IIIIII II
                        CCTCTC GGATCA AG
                        C____       C    G AC
GAM525  EDAR            AAGGGGAGACTCACTCATCAT     8358 TGGAAG        G_     A
                        GGGAGACTTA TATCAT
                        IIIIIIIIII IIIIII
                        CCCTCTGAGT GTAGTA
                        _____            GA    G
GAM525  GLTSCR1         TGGCAGGGGAGACGTTTTA-CAT   8365  A      TTAGTATCATA
                        TGG AGGGGAGAC
                        III IIIIIIIII
                        ACC TCCCCTCTG
                          G      CAAAATGTAII
GAM525  ITGA2           TGGAAGGGGCAGCCGTGGTAT     8362     _ A TA_   CATA
                        TGGAAGGGG AG CT  GTAT
                        IIIIIIIII II II   IIII
                        ACCTTCCCC TC GG  CATA
                          G _ CAC   IIIA
GAM525  JUNB            TGGAAGGGGGGGCTT-GTA       8364      AGA  A TCA
                        TGGAAGGGG  CTT GTA
                        IIIIIIIII  III III
                        ACCTTCCCC  GAA CAT
                          CCC _  III
GAM525  KIF5A           GGGGAGGGAGTTAGTATCA       8361 TGGAAG    AC     T
                        GGGAG TTAGTATCA
                        IIIII IIIIIIIII
                        CCCTC AATCATAGT
                        _____   __       C
GAM525  NR3C1           TGCAAGGGGAGATTGAGTA       8363 G      CTT   TCAT
                        TG AAGGGGAGA  AGTA
                        II IIIIIIIII  IIII
                        AC TTCCCCTCT  TCAT
                          G    AAC   IIIA
GAM525  SCNN1A          GGAAGGGGAATTGCCTAAGTAACA 8359 TG        A__   _ T TAI
                        GAAGGGGAG  CTTA GTA CA
                        IIIIIIIII  IIII III II
                        CTTCCCCTT  GGAT CAT GT
                          __       AAC   T  T TII
GAM525  SON             GGAAGGGGAG--TTA-CATCATA   8360 TG       AC G
                        GAAGGGGAG TTA TATCAT
                        IIIIIIIII III IIIIII
                        CTTCCCCTC AAT GTAGTA
                          __     __
GAM526  BAALC           GAAAGCTATGCAAAATTGCAATGTC 6909 AAAG  TG C      I
                        GTG AA TTGCAATGT
                        III II IIIIIIIII
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                        TAC  TT AACGTTACA
                        TCGA  GT  T         I
GAM526  BAALC           GAAAGCTATGCAAAATTGCAATGTC 6909 TGAAAG  TG  C          II
                        GTG  AA TTGCAATGTC
                        III  II IIIIIIIIII
                        TAC  TT AACGTTACAG
                        TTTCGA  GT  T          AI
GAM526  CALCRL          GAAAGA-GTGAAAGCTTTGCAATGT 6910 AAA  T    C___        I
                        GG GTGAA   TTGCAATG
                        II IIIII   IIIIIIII
                        TC CACTT   AACGTTAC
                        ___  T  TCGA        I
GAM526  CALCRL          GAAAGA-GTGAAAGCTTTGCAATGT 6910 TGA  T    C___        CI
                        AAGG GTGAA   TTGCAATGT
                        IIII IIIII   IIIIIIIII
                        TTTC CACTT   AACGTTACA
                        ___  T  TCGA       CI
GAM526  DCX             TGAAAGGTGTCAGACCTGAAA  6912        GA_   CAATGTC
                        TGAAAGGTGT  ACTTG
                        IIIIIIIIII  IIIII
                        ACTTTCCACA  TGGAC
                        GTC    TTTIIIC
GAM526  DCX             TGAAAGGTGTCAGACCTGAAA    6912 G     GA_   CAI
                        AAAGGTGT  ACTTG
                        IIIIIIII  IIIII
                        TTTCCACA  TGGAC
                        _     GTC   TTI
GAM526  DRD2            TGCAGGGTGTGAACTGTCCATCTC 6915 AAA       TGCA G  I
                        TG  GGTGTGAACT   AT TC
                        II  IIIIIIIIII   II II
                        AC  CCACACTTGA   TA AG
                        GTC       CAGG G  I
GAM526  DRD2            TGCAGGGTGTGAACTGTCCATCTC 6915 AAA       TGCAAI
                        GGTGTGAACT
                        IIIIIIIIII
                        CCACACTTGA
                        C__       CAGGTA
GAM526  GRB10           GGTGT-AACT-GCAATGTC      8379       AC     I
                        GGTGTGA TTGCAATGT
                        IIIIIII IIIIIIIII
                        CCACATT GACGTTACA
                        __        G
GAM526  ITK             TGAAAGGTGGTGCACCTTG      6911        _ A   III
                        TGAAAGGTG TG ACTT
                        IIIIIIIII II IIII
                        ACTTTCCAC AC TGGA
                        C G  ACI
GAM526  ITK             TGAAAGGTGGTGCACCTTG      6911        _ AA_  CAATGT
                        TGAAAGGTG TG  CTTG
                        IIIIIIIII II  IIII
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                         ACTTTCCAC AC  GAAC
                            C GTG    IIICTG
GAM526 MTF1             TGAAAGGTGAGGA-TTTCAA      6914      T_ ACTTGCAATGT
                         TGAAAGGTG GA
                         |||||||| ||
                         ACTTTCCAC CT
                            TC AAAGTTIIICT
GAM526 MTF1             TGAAAGGTGAGGA-TTTCAA      6914_      T_ ACTTGCAI
                          GAAAGGTG GA
                          ||||||| ||
                          CTTTCCAC CT
                           A     TC AAAGTIII
GAM526 NDRG3          AAGGA-TGGACTTGCAATG      6908    T A      I
                       AAGG GTG ACTTGCAAT
                       |||| ||| |||||||||
                       TTCC TAC TGAACGTTA
                        _  C      C
GAM526 NDRG3          AAGGA-TGGACTTGCAATG      6908 TGAAA  T A
                        GGTG GA CTTGCAATG
                        |||| || |||||||||
                        CTAC CT GAACGTTAC

                       _____  _ _
GAM526 OCRL          TGAAAGG-GAGA-CTAATGCAATGTC 6913      TGT ACT_    I
                      TGAAAGG  GA   TGCAATGTC
                      ||||||  ||   |||||||||
                      ACTTCC  CT   ACGTTACAG
                        CT_ GATT       I
GAM526 OCRL          TGAAAGG-GAGA-CTAATGCAATGTC 6913      TGT ACT_    I
                       GAAAGG  GA   TGCAATGT
                       ||||||  ||   ||||||||
                       CTTTCC  CT   ACGTTACA
                        CT_ GATT       I
GAM526 RORB        AAAAGTCTTGGACCTTGCAATGT   6905 AAGG_ T A      I
                      TG GA CTTGCAATG
                      || || |||||||||
                      AC CT GAACGTTAC
                    TCAGA _ G       I
GAM526 RORB        AAAAGTCTTGGACCTTGCAATGT   6905 TGAAAGG T A     CI
                      TG GA CTTGCAATGT
                      || || ||||||||||
                      AC CT GAACGTTACA
                    TTCAGA_ _ G      AT
GAM526 SRD5A2      AAACATGAGAGTTTGCAATGTC   6906 G  T AC      I
                     AA GTG GA TTGCAATGT
                     || ||| || |||||||||
                     TT TAC CT AACGTTACA
                      G  T CA       I
GAM526 SRD5A2      AAACATGAGAGTTTGCAATGTC   6906 TGAAAG  T AC
                     GTG GA TTGCAATGTC
                     ||| || |||||||||||
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                              TAC CT  AACGTTACAG
                         TG____   T  CA
GAM526 ZNF215       AAGGTGTGACGTGAC-TGCAA    6907        AC___    III
                         AAGGTGTGA    TTGCA
                         ||||||||    |||||
                         TTCCACACT    GACGT
                           GCACT    TII
GAM526 ZNF215       AAGGTGTGACGTGAC-TGCAA    6907 TGAAA GT   AC    T
                          G  GTGA  TTGCAA GT
                          |  ||||  ||||||| ||
                          C  CACT  GACGTT CA
                         CACA_ TG    __    _
GAM527 MUC3B         TACTG-ATATCAGTGGGTA      8393 AT  G  G     CT
                          ACTG ATG CAGTGGGTA
                          |||| ||| |||||||||
                          TGAC TAT GTCACCCAT
                          __  _  A    AI
GAM527 MX1         CTGGATGGC-G-GCGTTCTTC     8392 ATACTG    A  GGTA
                          GATGGC GTG    CTT
                          |||||| |||    |||
                          CTACCG CGC    GAA
                          _____     C  AA__
GAM528 BCRP2        AGAGCCTTGCGCGGCACAC      8398  _   T     II
                          AGA CCTT TGCGGCACA
                          ||| |||| |||||||||
                          TCT GGAA GCGCCGTGT
                           C   C    GI
GAM528 BCRP2        AGAGCCTTGCGCGGCACAC      8398 TGAAGA  T     CT
                          CCTT TGCGGCACAC
                          |||| |||||||||||
                          GGAA GCGCCGTGTG
                          C_____  C      AT
GAM528 COX7C       AAGACCTTTTTTTTCACGACCT    8397 A      GCGG  _  I
                          GACCTTTT   CAC ACC
                          ||||||||   ||| |||
                          CTGGAAAA   GTG TGG
                          _    AAAA  C  I
GAM528 COX7C       AAGACCTTTTTTTTCACGACCT    8397 TGAA     GCGG  _  G
                          GACCTTTT   CAC ACCT
                          ||||||||   ||| ||||
                          CTGGAAAA   GTG TGGA
                           ____   AAAA  C  A
GAM528 HUNK        AAGAC-TTTTGTAGGCACACCT    8396   C  C_    I
                          AGAC TTTTG GGCACACC
                          |||| ||||| |||||||||
                          TCTG AAAAC CCGTGTGG
                          _   AT    I
GAM528 HUNK        AAGAC-TTTTGTAGGCACACCT    8396 TGAA  C   C_
                          GAC TTTTG GGCACACCTG
                          ||| ||||| |||||||||||
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                              CTG AAAAC  CCGTGTGGAT
                              ____  _       AT
GAM528  IL16           CCTTCTGTCGGCACACCTG      8401      _       II
                              CCTTTTG CGGCACACCT
                              |||||| ||||||||||
                              GGAAGAC GCCGTGTGGA
                                    A       CI
GAM528  SIRPB2           TGAAGACCTTGCTCTGGGGCA      8402        ___  C  CACCTG
                              TGAAGACCT  TTTG GGCA
                              |||||||||  |||| ||||
                              ACTTCTGGA  AGAC CCGT
                               ACG   C   IIIGTC
GAM528  SIRPB2           TGAAGACCTTGCTCTGGGGCA      8402        ___  C  III
                              TGAAGACCT  TTTG GGC
                              |||||||||  |||| |||
                              ACTTCTGGA  AGAC CCG
                               ACG   C   TII
GAM528  TCF2           AGCCCTGTCACGGCACACC        8400 AGA  T TG      II
                              CCT T CGGCACAC
                              ||| | ||||||||
                              GGA A GCCGTGTG
                              TCG  C GT      GI
GAM528  TCF2           AGCCCTGTCACGGCACACC        8400 TGAAGA  T TG       T
                              CCT T CGGCACACC
                              ||| | |||||||||
                              GGA A GCCGTGTGG
                              _____   C GT        C
GAM528  WT1           AGACCAACTCTTCCAGGCACACCTG 8399 TGAA  _  TT C       II
                              GAC CTT  G GGCACACCTG
                              ||| ||| | ||||||||||
                              TTG GAA  T CCGTGTGGAC
                              GG__  A GG _      CA
GAM528  WT1           AGACCAACTCTTCCAGGCACACCTG 8399  _  TT C       I
                              GAC CTT  G GGCACACCT
                              ||| ||| | |||||||||
                              TTG GAA  T CCGTGTGGA
                                A  GG _      I
GAM529  BACE           TCT-TGGAGATGAGGTCTAA      8418  G    _       TATA
                              TCT TGGAGA GAGGTCTAA
                              ||| |||||| ||||||||||
                              AGA ACCTCT CTCCAGATT
                               _    A      IIIA
GAM529  BACE           TCT-TGGAGATGAGGTCTAA      8418  G   _      II
                              TCT TGGAGA GAGGTCTA
                              ||| |||||| |||||||||
                              AGA ACCTCT CTCCAGAT
                               _    A    TI
GAM529  BACH1           TGTAATGCTATGCAATATACAGAA 8425    G AC  __       II
                              TGTAA GC TGT TATACAGAA
                              ||||| || ||| |||||||||
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                        ACATT CG  ACG  ATATGTCTT
                         A  AT   TT         II
GAM529 BAZ2A          TGTAAGGCAGTGATGGACCCAGAA  8427      C  TTATA__     II
                        TGTAAGGCA TG     CAGAA
                        IIIIIIII II     IIIII
                        ACATTCCGT AC     GTCTT
                          C  TACCTGG    II
GAM529 BPAG1          AAGGTCACTAT-ATACAGAA     8405 TGTAAGG    T
                          CACTGT ATACAGAA
                          IIIIII IIIIIIII
                          GTGATA TATGTCTT
                      CA_____     _
GAM529 DHCR24          TGTAAGGCACTGAAATTAACTACAG 8424        TTA_____    AAIII
                        TGTAAGGCACTG     TACAG
                        IIIIIIIIIII     IIIII
                        ACATTCCGTGAC     ATGTC
                          TTTAATTG   IIIAA
GAM529 DIRC1          TGTGGAGAGAAATTCAATA     8431        C   II
                        TGTGGAGAGAGGT TAAT
                        IIIIIIIIIIII IIII
                        ACACCTCTCTTTA GTTA
                          A   TI
GAM529 DIRC1          TGTGGAGAGAAATTCAATA     8431 TCTG       C   TA
                          TGGAGAGAGGT TAATA
                          IIIIIIIIIII IIIII
                          ACCTCTCTTTA GTTAT
                     ____          A   CA
GAM529 ENAM          AAGACAGTTTTATACAGAA     8407 TGTAAG  CTG
                          GCA   TTATACAGAA
                          III   IIIIIIIIII
                          TGT   AATATGTCTT
                     _____    CAA
GAM529 HSPA4         AGGCACTCTGTTATACAGAA     8409 TGTAAG  A
                          GC CTGTTATACAGAA
                          II IIIIIIIIIII
                          TG GACAATATGTCTT
                     _____    A
GAM529 IRF1          AAGGCACTG-TATAAATAA     8408 TGTAAG    T  CAGA
                          GCACTGT ATA
                          IIIIIII III
                          CGTGACA TAT
                     _____       _ TTAT
GAM529 KCNK2          TAAGGCACTG----ACAGAA     8417 TGTA      TTAT
                          AGGCACTG   ACAG
                          IIIIIIII   IIII
                          TCCGTGAC   TGTC
                     ____     ____
GAM529 LOXL2         TGGAAGAGAGGTCTAGATAT     8422  _       ATAIII
                        TGGA GAGAGGTCTA
                        IIII IIIIIIIIII
```

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                          ACCT CTCTCCAGAT
                            T      CTATAI
GAM529 LOXL2             TGGAAGAGAGGTCTAGATAT     8422 TCTGTGG      _    A
                            AGAGAGGTCTA ATAT
                            ||||||||||| ||||
                            TCTCTCCAGAT TATA
                            _____       C   A
GAM529 LZTFL1           TGGAGAGAGTGTC-AATTTA    8423      _  T  ATII
                          TGGAGAGAG GTC AAT
                          |||||||||| ||| |||
                          ACCTCTCTC CAG TTA
                             A  _   AATI
GAM529 MST1R             TCTGTGGAGTGAGGGACCTAAT  8420      A  __    ATAA
                          TCTGTGGAG GAGG  TCTAAT
                          ||||||||| |||| ||||||
                          AGACACCTC CTCC  GGATTA
                             A   CT     IIIA
GAM529 MST1R             TCTGTGGAGTGAGGGACCTAAT  8420 CT    A  __    I
                            GTGGAG GAGG  TCTAA
                            |||||| |||| |||||
                            CACCTC CTCC  GGATT
                            __     A  CT   I
GAM529 MX1             TCTTTGCAAAGTAAGCTCTAATATA 8419 C TG  A  G      I
                            TG  GAG GAG TCTAATAT
                            ||  ||| ||| ||||||||
                            AC  TTC TTC AGATTATA
                            A  GT  A  G      I
GAM529 MX1             TCTTTGCAAAGTAAGCTCTAATATA 8419 TC__  TG  A  G      AII
                            TG  GAG GAG TCTAATATA
                            ||  ||| ||| |||||||||
                            AC  TTC TTC AGATTATAT
                          AGAA  GT  A  G       III
GAM529 OAS3             TGTGGAGAGTCAGGCTGTCTAA   8430         __    CTAIIIT
                            TGTGGAGAG AGGT
                            ||||||||| ||||
                            ACACCTCTC TCCG
                             AG   ACAGATT
GAM529 OAS3             TGTGGAGAGTCAGGCTGTCTAA   8430 TCTG      __  ___   TATAA
                            TGGAGAG AGGT  CTAA
                            ||||||| |||| ||||
                            ACCTCTC TCCG  GATT
                            ____      AG  ACA  CTIII
GAM529 PITX2           TGTACGAAA-TGTTATACA       8428   A CAC     GA
                            TGTA GG  TGTTATACA
                            |||| ||  |||||||||
                            ACAT CT  ACAATATGT
                             G TT_      II
GAM529 PLAG1          GTAGAGCCACTGTTATTAGACAAAA 8414 TGTA  G        ___   III
                            AG CACTGTTAT  ACAGAA
                            || ||||||||| ||||||
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                          TC GTGACAATA  TGTTTT
                         ATC_  G       ATC   TII
GAM529  PMCHL1        GTAAGTCATAATTATACAGAA     8415 TG   G CT        I
                        TAAG CA  GTTATACAGAA
                        IIII II  IIIIIIIIIII
                        ATTC GT  TAATATGTCTT
                        __  A AT        A
GAM529  PNUTL1        CTGTGGAGAAGGGGTGTAA      8412       A_  CTAII
                        CTGTGGAGAG  GGT
                        IIIIIIIIII III
                        GACACCTCTT  CCA
                          CC  CATTI
GAM529  PNUTL1        CTGTGGAGAAGGGGTGTAA      8412 TC      A_  C TATA
                        TGTGGAGAG  GGT TAA
                        IIIIIIIII III III
                        ACACCTCTT  CCA ATT
                         __        CC  C CIII
GAM529  PPP1R11       TCTGTCGCT-GAGGTCTAAGAGAA 8421     GGAGA      TATAAI
                        TCTGT   GAGGTCTAA
                        IIIII   IIIIIIIIII
                        AGACA   CTCCAGATT
                         GCGA_       CTCTTI
GAM529  PPP1R11       TCTGTCGCT-GAGGTCTAAGAGAA 8421_    GGAGA       TATAI
                        CTGT   GAGGTCTAA
                        IIII   IIIIIIIII
                        GACA   CTCCAGATT
                        A  GCGA_       CTCTI
GAM529  PRKY          TGTAATGCTTTTTATATACAGAA  8426     G ACTGT_     II
                        TGTAA GC    TATACAGAA
                        IIIII II    IIIIIIIII
                        ACATT CG    ATATGTCTT
                         A  AAAAT         II
GAM529  PTGFR          AAAGAAATCTTATACAGAA      8406 TGTAAGGCACTG
                           TTATACAGAA
                           IIIIIIIIII
                           AATATGTCTT
                         CTTTAG_____
GAM529  RABIF          CTGTAGCAGTGAGGAGCTAATATAA 8411 T_ TG A  AG T      I
                         G  G GAG  G CTAATATA
                         I  I III  I IIIIIIIII
                         C  C CTC  C GATTATAT
                        AT GT A  CT _      I
GAM529  RABIF          CTGTAGCAGTGAGGAGCTAATATAA 8411 TC    _ A  T_      II
                         TGTGG AG GAGG  CTAATATAA
                         IIIII II IIII  IIIIIIIII
                         ACATC TC CTCC  GATTATATT
                         __     G A  TC       TI
GAM529  TCFL4          GTAGAGAGAGGT-TGCTATAA     8416         __  ATATI
                        TGGAGAGAGGT CTA
                        IIIIIIIIIII III
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                              ATCTCTCTCCA GAT
                                 AC  ATIII
GAM529 TCFL4        GTAGAGAGAGGT-TGCTATAA   8416 TCTGTG      CTAA
                         GAGAGAGGT   TATA
                         ||||||||| ||||
                         CTCTCTCCA   ATAT
                         _____      ACG_
GAM529 TGFA         CTGATTGATAGAGGTCTAA    8410  TG_ G      II
                         CTG  GA AGAGGTCTA
                         ||| || |||||||||
                         GAC  CT TCTCCAGAT
                          TAA  A     TI
GAM529 TGFA         CTGATTGATAGAGGTCTAA    8410 TCTGTG G       TATA
                         GA AGAGGTCTAA
                         || |||||||||
                         CT TCTCCAGATT
                         ACTAA_ A       TIII
GAM529 TGFB1        TGTAAGGCACT-TCA-ACAG    8429        GTTAT  A
                         TGTAAGGCACT   ACAG
                         |||||||||| ||||
                         ACATTCCGTGA   TGTC
                           AGT__   I
GAM529 ZNF256       CTGTGGAGAAGTGCTCTGCTGATAA 8413    AG _  AATATAI
                         TGGAGAG  G TCT
                         ||||||| | |||
                         ACCTCTT  C AGA
                          CA G  CGACTII
GAM529 ZNF256       CTGTGGAGAAGTGCTCTGCTGATAA 8413 TC       AG _  AATATAAII
                         TGTGGAGAG  G TCT
                         |||||||||| | |||
                          ACACCTCTT  C AGA
                         __      CA G  CGACTATTC
GAM530 ANK1         TCACTGTTTACTCT-CTCT     8438       TCGTA     AGA
                         TCACTGTT   TGCTCT
                         ||||||||  ||||||
                         AGTGACAA   ATGAGA
                         _____      GAG
GAM530 HMGN3        CACTGATTA-T-TGCTCTAGA   8434 TC   TTTCGTA
                         ACTG   TGCTCTAGA
                         ||||   |||||||||
                         TGAC    ACGAGATCT
                         __  TAATA__
GAM530 MTMR8        CTGTCTCCTTGACTGCTCTAGA   8435 TCA G  CGTA       I
                         CT TTT  TGCTCTAGAG
                         || |||  |||||||||
                         GA GAA   ACGAGATCTT
                         A__ G  CTG_        A
GAM530 NPEPPS       TCACAGTTTCGTTATGCTCTA   8437 T    _   GAG
                         TCAC GTTTCGT ATGCTCTA
                         |||| ||||||| |||||||||
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                          AGTG CAAAGCA TACGAGAT
                           T      A        III
GAM530  SFRP4         TCACTGTTTCTGGTGCTGCTTAAGAG 8436        GTA___  CT  III
                          TCACTGTTTC    TGCT AGAG
                          |||||||||    |||| ||||
                          AGTGACAAAG    ACGA TCTC
                            ACCACG  AT   III
GAM530  ZNF36         TCACTGTTTAGAAAG-TCTA   8439      CGTATGC  GA
                          TCACTGTTT     TCTA
                          |||||||||     ||||
                          AGTGACAAA     AGAT
                            TCTTTC_  II
GAM531  COX15         ATAGGAAGCATGGCGCTGGCATC  8443 CATTGT  _        AI
                          AGGC TGGCGCTGGCATC
                          |||| |||||||||||||
                          TTCG ACCGCGACCGTAG
                          ATCC__   T       AI
GAM531  EML1          GTAGGCTGGTGATGTCATCA    8447 CATTGTAG   CGC  G
                          GCTGG  TG CATC
                          |||||  || ||||
                          CGACC  AC GTAG
                          _____   ACT  A
GAM531  EP300         AGGCTGGCGCCGCCGCCTCA    8442 CATTGTAG   G  G_
                          GCTG CGCT GCATC
                          |||| |||| |||||
                          CGGC GCGG TGTAG
                          CG_____   G   AG
GAM531  ETF1          TTGTAGGCTGCTGCGCTGACACCA  8448 CATT      __        I
                          GTAGGCTG GCGCTGGCATCA
                          |||||||| ||||||||||||
                          CATCCGAC CGCGACTGTGGT
                          ____     GA         A
GAM531  PCDHB9        ATTGTAGGCTGGGTGCGGTGGC-TCA 8445 CA        ___  C  A  II
                          TTGTAGGCTG  GCG TGGC TCA
                          ||||||||||  ||| |||| |||
                          AACATCCGAC  CGC ACCG AGT
                          __         CCA  C  _  AI
GAM531  PPP1R12B      ATGGTAGGCTGGGCGTGGGC   8444 CATT      _ CT  ATC
                          GTAGGCTGG CG GGC
                          ||||||||| || |||
                          CATCCGACC GC CCG
                          AC__      C AC  GII
GAM531  TCL1A         CATTGTAGGCTGGC-CAGGC-TCA   8446        GCT  A
                          CATTGTAGGCTGGC  GGC TCA
                          ||||||||||||||  ||| |||
                          GTAACATCCGACCG  CCG AGT
                            GT_  _
GAM532  AP1M1         AGGCTGGCGTCTCTCACCA    8450      _ GG  II
                          AGGCTGGCG CT  CATC
                          ||||||||| ||  ||||
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                        TCCGACCGC GA  GTGG
                           A  GA    TI
GAM532 COX15           ATAGGAAGCATGGCGCTGGCATC  8443 CATTGT  _          AI
                          AGGC TGGCGCTGGCATC
                          |||| ||||||||||||
                          TTCG ACCGCGACCGTAG
                       ATCC__   T        AI
GAM532 COX15           ATAGGAAGCATGGCGCTGGCATC  8443 TTGT   _        I
                          AGGC TGGCGCTGGCAT
                          |||| |||||||||||
                          TTCG ACCGCGACCGTA
                       TCC_   T      I
GAM532 EML1          GTAGGCTGGTGATGTCATCA       8447       CGC  G  I
                         TAGGCTGG  TG CATC
                         |||||||| || ||||
                         ATCCGACC  AC GTAG
                          ACT  A   I
GAM532 EML1          GTAGGCTGGTGATGTCATCA       8447 CATTGTAG    CGC  G
                            GCTGG  TG CATC
                            ||||| || ||||
                            CGACC  AC GTAG
                          _____    ACT  A
GAM532 EP300         AGGCTGGCGCCGCCGCCTCA       8442         __  ATCIII
                         AGGCTGGCGCTG GC
                         ||||||||||| ||
                         TCCGACCGCGGC  CG
                            GG  GAGTII
GAM532 EP300         AGGCTGGCGCCGCCGCCTCA       8442 CATTGTAG   G  G_
                         GCTG CGCT  GCATC
                         |||| |||| |||||
                         CGGC GCGG  TGTAG
                       CG_____    G  AG
GAM532 ETF1         TTGTAGGCTGCTGCGCTGACACCA  8448 CATT      __        I
                       GTAGGCTG GCGCTGGCATCA
                       |||||||| |||||||||||
                       CATCCGAC CGCGACTGTGGT
                         ____      GA       A
GAM532 ETF1         TTGTAGGCTGCTGCGCTGACACCA  8448 TG       __       I
                        TAGGCTG GCGCTGGCATC
                        ||||||| |||||||||||
                        ATCCGAC CGCGACTGTGG
                          __     GA       I
GAM532 LNK          TGTAGGCTGGGCGCGGTGGC       8464         _  T III
                       TGTAGGCTGG CGC GG
                       |||||||||| ||| ||
                       ACATCCGACC GCG CC
                          C _ ACC
GAM532 PCDHB9       ATTGTAGGCTGGGTGCGGTGGC-TCA 8445         ___  C  ATCI
                       GTAGGCTG  GCG TGGC
                       |||||||| ||| ||||
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                    CATCCGAC  CGC ACCG
                      CCA  C   IIIC
GAM532 PCDHB9      ATTGTAGGCTGGGTGCGGTGGC-TCA 8445 CA       ___   C  A  II
                    TTGTAGGCTG  GCG TGGC TCA
                    |||||||||  ||| |||| |||
                    AACATCCGAC  CGC ACCG AGT
                      __       CCA  C  _  AI
GAM532 PPP1R12B    ATGGTAGGCTGGGCGTGGGC      8444 ATT      C _   II
                      GTAGGCTGG GC TGG
                      ||||||||| || |||
                      CATCCGACC CG ACC
                      TAC       _  C  CG
GAM532 PPP1R12B    ATGGTAGGCTGGGCGTGGGC      8444 CATT     _ CT  ATC
                      GTAGGCTGG CG  GGC
                      ||||||||| || |||
                      CATCCGACC GC  CCG
                      AC__       C  AC  GII
GAM532 TCL1A      CATTGTAGGCTGGC-CAGGC-TCA  8446        GCT  A
                    CATTGTAGGCTGGC  GGC TCA
                    |||||||||||||  ||| |||
                    GTAACATCCGACCG  CCG AGT
                          GT_  _
GAM532 TCL1A      CATTGTAGGCTGGC-CAGGC-TCA  8446        GCT  ATI
                    CATTGTAGGCTGGC  GGC
                    |||||||||||||  |||
                    GTAACATCCGACCG  CCG
                          GT_ AGT
GAM532 YES1       TGTAGGCTGGGCGCGGTGGC-TCA  8466 T     _  __    ATCI
                     AGGCTGG CGC  TGGC
                     ||||||| ||| ||||
                     TCCGACC GCG  ACCG
                     _     C  CC  AIII
GAM533 ACTN1      GAGATGGGCGACGGCGGAGGTGCAA 8474 TG     _  _  A _  AII
                    AGATGGGC ACG TGGA GT CAA
                    |||||||| ||| |||| || |||
                    TCTACCCG TGC GCCT CA GTT
                    __        C  C  C C  CII
GAM533 ADORA3     TGAGATGGGCCAAGAGGAAGT     8483        ACGT_   CAAA
                    TGAGATGGGC    GGAAGT
                    ||||||||||     ||||||
                    ACTCTACCCG    CCTTCA
                       GTTCT     IIIA
GAM533 ARHGDIB    TGAGATGGAGACGTGGAAG       8486      C     TCAA
                    TGAGATGGG ACGTGGAAG
                    ||||||||| ||||||||||
                    ACTCTACCT TGCACCTTC
                        C    IIIA
GAM533 BMP1       TGTGAGGCCCACGTGGAAG       8488 TGA T G_    TCAA
                    GA GG  CACGTGGAAG
                    II II  |||||||||||
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                              CT CC  GTGCACCTTC
                            ACA _  GG        IIIA
GAM533 CALM3          TGGGATCTGCACGTGGAA-TCA    8490  A  GG       G  AA
                            TG GAT  GCACGTGGAA TCA
                            II III  IIIIIIIIII III
                            AC CTA  CGTGCACCTT AGT
                              C  GA        _  II
GAM533 CCBL1          TGTGATCGGTACATGGTGGAAGTC   8484 TGA  G  C  ___      AAAI
                            GAT GG AC  GTGGAAGTC
                            III II II  IIIIIIIII
                            CTA CC TG  CACCTTCAG
                            ACA  G A TAC      IIIA
GAM533 CDC25B         TGAGATGGG--CGT-AAAGTCAAA   8491        ACGTG
                            TGAGATGGGC   GAAGTCAAA
                            IIIIIIIIII   IIIIIIIII
                            ACTCTACCCG   TTTCAGTTT
                                CA___
GAM533 EPB72          ATGAGTCA-GTGGAAGTCAAA    8473 TGAGATGGG  C
                            CA GTGGAAGTCAA
                            II IIIIIIIIIII
                            GT CACCTTCAGTT
                            CA_____  _
GAM533 FOXD2          GAGATGGGCGC-TGGACGT     8475 TG    ACG   A CA
                            AGATGGGC  TGGA GT
                            IIIIIIII  IIII II
                            TCTACCCG  ACCT CA
                            __     CG_  G CI
GAM533 GPC5           TGAGCTGCAGACGTGGAAG    8487   A _  C     TCAA
                            TGAG TG GG ACGTGGAAG
                            IIII II II IIIIIIIII
                            ACTC AC TC TGCACCTTC
                              G  G  _      IIIA
GAM533 GPX3           TGGGCAGAGAGGTGGAAGTCA    8492 TG  T  CAC      AA
                            AGA GGG  GTGGAAGTCA
                            III III  IIIIIIIIII
                            TCT CTC  CACCTTCAGT
                            __  _ ___        CC
GAM533 HTR2C          TGAAATGGGCACGTATGGAA    8485          __  GTCAA
                            TGAGATGGGCACGT GGAA
                            IIIIIIIIIIIII IIII
                            ACTTTACCCGTGCA CCTT
                              TA   IIIAA
GAM533 MAPK9          AGATGGGCAAGTCCAAG-CAA    8472 TGAG    C  GG  T
                            ATGGGCA GT  AAG CAA
                            IIIIIII II  III III
                            TACCCGT CA  TTC GTT
                            ____      T  GG  _
GAM533 MSR1           GAGAAGGCCATGTGGAAGTCA    8476 TG  T  G  C       AA
                            AGA GG CA GTGGAAGTCA
                            III II II IIIIIIIII
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                                 TCT CC GT CACCTTCAGT
                                 __  T G A       CI
GAM533 NEBL          TGGGAGGGAAGCACGTGGAA    8482 T__  AT        GTCAA
                         GAG  GGGCACGTGGAA
                         III  IIIIIIIIIII
                         CTC  TTCGTGCACCTT
                         ACC  CC         IIIAA
GAM533 NOLA1          TGACGCTGAGC-CGTGGAAGT   8480  GA_  A       CAA
                         TGA  TGGGC CGTGGAAGT
                         III  IIIII IIIIIIIII
                         ACT  ACTCG GCACCTTCA
                         GCG   _      III
GAM533 NRXN3          AGATGGGCAGTTTGAATTC     8471 TGAG    CG_  AG  A
                         ATGGGCA  TGGA TCA
                         IIIIIIII IIII III
                         TACCCGT  ACTT GGT
                         ____       CAA  AA  I
GAM533 RNF26         GGGCACGTGGCCCCAAAGTCA    8479 TGAGATG  ACGTG    AA
                         GGC    GAAGTCA
                         III    IIIIIII
                         CCG    TTTCAGT
                         CA_____  GGG__     CC
GAM533 RPA3          GAGATGGGC-CGCGG-GGTCA    8477 TG    A  AA  A
                         AGATGGGC CGTGG GTCA
                         IIIIIIII IIIII IIII
                         TCTACCCG GCGCC CAGT
                         __     _   C_  A
GAM533 RPH3AL         TGAGATGGG-GGTTGGGAGTCA  8489       CACG A  AA
                         TGAGATGGG  TGG AGTCA
                         IIIIIIIII  III IIIII
                         ACTCTACCC  ACC TCAGT
                           CCA_  C   II
GAM533 SDS           GATGGGCACAGAGCAGTCA      8478 TGAGAT   T A  A
                         GGGCACG GG AGTCA
                         IIIIIII II IIIII
                         CCCGTGT TC TCAGT
                         _____      C G  G
GAM533 SELL          TGAGATGCTAGGT--GTGGAAGTCA 8481     ___ CAC      AAI
                         TGAGATG GG  GTGGAAGTCA
                         IIIIIII II  IIIIIIIIII
                         ACTCTAC CC  CACCTTCAGT
                         GAT A__        III
GAM534 ARHGAP6          TAAGAGTAGCAT---GTTTTA   8503         TAGGTAI
                         TAAGAGTAGCAT
                         IIIIIIIIIIII
                         ATTCTCATCGTA
                             CAAAATI
GAM534 ARHGAP6          TAAGAGTAGCAT---GTTTTA   8503         TAGGTATTAG
                         TAAGAGTAGCAT
                         IIIIIIIIIIII
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                                  ATTCTCATCGTA
                                   CAAAATlllG
GAM534 ATRN        TAGCATTAGCTTAAGTTAGTG    8506      G_  __    lll
                          TAGCATTAG TA TTAGT
                          llllllll ll lllll
                          ATCGTAATC AT AATCA
                               GA TC   Cll
GAM534 ATRN        TAGCATTAGCTTAAGTTAGTG    8506 TAAGAG   A    AT
                          TAGC TTAGGT TAGTG
                          llll llllll lllll
                          ATCG AATTCA ATCAC
                          _____  _   __
GAM534 CD34        TAA-AGTAGCATTATCTGGTA     8500 TA        ___    TTAGT
                         AGAGTAGCATTA GGTA
                         llllllllllll llll
                         TTTCATCGTAAT CCAT
                         A_         AGA  lllGT
GAM534 CD34        TAA-AGTAGCATTATCTGGTA     8500 TA        ___    lll
                         AGAGTAGCATTA GGT
                         llllllllllll lll
                         TTTCATCGTAAT CCA
                         A_         AGA  Tll
GAM534 DEC1        AAGAGTAGC-TCTGGGATT     8496      A A TATl
                         AAGAGTAGC TT GG
                         llllllllll ll ll
                         TTCTCATCG AG CC
                          _ A CTAA
GAM534 DEC1        AAGAGTAGC-TCTGGGATT     8496 TA    A A T  AG
                         AGAGTAGC TT GG ATT
                         llllllll ll ll lll
                         TCTCATCG AG CC TAA
                          __   _ A C  Gl
GAM534 EEF1A1      TAAGAGTGGGGTGGCAGGTATTAG 8499    AGCAT__     TGl
                         TAAGAGT    TAGGTATTAG
                         lllllll    llllllllll
                         ATTCTCA    GTCCATAATC
                          CCCCACC          lll
GAM534 EEF1A1      TAAGAGTGGGGTGGCAGGTATTAG 8499 AA   AGCAT__       l
                         GAGT    TAGGTATTA
                         llll    lllllllll
                         CTCA    GTCCATAAT
                          __   CCCCACC       l
GAM534 FMR2        TAAGAGTAGCATT-GCTAT     8502        AGGTAl
                         TAAGAGTAGCATT
                         lllllllllllll
                         ATTCTCATCGTAA
                          CGATAl
GAM534 FMR2        TAAGAGTAGCATT-GCTAT     8502        AGGTATTAG
                         TAAGAGTAGCATT
                         lllllllllllll
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                              ATTCTCATCGTAA
                               CGATAIIIG
GAM534  MADH4           AACAGTGAGACATTAGGTA-GAGTG 8495 A  TA       TTI
                              GAG GCATTAGGTA
                              III IIIIIIIIII
                              CTC TGTAATCCAT
                              A   __        CTC
GAM534  MADH4           AACAGTGAGACATTAGGTA-GAGTG 8495 TAA__ TA      TT  I
                              GAG GCATTAGGTA AGTG
                              III IIIIIIIIII IIII
                              CTC TGTAATCCAT TCAC
                         TGTCA __       C_  T
GAM534  MAPK14          TAGCATTAGTTATTGGGAGTG    8507       G  AGTIII
                             TAGCATTAG TATT
                             IIIIIIIIII IIII
                             ATCGTAATC ATAA
                               A  CCCTCA
GAM534  P4HA1          TAAGAG--GCA--AGGTATTAG  8504    TA TT
                            TAAGAG GCA AGGTATTAG
                            IIIIII III IIIIIIIII
                            ATTCTC CGT TCCATAATC
                                 __  __
GAM534  P4HA1          TAAGAG--GCA--AGGTATTAG  8504 _  TA TT
                            AAGAG GCA AGGTATTA
                            IIIII III IIIIIIII
                            TTCTC CGT TCCATAAT
                         A   __  __
GAM534  RASAL1        AGGAGCA--AG-TATTAGTG   8497 _ T  TTA
                           G AGCA  GGTATTAGT
                           I IIII  IIIIIIIII
                           C TCGT  TCATAATCA
                         T C  ___
GAM534  RFX5         TAAGAGTAGCCT--GGTGTTAG   8505      ATTA A  T
                          TAAGAGTAGC  GGT TTAG
                          IIIIIIIIII  III IIII
                          ATTCTCATCG  CCA AATC
                             GA__ C  I
GAM534  RFX5         TAAGAGTAGCCT--GGTGTTAG   8505      ATTA ATTI
                          TAAGAGTAGC  GGT
                          IIIIIIIIII  III
                          ATTCTCATCG  CCA
                             GA__  CAAT
GAM534  SERPINB13      TAAGAG---CATTAGGTAT    8501 TAA  T
                           GAG AGCATTAGGTA
                           III IIIIIIIIIII
                           TTC TCGTAATCCAT
                           A__  _
GAM534  SERPINB13      TAAGAG---CATTAGGTAT    8501 TAA  T        TA
                           GAG AGCATTAGGTAT
                           III IIIIIIIIIIII
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                              TTC TCGTAATCCATA
                             A__   _        II
GAM534  TEX15          TAA-AGAAGCAGCTTAGGTATT   8498    _    A     I
                          AAGA GTAGC TTAGGTAT
                          |||| ||||| |||||||||
                          TTCT CGTCG AATCCATA
                             T   _        I
GAM534  TEX15          TAA-AGAAGCAGCTTAGGTATT   8498 T_  _   A      AGTG
                          AAGA GTAGC TTAGGTATT
                          |||| ||||| |||||||||
                          TTCT CGTCG AATCCATAA
                          AT  T  _      IIIG
GAM535  APBB2            TGTCCATGTGTCAAAGAGCTT   8514   _     _T   ACTGA
                          TGTC ATGTGTCAA G GCTT
                          |||| ||||||||| | ||||
                          ACAG TACACAGTT C CGAA
                            G     T T   IIIAG
GAM535  ARHGEF12         TGTTA-GTGTCAAGTGGCTAC   8517  CAT     C    TG
                          TGT  GTGTCAAGTG TTAC
                          |||  |||||||||| ||||
                          ACA  CACAGTTCAC GATG
                            AT_      C  II
GAM535  CARPX           TGT-ATGTG-CAAGTGCTT   8516  C   T     ACT
                          TGT ATGTG CAAGTGCTT
                          ||| ||||| |||||||||
                          ACA TACAC GTTCACGAA
                            _    _       III
GAM535  GDA           ATTTGTCAAGTGAATACTG    8510 TGTCATGT    CT
                           GTCAAGTG TACTG
                           |||||||| |||||
                           CAGTTCAC ATGAC
                           _____      TT
GAM535  OGT           TGTCATGTTTTCAAGTGCT    8515    G_     TACTG
                          TGTCATGT TCAAGTGCT
                          |||||||| |||||||||
                          ACAGTACA AGTTCACGA
                            AA    IIIAG
GAM535  POP2           GTGATTTATTGAGTGCTTACT   8511 TGTCATG  CA     GA
                          TGT  AGTGCTTACT
                          |||  ||||||||||
                          ATA  TCACGAATGA
                          ACTAA__  AC     AI
GAM535  RAB23          TGTCAGATGAAAACTGCTTACTG   8518    T  TC  G     AI
                          TGTCA GTG  AA TGCTTACTG
                          ||||| ||| || |||||||||
                          ACAGT TAC  TT ACGAATGAC
                            C  TT  G     II
GAM535  TRIM9          TCATGTGTC--TTGCTTACT   8512 TGTC    AAG
                          ATGTGTC TGCTTACT
                          ||||||| ||||||||
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                        TACACAG   ACGAATGA
                        ____        A__
GAM535  UBQLN2        TGTACA-GTGCCAATTGTGCTTACTG 8513  _ T    __        AII
                        TGT CA GTGTCAA  GTGCTTACTG
                        III II IIIIIII  IIIIIIIIII
                        ACA GT CACGGTT  CACGAATGAC
                          T _    AA        III
GAM536  ADCY1         TGAGGCCCGACACGCAGTA      8526      _ A TTATGGAG
                        TGAGGCCCG CAC CA
                        IIIIIIIII III II
                        ACTCCGGGC GTG GT
                          T  C  CATIIIGG
GAM536  BAZ2A         GGTCCGCACACAGTACAGAG      8525 TGAGGC      T
                          CCGCACACA TATGGAG
                          IIIIIIIII IIIIIII
                          GGCGTGTGT ATGTCTC
                        _____        C
GAM536  EGLN2         GACGCCTCCCAACACATTAT      8521 _ AGG   C      GGAG
                        TG  CCCG ACACATTAT
                        II  IIII IIIIIIIII
                        GC  GGGT TGTGTAATA
                          T GGA  _       GIII
GAM536  RAD18         TGAGACTC-CACACATTAT      8527    _      CATTATGGA
                        TGAGGC CCGCACA
                        IIIIII IIIIIII
                        ACTCTG GGTGTGT
                          A     AATAIIIGG
GAM536  RORB          GAGGCC---ACACATTATG      8523 TG   CGC      G
                        AGGCC  ACACATTATG
                        IIIII  IIIIIIIIII
                        TCCGG  TGTGTAATAC
                        __  ___      A
GAM536  TEM8          GAGGCCCGC---TATTAAGGAGG 8524 TG    ACAC   T
                        AGGCCCGC  ATTA GGAG
                        IIIIIIII  IIII IIII
                        TCCGGGCG  TAAT CCTC
                        __    A___   T
GAM536  UBE2I         GAGGCCCGCACTCAGGTTCTGG   8522 TG    A TTA__ AGG
                        AGGCCCGCAC CA    TGG
                        IIIIIIIIII II    III
                        TCCGGGCGTG GT    ACC
                          __      A CCAAG  CII
GAM537  APG5L         TCAACCAAAGCCAAACCTA      8542   __       A AAAGGT
                        TCAA AAAGCCAAA CTA
                        IIII IIIIIIIII III
                        AGTT TTTCGGTTT GAT
                          GG     G  IIICTG
GAM537  APG5L         TCAACCAAAGCCAAACCTA      8542   __       ACTIII
                        TCAA AAAGCCAAA
                        IIII IIIIIIIII
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                         AGTT  TTTCGGTTT
                          GG        GGATII
GAM537 BIG1              CAAAAAGGGCAAAACTAAAA      8538       C_        II
                          CAAAAAG CAAAACTAAA
                          IIIIIII IIIIIIIIII
                          GTTTTTC GTTTTGATTT
                              CC        TI
GAM537 BIG1              CAAAAAGGGCAAAACTAAAA      8538 TC    C_        GT
                            AAAAAG CAAAACTAAAAG
                            IIIIII IIIIIIIIIII
                            TTTTTC GTTTTGATTTTT
                             __        CC        II
GAM537 C7            AATAAGGAATAAATAAAAGGTC    8533 TCAAAAAGCCAAAAC
                                   TAAAAGGTC
                                   IIIIIIIII
                                   ATTTTCCAG
                      ATTCCTTATTT____
GAM537 CCNT2            AAAAGCCAAGCAACAAAAA      8535       AACTAAAIII
                          AAAAGCCAA
                          IIIIIIIII
                          TTTTCGGTT
                            CGTTGTTTTT
GAM537 CCNT2            AAAAGCCAAGCAACAAAAA      8535 TCAAAA    __  T
                           AGCCAA  AAC AAAAGGT
                           IIIIII  III IIIIIII
                           TCGGTT  TTG TTTTTTA
                          _____      CG  _
GAM537 COX15        TCAAAAAG-CAAAACAAAAA      8546     C    T   GT
                       TCAAAAAGC AAAAC AAAAG
                       IIIIIIIII IIIII IIIII
                       AGTTTTTCG TTTTG TTTTT
                            _    _    II
GAM537 COX15        TCAAAAAG-CAAAACAAAAA      8546 _    C   TAAAI
                         CAAAAAGC AAAAC
                         IIIIIIII IIIII
                         GTTTTTCG TTTTG
                      A      _    TTTTI
GAM537 EXT2         TCAAAAAGCCAAACCAAAGAGG      8548         A   _  TC
                       TCAAAAAGCCAAA CTAAA AGG
                       IIIIIIIIIIIII IIIII III
                       AGTTTTTCGGTTT GGTTT TCC
                            _    C  II
GAM537 EXT2         TCAAAAAGCCAAACCAAAGAGG      8548         A   AGI
                         CAAAAAGCCAAA CTAAA
                         IIIIIIIIIII IIIII
                         GTTTTTCGGTTT GGTTT
                            _     CTC
GAM537 GLS          AAAGCCAAAACAAAAAGATC      8536        T   I
                       AAGCCAAAAC AAAAGGT
                       IIIIIIIIII IIIIIII
```

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                    TTCGGTTTTG TTTTCTA
                        T       I
GAM537 GLS          AAAGCCAAAACAAAAAGATC      8536 TCAAAAAG      T
                        CCAAAAC AAAAGGT
                        |||||||| |||||||
                        GGTTTTG TTTTCTA
                        _____        T
GAM537 GPR85        TCAAAAAG-CAAAACCATAA      8547      C     AAAGGT
                        TCAAAAAGC AAAACTA
                        |||||||||| ||||||||
                        AGTTTTTCG TTTTGGT
                             _     ATTIII
GAM537 GPR85        TCAAAAAG-CAAAACCATAA      8547 _    C     AAI
                        CAAAAAGC AAAACTA
                        |||||||| |||||||
                        GTTTTTCG TTTTGGT
                        A      _      ATI
GAM537 HOXC4        TCCAAAAGCC-AAACAAAA       8544 A        ACTAAAAGG
                        TC AAAAGCCAAA
                        || ||||||||||
                        AG TTTTCGGTTT
                        G         GTTTTIIIC
GAM537 HOXC4        TCCAAAAGCC-AAACAAAA       8544 A        ACTAAI
                        TC AAAAGCCAAA
                        || ||||||||||
                        AG TTTTCGGTTT
                        G         GTTTTI
GAM537 LTB4R        AAGCCAAAATCCAAATGGTC      8537          _    A  II
                        AAGCCAAAA CTAAA GGT
                        ||||||||| ||||| |||
                        TTCGGTTTT GGTTT CCA
                            A    A  GI
GAM537 LTB4R        AAAAAG---AAACTAAAAAGTC    8532 _     CCA
                        AAAAG  AAACTAAAAGGT
                        |||||  ||||||||||||
                        TTTTC  TTTGATTTTTCA
                        T     ___
GAM537 LTB4R        AAAAAG---AAACTAAAAAGTC    8532 TCAA  CCA
                        AAAG   AAACTAAAAGGT
                        ||||   ||||||||||||
                        TTTC   TTTGATTTTTCA
                        _____   ___
GAM537 PCBP1        CAAAA---CAAAACTAAAA       8539 TCAA    C
                        AAAGC AAAACTAAAAG
                        ||||| ||||||||||||
                        TTTTG TTTTGATTTTT
                        _____   ___
GAM537 PRL          TCAAAAGAGATACAACTAAAAG    8543    _ CCAA      GTC
                        TCAAAA AG   AACTAAAAG
                        |||||| ||    |||||||||
```

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                        AGTTTT TC   TTGATTTTC
                         C  TATG        III
GAM537 SELL             CAAAACCCCCAAACTAAAA     8540    AG  A     II
                          CAAAA  CC AAACTAAA
                          |||||  ||  |||||||||
                          GTTTT  GG TTTGATTT
                           GG  G      TI
GAM537 SELL             CAAAACCCCCAAACTAAAA     8540 TCA  G  A_      GT
                           AAAA CC  AAACTAAAAG
                           |||| ||  |||||||||||
                           TTTT GG  TTTGATTTTT
                           ___  G  GG       II
GAM537 SH3BP2           TCAAAAACAAAAAACTAAAA     8545     GCC      GGT
                          TCAAAAA  AAAACTAAAA
                          |||||||  |||||||||||
                          AGTTTTT  TTTTGATTTT
                             GTT         III
GAM537 TPK1             CAGAAAACTAATACTAAAAGGT   8541 AA    C  A      I
                           AAAGC AA ACTAAAAGG
                           ||||| ||  |||||||||
                           TTTTG TT TGATTTTCC
                           TC    A A       I
GAM537 TPK1             CAGAAAACTAATACTAAAAGGT   8541 TCAA   C  A      C
                           AAAGC AA ACTAAAAGGT
                           ||||| ||  ||||||||||
                           TTTTG TT TGATTTTCCA
                           TC__   A  A       T
GAM537 UVRAG           AAAAAGCAGACAAATAGCTAAAAGGT 8530 AAA  C   A__      I
                          AG CAAA  CTAAAAGG
                          || ||||   |||||||||
                          TC GTTT  GATTTTCC
                          G__  T  ATC       I
GAM537 UVRAG           AAAAAGCAGACAAATAGCTAAAAGGT 8530 TCAA   ___  A__      CII
                          AAAGC  CAAA  CTAAAAGGT
                          |||||  ||||  |||||||||
                          TTTCG  GTTT  GATTTTCCA
                           ____   TCT  ATC      CTI
GAM537 WASF3          AACAGCAATCAAAACTAAAACGGTC 8534 AAAGC         _  I
                          CAAAACTAAAA GGT
                          |||||||||||| |||
                          GTTTTGATTTT CCA
                          GTTA_      G  I
GAM537 ZIC1           AAAAAGCCAAA--GAAAAGG      8531      ACTAAAAI
                          AAAAAGCCAAA
                          |||||||||||
                          TTTTTCGGTTT
                           CTTTTCCI
GAM537 ZIC1           AAAAAGCCAAA--GAAAAGG      8531 TCAA      ACT
                           AAAGCCAAA  AAAAGG
                           |||||||||  ||||||
```

```
                          TTTCGGTTT  TTTTCC
                          ___        C__
GAM538 COL19A1        AGCACC--ATTGTAGGTATTGC    8558 AA   G  T        G
                         GCA CT ATTGTAGGTGT GC
                         ||| || |||||||||| ||
                         CGT GG TAACATCCATA CG
                         __  _ _         A
GAM538 CUBN          CAGCTTATTCT--CTGTGGC    8560 AAGCAG    GTAGG
                         CTTATT   TGTGG
                         ||||||   |||||
                         GAATAA   ACACC
                         _____   GAG__
GAM538 CYLN2         AGCAGCTTA--G-AGGTGTG    8556 AA     TTGT    G
                         GCAGCTTA AGGTGTG
                         |||||||| |||||||
                         CGTCGAAT TCCACAC
                         __     C___    A
GAM538 EN2          GCAGACACTTATTGTAAGTGTG    8561 AA  G        G
                         GCA CTTATTGTAGGTGTG CG
                         ||| |||||||||||||| ||
                         TGT GAATAACATTCACAC GC
                         TC  _         _
GAM538 GLI2         AGCA--TTATTGTAGGAGT    8555 AA  GC      T GG
                         GCA  TTATTGTAGG GT
                         |||  |||||||||| ||
                         CGT  AATAACATCC CA
                         __  __        T GI
GAM538 KIAA0857       AGCAGCTTAATGGATGGATGG    8557 AA     T TA_ T  CG
                         GCAGCTTA TG  GG GTGG
                         |||||||| ||  || ||||
                         CGTCGAAT AC  CC TACC
                         __    T CTA _  CI
GAM538 PCDHB9       AAGAAAATTATTGTAGGCTGGGTGCG 8553   C  C       GTG__  II
                         AAG AG TTATTGTAGGT   GCG
                         ||| || |||||||||||   |||
                         TTC TT AATAACATCCG   CGC
                          T T         ACCCA  II
GAM538 PCSK1        AAGCCAGC--ATTGTAGGTG    8551  _ TT       TGG
                         AAGC AGC ATTGTAGGTG
                         |||| ||| ||||||||||
                         TTCG TCG TAACATCCAC
                          G  __         III
GAM538 RARB        GCTTATCCTCTAGGTGTGG    8563 AAGCAGCTTA G     C
                           TT TAGGTGTGG
                           || |||||||||
                           GA ATCCACACC
                         AG_____ G      T
GAM538 TEM7R        AGCAGCTTAGAGCTTGTTTGTGTG  8554 AA     ____  AG   GCGI
                         GCAGCTTA TTGT GTGTG
                         |||||||| |||| |||||
```

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                              CGTCGAAT   AACA CACAC
                          __      CTCG   AA    AIII
GAM538  TNKS            AAACAGCTTATTTCTAGGCTGT  8552        G_    GTGGCG
                          AAGCAGCTTATT TAGGT

                          IIIIIIIIIII IIIII
                          TTTGTCGAATAA ATCCG
                              AG    ACAIII
GAM538  TNNT1           GCGGCCT-TGGTAGGTGTGG      8562 AAGCA  ATT       C
                            GCTT GTAGGTGTGG

                            IIII IIIIIIIIII
                            CGGA CATCCACACC
                          C____ AC_     A
GAM538  XT3            CAGCTTATTGGAGG-GTGG        8559 AAGCAG    T  T
                          CTTATTG AGG GTGG

                          IIIIIIII III IIII
                          GAATAAC TCC CACC
                          _____      C _
GAM539  ZNF264          GGAAGGGGTCAGGCTCGTACAAG  8566 TG   CGAC__  C      AI
                          GAAG    GGC CGTACAAAG

                          IIII    III IIIIIIIII
                          CTTC    CCG GCATGTTC
                            __  CCCAGT  A     CI
GAM540  BCL6           TGTCCGGCCTTTCCTAGAAACTTC  8571        ___ _       ATACI
                          TGTCCGGCC  CTT GAAATTTC

                          IIIIIIIII  III IIIIIIII
                          ACAGGCCGG  GGA CTTTGAAG
                            AAA  T      IIICA
GAM540  BCL6           TGTCCGGCCTTTCCTAGAAACTTC  8571 GTCC   ___ _      I
                            GGCC  CTT GAAATTT

                            IIII  III IIIIIII
                            CCGG  GGA CTTTGAA
                          ____     AAA  T    I
GAM540  PTPRD          TGTCCGATC--TGAAATTTCA      8572        CCC       TA
                          TGTCCGG  TTGAAATTTCA

                          IIIIIII  IIIIIIIIIII
                          ACAGGCT  GACTTTAAAGT
                            A__        II
GAM540  PTPRD          TGTCCGATC--TGAAATTTCA      8572 _     CCC        I
                          GTCCGG  TTGAAATTTC

                          IIIIII  IIIIIIIIII
                          CAGGCT  GACTTTAAAG
                          A    A__       I
GAM540  SAA4          TCCAGC---TGAAATTTCA       8570    CCT
                          TCCGGC  TGAAATTTC

                          IIIIII  IIIIIIIII
                          AGGTCG  ACTTTAAAG
                                   ___
GAM540  SAA4          TCCAGC---TGAAATTTCA         8570 TGTC  CCT
                          CGGC  TGAAATTTCA

                          IIII  IIIIIIIIII
```

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                          GTCG  ACTTTAAAGT
                          ____  ___
GAM540  WT1          TCCGGCCCTGGAGACGTTCA     8569      T AATTTCII
                       TCCGGCCCT GA
                       |||||||| ||
                       AGGCCGGGA CT
                          C CTGCAAGT
GAM540  WT1          TCCGGCCCTGGAGACGTTCA     8569 TGTC    T A _  TA
                       CGGCCCT GA AT TTCA
                       ||||||| || || ||||
                       GCCGGGA CT TG AAGT
                       ____     C C C  CG
GAM541  ANK3       CATTTAAAAAGATCCTCTCAAGCA  8576 TC     _ GG  _ AI
                      ATTTAAAAA AT  TTTCA GCA
                      ||||||||| ||  ||||| |||
                      TAAATTTTT TA  AGAGT CGT
                      __        C GG   T GI
GAM541  EGFL5      TTTAAAAAAAATGTTTCAGGAA  8577 TCATTT    G   CAA
                       AAAAAATG TTTCAG
                       |||||||| ||||||
                       TTTTTTAC AAAGTC
                     TT____      _   CTT
GAM541  MBNL       ATTTCCAAGCTGCTTTCAGCAA   8575 TCA   AAAA  G
                       TTTAA   TG TTTCAGCAA
                       |||||   || |||||||||
                       AGGTT   AC AAAGTCGTT
                     A__   CG__  G
GAM541  TOX       TTTAAAAAAAAGTGTTCAGCAA   8578 TCATTT    T _
                       AAAAAA GGT TTCAGCAA
                       |||||| ||| |||||||||
                       TTTTTT TCA AAGTCGTT
                     _____     T C
GAM542  ADCY2       AGCAAGCACAGT--GCAAGTGGC  8590 _      CTAG    I
                       GCAAGCACA  GCAGGTGG
                       |||||||||  ||||||||
                       CGTTCGTGT  CGTTCACC
                     T     CA__    I
GAM542  ADCY2       AGCAAGCACAGT--GCAAGTGGC  8590 CA      CTAG
                       GCAAGCACA  GCAGGTGGC
                       |||||||||  |||||||||
                       CGTTCGTGT  CGTTCACCG
                            CA__
                     __
GAM542  APBB2       AGCAAGCACCCAAGG-AGGT    8586 _    A  C  I
                       GCAAGCAC CTAGG AGG
                       |||||||| ||||| |||
                       CGTTCGTG GGTTC TCC
                     T    _   C I
GAM542  APBB2       AGCAAGCACCCAAGG-AGGT    8586 CA    A  C  GG
                       GCAAGCAC CTAGG AGGT
                       |||||||| ||||| ||||
```

```
                              CGTTCGTG GGTTC TCCA
                              __      _   C  GI
GAM542 CAPG          AGCAAGCA-----GGCAGGTGG  8588 _     CACTA
                        GCAAGCA   GGCAGGT
                        |||||||   |||||||
                        CGTTCGT   CCGTCCA
                     T         _____
GAM542 CAPG          AGCAAGCA-----GGCAGGTGG  8588 CA     CACTA
                        GCAAGCA   GGCAGGTG
                        |||||||   ||||||||
                        CGTTCGT   CCGTCCAC
                           __    _____
GAM542 CYP4A11         CAGGAAG-ACAGGACGGCAGGTGG  8599  C  C  CTA_     CI
                         CAG AAG ACA   GGCAGGTGG
                         ||| ||| |||   |||||||||
                         GTC TTC TGT   CCGTCCACC
                          C  _  CCTG       II
GAM542 CYP4A11         CAGGAAG-ACAGGACGGCAGGTGG  8599  C  C  CTA_      I
                          AG AAG ACA   GGCAGGTG
                          || ||| |||   ||||||||
                          TC TTC TGT   CCGTCCAC
                          C  _  CCTG        I
GAM542 DNASE1L1       ACACTACCTGGCAGGTGGC    8584    ___       III
                        ACACTA  GGCAGGTGG
                        ||||||  |||||||||
                        TGTGAT  CCGTCCACC
                            GGA       GII
GAM542 DRG2           CAGGGAGACGAGGCAGGTGG    8593 AAGCAC  T     I
                         AC AGGCAGGTG
                         || |||||||||
                         TG TCCGTCCAC
                        TCCCTC  C      I
GAM542 DRG2           CAGGGAGACGAGGCAGGTGG    8593 CAGCAAGCAC  T
                         AC AGGCAGGTGG
                         || ||||||||||
                         TG TCCGTCCACC
                        CCTC_____  C
GAM542 FBXW1B         GCAAGCACACGTATAAAGGTG    8606 C      _  GGC   I
                         AAGCACAC TA  AGGT
                         |||||||| ||  ||||
                         TTCGTGTG AT  TCCA
                         _      C ATT   I
GAM542 FBXW1B         GCAAGCACACGTATAAAGGTG    8606 CAGC     _  GGC   GC
                         AAGCACAC TA  AGGTG
                         |||||||| ||  |||||
                         TTCGTGTG AT  TCCAC
                         ____         C ATT   AA
GAM542 FZD7          CAAGCACAC--CGCAGGAGGC    8594 _      AG  T I
                        AAGCACACT GCAGG GG
                        ||||||||| ||||| ||
```

```
                    TTCGTGTGG CGTCC CC
                  G       T I
GAM542 FZD7       CAAGCACAC--CGCAGGAGGC  8594 CAGCAA    AG   T
                      GCACACT GCAGG GG
                      ||||||| ||||| ||
                      CGTGTGG CGTCC CC
                  _____    __    T
GAM542 GPR44      CAAGTCCAC--GGCAGGTGG   8592 _ CA TA    I
                      AAG CAC GGCAGGTG
                      ||| ||| ||||||||
                      TTC GTG CCGTCCAC
                   G  AG  __    I
GAM542 GPR44      CAAGTCCAC--GGCAGGTGG   8592 CAGCAAGCA TA
                        CAC GGCAGGTG
                        ||| ||||||||
                        GTG CCGTCCAC
                  CAG_____  __
GAM542 LOXL2      AGCAAGCAC-CAAGCGTAGGTAGC 8585     AC  __   I
                      GCAAGCAC TAGGC AGGTGG
                      |||||||| ||||| ||||||
                      CGTTCGTG GTTCG TCCATC
                         __   CA    I
GAM542 LOXL2      AGCAAGCAC-CAAGCGTAGGTAGC 8585 CA     AC  __    I
                        GCAAGCAC TAGGC AGGTGGC
                        |||||||| ||||| |||||||
                        CGTTCGTG GTTCG TCCATCG
                     __     __  CA    G
GAM542 LPIN1      CAG-AAGC-CAGAAGGCAGGTG  8600  C  A CT     G
                      CAG AAGC CA AGGCAGGTG
                      ||| |||| || |||||||||
                      GTC TTCG GT TCCGTCCAC
                       _  _ CT     I
GAM542 LPIN1      CAG-AAGC-CAGAAGGCAGGTG  8600  C  A CT    I
                      CAG AAGC CA AGGCAGG
                      ||| |||| || |||||||
                      GTC TTCG GT TCCGTCC
                       _  _ CT    A
GAM542 MATK       CAG-AGGGAAACTGAGGCAGGTG 8598  CAAGCAC _    GC
                      CAG    ACT AGGCAGGTG
                      |||    ||| |||||||||
                      GTC    TGA TCCGTCCAC
                       TCCCTT_  C      II
GAM542 MATK       CAG-AGGGAAACTGAGGCAGGTG 8598 AGCAAGCAC _   I
                          ACT AGGCAGGT
                          ||| ||||||||
                          TGA TCCGTCCA
                   TCTCCCTT_  C    I
GAM542 MFAP4      CAGCTTAGCACACTAG---GGTGGC 8595  A_     CA GI
                      CAGC AGCACACTAGG GGT
                      |||| ||||||||||| |||
```

```
                       GTCG TCGTGTGATCC CCG
                        AA          CA   II
GAM542 MFAP4           CAGCTTAGCACACTAG---GGTGGC   8595   A_          CAG
                       CAGC AGCACACTAGG GTGGC
                       |||| |||||||||| |||||
                       GTCG TCGTGTGATCC CACCG
                        AA              ___
GAM542 MGAT1           CAGGAAGGACA---GGCAGGTG   8601   C  C CTA     G
                       CAG AAG ACA  GGCAGGTG
                       ||| ||| |||  ||||||||
                       GTC TTC TGT  CCGTCCAC
                        C   C  ___   I
GAM542 MGAT1           CAGGAAGGACA---GGCAGGTG   8601   C  C CTA   I
                       CAG AAG ACA  GGCAGG
                       ||| ||| |||  ||||||
                       GTC TTC TGT  CCGTCC
                        C   C  ___     A
GAM542 MYD88           AAGCTCTCT--GCAGGTGGC    8583 _  ACA AG     I
                       AGC  CT GCAGGTGG
                       |||  || ||||||||
                       TCG  GA CGTCCACC
                        T  A__ GA      I
GAM542 NTS             CAG-AAGCACACT--GAAGGGGGC   8602   C       __  CA  GI
                       CAG AAGCACACT AGG GGT
                       ||| ||||||||| ||| |||
                       GTC TTCGTGTGA TCC CCG
                        _          CT  C_ II
GAM542 NTS             CAG-AAGCACACT--GAAGGGGGC   8602   C       A C T
                       CAG AAGCACACT GG AGG GGC
                       ||| ||||||||| || ||| |||
                       GTC TTCGTGTGA CT TCC CCG
                        _          _ _ C
GAM542 PAK4            CAG-AAGTGCCCTCAGGCAGGTG   8597   C CACA _      GC
                       CAG AAG   CT AGGCAGGTG
                       ||| |||   || |||||||||
                       GTC TTC   GA TCCGTCCAC
                        _  ACGG  G        II
GAM542 PAK4            CAG-AAGTGCCCTCAGGCAGGTG   8597 AGCAA_ ACAC      I
                        GC  TAGGCAGGT
                        ||  |||||||||
                        CG  GTCCGTCCA
                       TCTTCA GGA_       I
GAM542 PCMT1           AAGCACACTCGGAGCAGGT    8581          A__    III
                       AAGCACACT GGCAGG
                       ||||||||| ||||||
                       TTCGTGTGA TCGTCC
                         GCC    AII
GAM542 PIGR            AGGAAAAAC-CTAGGCAGGTG    8587 CAGCAAGCACA        G
                       CTAGGCAGGTG
                       |||||||||||
```

```
                                       GATCCGTCCAC
                         CCTTTTTG___           A
GAM542  PIGR             AGGAAAAAC-CTAGGCAGGTG     8587 GCAAGCACA        I
                                  CTAGGCAGGT
                                  ||||||||||
                                  GATCCGTCCA
                         TCCTTTTTG        I
GAM542  PTK2B            AAG-ACGC-AGGCAGGTGGC     8582 AGCAC  _         I
                                 AC TAGGCAGGTGG
                                 || |||||||||||
                                 TG GTCCGTCCACC
                         TTC__  C       I
GAM542  SCN2B            CAAGCAC--TGGGCAGGTGG     8591 _     ACTA       I
                                AAGCAC  GGCAGGTG
                                ||||||  ||||||||
                                TTCGTG  CCGTCCAC
                         G     AC__       I
GAM542  SCN2B            CAAGCAC--TGGGCAGGTGG     8591 CAGCAAGCA   A
                                CACT GGCAGGTG
                                |||| ||||||||
                                GTGA CCGTCCAC
                         C_____        C
GAM542  SEMG1            AGGAAGCA---TGGGCAGGTGG    8589 _ C    CACTA
                                 G AAGCA    GGCAGGTG
                                 | |||||    ||||||||
                                 C TTCGT    CCGTCCAC
                         T C    AC___
GAM542  SEMG1            AGGAAGCA---TGGGCAGGTGG    8589 CAGC    CACTA
                                  AAGCA    GGCAGGTGG
                                  |||||    |||||||||
                                  TTCGT    CCGTCCACC
                         CC__    AC___
GAM542  SLC12A4          GCAAGCAGGGCT-GGCAGGTGG     8605     CA_ A      I
                                 CAAGCA  CT GGCAGGTG
                                 ||||||  || |||||||||
                                 GTTCGT  GA CCGTCCAC
                           CCC _        I
GAM542  SLC12A4          GCAAGCAGGGCT-GGCAGGTGG     8605 CAGC    CA_ A       C
                                  AAGCA  CT GGCAGGTGG
                                  |||||  || ||||||||||
                                  TTCGT  GA CCGTCCACC
                           ____  CCC _        C
GAM542  SLC7A5           CAGCAATGCAC-C-AGGCAGGTGG  8596       GCA         C
                                 CAGCAA  CACTAGGCAGGTGG
                                 ||||||  |||||||||||||
                                 GTCGTT  GTGGTCCGTCCACC
                           AC_         I
GAM542  SLC7A5           CAGCAATGCAC-C-AGGCAGGTGG  8596 _    GCA          I
                                  AGCAA  CACTAGGCAGGTG
                                  |||||  |||||||||||||
```

```
                         TCGTT  GTGGTCCGTCCAC
                        G    AC_          I
GAM542  TEM8     CAGCAATGTCACT--GCAGGTGGC  8603     GCA   AG
                         CAGCAA  CACT GCAGGTGGC
                         |||||| |||| |||||||||
                         GTCGTT  GTGA CGTCCACCG
                               ACA    __
GAM542  TEM8     CAGCAATGTCACT--GCAGGTGGC  8603 _   GCA   AG     I
                          AGCAA  CACT GCAGGTGG
                          ||||| |||| ||||||||
                          TCGTT  GTGA CGTCCACC
                         G    ACA  __       I
GAM542  TMEM1     GCAAGCACAGTGCTGGGCAGG     8604        ___ A   III
                          GCAAGCACA  CT GGCAG
                          |||||||||  || |||||
                          CGTTCGTGT  GA CCGTC
                               CAC  C   CII
GAM542  TMEM1     GCAAGCACAGTGCTGGGCAGG     8604 CAGC    ___ A   TGGC
                          AAGCACA  CT GGCAGG
                          |||||||  || ||||||
                          TTCGTGT  GA CCGTCC
                          ____       CAC  C    TTII
GAM542  UNC13    GCAGGGAGACTCCCAGGCAGGTGGC  8607 A C  A_        I
                          C AG AC  CTAGGCAGGTGG
                          | || ||  ||||||||||||
                          C TC TG  GGTCCGTCCACC
                          C _  AG          I
GAM542  UNC13    GCAGGGAGACTCCCAGGCAGGTGGC  8607 C  CA C A_         II
                          AG AG AC  CTAGGCAGGTGGC
                          || || ||  |||||||||||||
                          TC TC TG  GGTCCGTCCACCG
                          _ CC _ AG         GG
GAM543  ARSF     GAGTGGTGGTTCACGCCTGTAATCCC 8614 TAGA    C ___ AG_    II
                          GTGGTGG TC  CC  AATCCC
                          ||||||| ||  ||  ||||||
                          CACCACC AG  GG  TTAGGG
                          ____       A TGC ACA    TC
GAM543  ATP5B    GATTGGTG-CACC-AGAATCC     8616 TAGAG   G TC
                          TGGTG C  CCAGAATCC
                          ||||| |  |||||||||
                          ACCAC G  GGTCTTAGG
                          A____    _ T_
GAM543  CD1A     TAAAGTGAAATGGCTCCCAG      8619       __        AATCC
                          TAGAGTG  GTGGCTCCCAG
                          |||||||  ||||||||||
                          ATTTCAC  TACCGAGGGTC
                               TT      IIICC
GAM543  CRY2     TAGGGAGGCAGATGCCAGAATCCC  8620 TAG  T T  TC___        I
                          AG GG GGC   CCAGAATCCC
                          || || |||   |||||||||
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                        TC CC CCG    GGTCTTAGGG
                        A__ _ T  TCTAC        I
GAM543  ENAM            GAGTGGTGGCTCATTCAGCATCC   8615 TAGA        C__ A  CI
                        GTGGTGGCTC  CAG ATCC
                        IIIIIIIIII  III IIII
                        CACCACCGAG  GTC TAGG
                        ____           TAA G   AT
GAM543  KIFC3           GAGGGCGTGGCTCCCAGGTTCC    8612 TAGAGTG      AA  C
                        GTGGCTCCCAG  TCC
                        IIIIIIIIII  III
                        CACCGAGGGTC AGG
                        CCCG___          CA  T
GAM543  NRXN1           GTGGCTGCTCCCAGATTTCC      8617 TAGAGTGGTG      A_
                        GCTCCCAGA  TCC
                        IIIIIIIII  III
                        CGAGGGTCT  AGG
                        GA_____        AA
GAM543  PRSS8           AGAGGGAAGGATCCCAGAATCC    8611 TA  T T_ C      C
                        GAG GG  GG TCCCAGAATCC
                        III II  II IIIIIIIIII
                        CTC CC  CC AGGGTCTTAGG
                        __ _ TT T        C
GAM543  RPP30           GTGGTGGCTCATGTAATCCC      8618 TAGAGTGG    CCAG
                        TGGCTC  AATCC
                        IIIIII  IIIII
                        ACCGAG  TTAGG
                        _____      TACA
GAM543  SMAC            GAGTGGTGGCACGCTCCTGTAATCCC 8613 TAGA    ____ CAG    II
                        GTGGTGGC  TCC  AATCCC
                        IIIIIIII  III  IIIIII
                        CACCACCG  AGG  TTAGGG
                        ____        TGCG ACA    TC
GAM543  TBXAS1          AGAGTGGTGGTCTTCCAGA       8610 TA      _ C   ATCC
                        GAGTGGTGG CT CCAGA
                        IIIIIIIII II IIIII
                        CTCACCACC GA GGTCT
                        __      A A   AIII
GAM544  ADAMTS4         GTGGTGGCTCACACCTGTAATCCC  8629 TGGT    ___ AA_  I
                        GGCTC  CC  AATCC
                        IIIII  II  IIIII
                        CCGAG  GG  TTAGG
                        ____       TGT ACA   I
GAM544  ADCY6           GTGGTGGCTCACGTCCGTAATCCC  8628 TGGT    ____ AA   I
                        GGCTC   CC  AATCC
                        IIIII   II  IIIII
                        CCGAG   GG  TTAGG
                        ____       TGCA CA   I
GAM544  ALDH1B1         GTTGTGGCTCCCACCTGTAATCCC  8632 TGGT      A____    I
                        GGCTCCCA  AATCC
                        IIIIIIII  IIIII
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                          CCGAGGGT    TTAGG
                          ____        GGACA    I
GAM544 ARAF1       GAGATGGAGGAGCTCCCAAAAT   8624  _   T__          III
                          GAG TGG   GGCTCCCAAAA
                          ||| |||   ||||||||||
                          CTC ACC   TCGAGGGTTTT
                           T   TCC          AII
GAM544 ARAF1       GAGATGGAGGAGCTCCCAAAAT   8624 TAGA  T__          CCC
                          GTGG   GGCTCCCAAAAT
                          ||||   ||||||||||||
                          TACC   TCGAGGGTTTTA
                          C___   TCC          AAI
GAM544 CD1A        TAAAGTGAAATGGCTCCCA       8634       __          AAATCC
                          TAGAGTG  GTGGCTCCCA
                          |||||||  ||||||||||
                          ATTTCAC  TACCGAGGGT
                           TT         IIICCC
GAM544 CD1A        TAAAGTGAAATGGCTCCCA       8634       __          III
                          TAGAGTG  GTGGCTCCC
                          |||||||  |||||||||
                          ATTTCAC  TACCGAGGG
                           TT         TII
GAM544 CDC6        TGGTGGCTCACGCCTATAATCCC  8638        ___ AA_     IIIG
                          TGGTGGCTC  CC  AATCC
                          |||||||||  ||  |||||
                          ACCACCGAG  GG  TTAGG
                           TGC ATA      GIII
GAM544 CLECSF12    GTGGTGGCTCACATCTGTAATCCC  8631 TGGT    C A____    I
                          GGCTC CA    AATCC
                          ||||| ||    |||||
                          CCGAG GT    TTAGG
                          ____    T AGACA    I
GAM544 CYP1A2      GTGGTGGCTCACACCTGTAATCCC  8629 TGGT    ___ AA_   I
                          GGCTC  CC  AATCC
                          |||||  ||  |||||
                          CCGAG  GG  TTAGG
                          ____     TGT ACA    I
GAM544 DSCR3       GTGGTGGCTCACACCTGTAATCCC  8629 TGGT    ___ AA_   I
                          GGCTC  CC  AATCC
                          |||||  ||  |||||
                          CCGAG  GG  TTAGG
                          ____     TGT ACA    I
GAM544 FZD4        GTGGTGGCTCACACTTGTAATCCC  8630 TGGT    C A____    I
                          GGCTC CA    AATCC
                          ||||| ||    |||||
                          CCGAG GT    TTAGG
                          ____    T GAACA    I
GAM544 GABPB1      TGGTCGGCGCCCAAAATCCC      8636  _   T        II
                          TGGT GGC  CCCAAAATCC
                          |||| |||  ||||||||||
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                        ACCA CCG GGGTTTTAGG
                          G   C         GI
GAM544 IL11          GTGGTGGCTCACACCTGTAATCCC  8629 TGGT    ___  AA_    I
                        GGCTC  CC  AATCC
                        |||||  ||  |||||
                        CCGAG  GG  TTAGG
                        ____       TGT  ACA    I
GAM544 IL17E         GAGTGGTGGCCTCCAGAAAT      8626       TC  AAAII
                        GAGTGGTGGC  CCA
                        |||||||||| |||
                        CTCACCACCG  GGT
                          GA  CTTTA
GAM544 IL17E         GAGTGGTGGCCTCCAGAAAT      8626 TAGA      TC  AAATCC
                        GTGGTGGC  CCA
                        |||||||| |||
                        CACCACCG  GGT
                        ____        GA  CTTTAC
GAM544 KRT9         GAGTGCTACCGGCTCCCAA        8625    G___       III
                        GAGTG  TGGCTCCCA
                        |||||  |||||||||
                        CTCAC  GCCGAGGGT
                          GATG      TII
GAM544 KRT9         GAGTGCTACCGGCTCCCAA        8625 TAGA GG_       AATCC
                        GT  TGGCTCCCAA
                        ||  ||||||||||
                        CG  GCCGAGGGTT
                        CA__  ATG       CAIII
GAM544 PCDH11X        AGAGTGGTGGGTAATAAAA      8623        CTCCCAAAII
                        AGAGTGGTGG
                        ||||||||||
                        TCTCACCACC
                          CATTATTTTI
GAM544 PCDH11X        AGAGTGGTGGGTAATAAAA      8623 TA       CTCCCAAAATCC
                        GAGTGGTGG
                        |||||||||
                        CTCACCACC
                        __        CATTATTTTTII
GAM544 PCDH11Y        AGAGTGGTGGGTAATAAAA      8623        CTCCCAAAII
                        AGAGTGGTGG
                        ||||||||||
                        TCTCACCACC
                          CATTATTTTI
GAM544 PCDH11Y        AGAGTGGTGGGTAATAAAA      8623 TA       CTCCCAAAATCC
                        GAGTGGTGG
                        |||||||||
                        CTCACCACC
                        __        CATTATTTTTII
GAM544 PDE4D         GTGGCTCCCAGAGGATCCC       8627        AA__   III
                        GTGGCTCCCA  ATCC
                        ||||||||||  ||||
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                              CACCGAGGGT   TAGG
                               CTCC   GII
GAM544  PDE4D          GTGGCTCCCAGAGGATCCC      8627 TAGAGT  T  C     ATCC
                           GG GG TCCCAAA
                           II II IIIIIII
                           TC CC AGGGTTT
                            GG____  T  T    GTTT
GAM544  RPP30          GTGGTGGCTCATGTAATCCC     8618        CCAA   I
                           TGGTGGCTC  AATCC
                           IIIIIIIII  IIIII
                           ACCACCGAG  TTAGG
                            TACA   I
GAM544  RPP30          GTGGTGGCTCATGTAATCCC     8618 TAGAGTGG    CCAA
                            TGGCTC  AATCC
                            IIIIII  IIIII
                            ACCGAG   TTAGG
                           _____   TACA
GAM544  SAS         TATAGTC-TGGCTCCCACTAAAAT  8635 TAGA   __     AAATCCCI
                          GTGGT GGCTCCCA
                          IIIII IIIIIIII
                          TATCA CCGAGGGT
                          A___   GA     GATTTTAI
GAM544  SAS         TATAGTC-TGGCTCCCACTAAAAT  8635 TAGAGTGG     AI
                            TGGCTCCCA
                            IIIIIIIII
                            ACCGAGGGT
                          AG_____       GA
GAM544  SORCS1       TGGTCACTTCCCAAAATGCC    8637  G  _    _ II
                         TGGT GCT CCCAAAAT CC
                         IIII III IIIIIIII II
                         ACCA TGA GGGTTTTA GG
                           G   A    C II
GAM544  TP53         GTGGTGGCTCACAATTGTAATCCC  8633 TGGT   C  ____   I
                          GGCTC CAA   AATCC
                          IIIII III   IIIII
                          CCGAG GTT   TTAGG
                          ____    T  AACA   I
GAM544  UGDH          GTGGTGGCTCACACCTGTAATCCC  8629 TGGT   ___ AA_  I
                          GGCTC  CC  AATCC
                          IIIII  II  IIIII
                          CCGAG  GG  TTAGG
                           ____    TGT ACA   I
GAM545  ADAMTS4         GTGGTGGCTCACACCTGTAATCCC  8629 TGGT   ___ AA_  I
                          GGCTC  CC  AATCC
                          IIIII  II  IIIII
                          CCGAG  GG  TTAGG
                           ____     TGT ACA   I
GAM545  ADCY6         GTGGTGGCTCACGTCCGTAATCCC  8628 TGGT   ____ AA  I
                          GGCTC   CC AATCC
                          IIIII   II IIIII
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                        CCGAG  GG TTAGG
                   ____     TGCA CA    I
GAM545 ALDH1B1          GTTGTGGCTCCCACCTGTAATCCC  8632 TGGT       A____       I
                        GGCTCCCA    AATCC
                        ||||||||    |||||
                        CCGAGGGT    TTAGG
                   ____        GGACA    I
GAM545 ARAF1            GAGATGGAGGAGCTCCCAAAAT  8624  _  T__        III
                        GAG TGG  GGCTCCCAAAA
                        ||| |||  ||||||||||
                        CTC ACC  TCGAGGGTTTT
                         T  TCC         AII
GAM545 ARAF1            GAGATGGAGGAGCTCCCAAAAT  8624 TAGA  T__        CCC
                        GTGG  GGCTCCCAAAAT
                        ||||  |||||||||||
                        TACC  TCGAGGGTTTTA
                         C___  TCC         AAI
GAM545 CD1A         TAAAGTGAAATGGCTCCCA      8634      __        AAATCC
                        TAGAGTG GTGGCTCCCA
                        ||||||| ||||||||||
                        ATTTCAC TACCGAGGGT
                          TT       IIICCC
GAM545 CD1A         TAAAGTGAAATGGCTCCCA      8634      __         III
                        TAGAGTG GTGGCTCCC
                        ||||||| |||||||||
                        ATTTCAC TACCGAGGG
                          TT       TII
GAM545 CDC6        TGGTGGCTCACGCCTATAATCCC   8638       ___ AA_   IIIG
                        TGGTGGCTC CC AATCC
                        ||||||||| || |||||
                        ACCACCGAG GG TTAGG
                          TGC ATA   GIII
GAM545 CLECSF12        GTGGTGGCTCACATCTGTAATCCC  8631 TGGT    C A____      I
                        GGCTC CA    AATCC
                        ||||| ||    |||||
                        CCGAG GT    TTAGG
                   ____       T AGACA     I
GAM545 CYP1A2          GTGGTGGCTCACACCTGTAATCCC  8629 TGGT     ___ AA_   I
                        GGCTC CC  AATCC
                        ||||| || |||||
                        CCGAG GG  TTAGG
                   ____        TGT ACA   I
GAM545 DSCR3          GTGGTGGCTCACACCTGTAATCCC  8629 TGGT     ___ AA_   I
                        GGCTC CC  AATCC
                        ||||| || |||||
                        CCGAG  GG  TTAGG
                   ____          TGT ACA   I
GAM545 FZD4         GTGGTGGCTCACACTTGTAATCCC  8630 TGGT    C A____      I
                        GGCTC CA    AATCC
                        ||||| ||    |||||
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                              CCGAG GT   TTAGG
                              ____   T GAACA   I
GAM545  GABPB1        TGGTCGGCGCCCAAAATCCC    8636   _  T      II
                              TGGT GGC CCCAAAATCC
                              IIII III IIIIIIIIII
                              ACCA CCG GGGTTTTAGG
                               G    C      GI
GAM545  IL11         GTGGTGGCTCACACCTGTAATCCC 8629 TGGT   ___  AA_   I
                              GGCTC  CC  AATCC
                              IIIII II  IIIII
                              CCGAG  GG  TTAGG
                              ____    TGT  ACA   I
GAM545  IL17E      GAGTGGTGGCCTCCAGAAAT    8626       TC  AAAII
                              GAGTGGTGGC CCA
                              IIIIIIIIII III
                              CTCACCACCG GGT
                                GA  CTTTA
GAM545  IL17E      GAGTGGTGGCCTCCAGAAAT    8626 TAGA    TC  AAATCC
                              GTGGTGGC CCA
                              IIIIIIII III
                              CACCACCG GGT
                              ____      GA  CTTTAC
GAM545  KRT9        GAGTGCTACCGGCTCCCAA     8625   G___       III
                              GAGTG TGGCTCCCA
                              IIIII IIIIIIIIII
                              CTCAC GCCGAGGGT
                               GATG      TII
GAM545  KRT9        GAGTGCTACCGGCTCCCAA     8625 TAGA GG_      AATCC
                              GT TGGCTCCCAA
                              II IIIIIIIIII
                              CG GCCGAGGGTT
                              CA__ ATG      CAIII
GAM545  PCDH11X      AGAGTGGTGGGTAATAAAA     8623       CTCCCAAAII
                              AGAGTGGTGG
                              IIIIIIIIII
                              TCTCACCACC
                               CATTATTTTI
GAM545  PCDH11X      AGAGTGGTGGGTAATAAAA     8623 TA      CTCCCAAAATCC
                              GAGTGGTGG
                              IIIIIIIII
                              CTCACCACC
                              __      CATTATTTTTII
GAM545  PCDH11Y      AGAGTGGTGGGTAATAAAA     8623       CTCCCAAAII
                              AGAGTGGTGG
                              IIIIIIIIII
                              TCTCACCACC
                               CATTATTTTI
GAM545  PCDH11Y      AGAGTGGTGGGTAATAAAA     8623 TA      CTCCCAAAATCC
                              GAGTGGTGG
                              IIIIIIIII
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                      CTCACCACC
                      __      CATTATTTTTII
GAM545  PDE4D         GTGGCTCCCAGAGGATCCC     8627        AA__    III
                      GTGGCTCCCA   ATCC
                      IIIIIIIII    IIII
                      CACCGAGGGT   TAGG
                           CTCC   GII
GAM545  PDE4D         GTGGCTCCCAGAGGATCCC     8627 TAGAGT T  C     ATCC
                      GG GG TCCCAAA
                      II II IIIIIIII
                      TC CC AGGGTTT
                      GG____  T T    GTTT
GAM545  RPP30         GTGGTGGCTCATGTAATCCC    8618        CCAA   I
                      TGGTGGCTC   AATCC
                      IIIIIIIII   IIIII
                      ACCACCGAG   TTAGG
                           TACA   I
GAM545  RPP30         GTGGTGGCTCATGTAATCCC    8618 TAGAGTGG     CCAA
                      TGGCTC   AATCC
                      IIIIII   IIIII
                      ACCGAG   TTAGG
                      _____   TACA
GAM545  SAS          TATAGTC-TGGCTCCCACTAAAAT  8635 TAGA    __      AAATCCCI
                      GTGGT GGCTCCCA
                      IIIII IIIIIIII
                      TATCA CCGAGGGT
                       A___   GA    GATTTTAI
GAM545  SAS          TATAGTC-TGGCTCCCACTAAAAT  8635 TAGAGTGG       AI
                         TGGCTCCCA
                         IIIIIIIII
                         ACCGAGGGT
                      AG_____     GA
GAM545  SORCS1        TGGTCACTTCCCAAAATGCC     8637   G  _    _  II
                      TGGT GCT CCCAAAAT CC
                      IIII III IIIIIIII II
                      ACCA TGA GGGTTTTA GG
                         G   A    C II
GAM545  TP53          GTGGTGGCTCACAATTGTAATCCC  8633 TGGT    C  ____    I
                      GGCTC CAA   AATCC
                      IIIII III   IIIII
                      CCGAG GTT   TTAGG
                       ____   T  AACA    I
GAM545  UGDH          GTGGTGGCTCACACCTGTAATCCC  8629 TGGT   ___ AA_   I
                      GGCTC  CC   AATCC
                      IIIII  II   IIIII
                      CCGAG  GG   TTAGG
                      ____     TGT  ACA   I
GAM546  A1BG          GTGGTGGCTCACCCCTGTAATCCC  8688 TGGT   _ AG___    I
                      GGCTC CC    AATCC
                      IIIII II    IIIII
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                              CCGAG GG    TTAGG
                              ____   T GGACA     I
GAM546  ADCY6           GTGGTGGCTCACGTCCGTAATCCC 8628 TGGT    ____  AG    I
                              GGCTC   CC AATCC
                              |||||  || |||||
                              CCGAG   GG TTAGG
                                   TGCA CA    I
GAM546  ARSF           GAGTGGTGGTTCACGCCTGTAATCCC 8614 A   G_ T CAG    I
                              GTGGT GC CC  AATCC

                              ||||| || ||  |||||
                              CACCA TG GG  TTAGG
                              _   AG C ACA    I
GAM546  ARSF           GAGTGGTGGTTCACGCCTGTAATCCC 8614 TAGA    C ___ AG_    II
                              GTGGTGG TC  CC  AATCCC

                              |||||||| ||  ||  ||||||
                              CACCACC AG  GG  TTAGGG
                              ____    A TGC  ACA    TC
GAM546  ATP5B          GATTGGTG-CACC-AGAATCC    8616 AG_   G TC     I
                              TGGTG C  CCAGAATC

                              ||||| |  |||||||||
                              ACCAC G  GGTCTTAG
                              CTA    _T_     I
GAM546  ATP5B          GATTGGTG-CACC-AGAATCC    8616 TAGAG   G TC
                              TGGTG C  CCAGAATCC

                              ||||| |  |||||||||
                              ACCAC G  GGTCTTAGG
                              A____   _T_
GAM546  CCNF           TGCTGGCTCCCAGGCTCCC      8714  G     AA  II
                              TG TGGCTCCCAG TCC

                              || |||||||||| |||
                              AC ACCGAGGGTC AGG
                               G     CG  GI
GAM546  CD1A           TAAAGTGAAATGGCTCCCAG     8619      __       AATCC
                              TAGAGTG GTGGCTCCCAG

                              ||||||| |||||||||||
                              ATTTCAC TACCGAGGGTC
                               TT     IIICC
GAM546  CD1A           TAAAGTGAAATGGCTCCCAG     8619      __       III
                              TAGAGTG GTGGCTCCCA

                              ||||||| ||||||||||
                              ATTTCAC TACCGAGGGT
                               TT     CII
GAM546  CLECSF12        GTGGTGGCTCACATCTGTAATCCC 8631 TGGT   C G____    I
                              GGCTC CA    AATCC

                              ||||| ||    |||||
                              CCGAG GT    TTAGG
                              ____    T AGACA    I
GAM546  CRY2           TAGGGAGGCAGATGCCAGAATCCC 8620 AG T T TC___      I
                              AG GG GGC    CCAGAATCC

                              || || |||    |||||||||
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                          TC CC CCG    GGTCTTAGG
                          __ _ T  TCTAC        I
GAM546  CRY2        TAGGGAGGCAGATGCCAGAATCCC  8620 TAG  T  T  TC___        I
                          AG GG GGC    CCAGAATCCC
                          || || |||   ||||||||||
                          TC CC CCG    GGTCTTAGGG
                          A__ _ T  TCTAC        I
GAM546  CRY2        TGGCTGCCTCC-AGAATCCC      8708   G TC      II
                          TGGT GC  CCAGAATCC
                          |||| || |||||||||
                          ACCG CG  GGTCTTAGG
                          A GA      GI
GAM546  CYP1A2       GTGGTGGCTCACACCTGTAATCCC  8629 TGGT    ___ AG_   I
                          GGCTC  CC  AATCC
                          ||||| || |||||
                          CCGAG  GG  TTAGG
                          ____      TGT ACA   I
GAM546  DNASE1L1       GTGGTGGCTCATGCCTGTAATCCC  8694 TGGT    ___ AG_   I
                          GGCTC  CC  AATCC
                          ||||| || |||||
                          CCGAG  GG  TTAGG
                          ____      TAC ACA   I
GAM546  DSCR3         GTGGTGGCTCACACCTGTAATCCC  8629 TGGT    ___ AG_   I
                          GGCTC  CC  AATCC
                          ||||| || |||||
                          CCGAG  GG  TTAGG
                          ____      TGT ACA   I
GAM546  ENAM        GAGTGGTGGCTCATTCAGCATCC  8615 TAGA       C__  A  CI
                          GTGGTGGCTC  CAG ATCC
                          |||||||||| ||| ||||
                          CACCACCGAG  GTC TAGG
                          ____         TAA  G  AT
GAM546  ENAM        GAGTGGTGGCTCATTCAGCATCC  8615 AG       C__  A  I
                          TGGTGGCTC  CAG ATC
                          ||||||||| ||| |||
                          ACCACCGAG  GTC TAG
                          __         TAA  G  I
GAM546  FZD4        GTGGTGGCTCACACTTGTAATCCC  8630 TGGT    C G____      I
                          GGCTC CA    AATCC
                          ||||| ||    |||||
                          CCGAG GT    TTAGG
                          ____      T GAACA   I
GAM546  HCS        TGGTGGCTCACGCCTGCAATCCC  8712          ___ AG_  IIIG
                          TGGTGGCTC  CC  AATCC
                          ||||||||| || |||||
                          ACCACCGAG  GG  TTAGG
                          TGC ACG    GIII
GAM546  IGF1        GTGGTGGCTCATGCCTGTAATCCC  8694 TGGT    ___ AG_   I
                          GGCTC  CC  AATCC
                          ||||| || |||||
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                    CCGAG  GG  TTAGG
                  ____  TAC  ACA    I
GAM546  IL11       GTGGTGGCTCACACCTGTAATCCC  8629 TGGT    ___ AG_   I
                    GGCTC  CC  AATCC
                    |||||  ||  |||||
                    CCGAG  GG  TTAGG
                   ____  TGT  ACA    I
GAM546  KIFC3       GAGGGCGTGGCTCCCAGGTTCC   8612 GAGTG        AAI
                       GTGGCTCCCAG
                       ||||||||||
                       CACCGAGGGTC
                     CG___        CAA
GAM546  KIFC3       GAGGGCGTGGCTCCCAGGTTCC   8612 TAGAGTG       AA  C
                       GTGGCTCCCAG TCC
                       |||||||||| |||
                       CACCGAGGGTC AGG
                    CCCG___        CA  T
GAM546  NRXN1       GTGGCTGCTCCCAGATTTCC      8617  G       ATCCI
                     TGGT GCTCCCAGA
                     |||| |||||||||
                     ACCG CGAGGGTCT
                       A       AAAGI
GAM546  NRXN1       GTGGCTGCTCCCAGATTTCC      8617 TAGAGTGGTG      A_
                        GCTCCCAGA TCC
                        ||||||||| |||
                        CGAGGGTCT AGG
                    GA_____      AA
GAM546  PDE4D       GTGGCTCCCAGAGGATCCC        8627            __  III
                     GTGGCTCCCAGA ATCC
                     ||||||||||| ||||
                     CACCGAGGGTCT TAGG
                        CC  GII
GAM546  PRSS8       AGAGGGAAGGATCCCAGAATCC    8611   T T_  C       I
                    GAG GG  GG TCCCAGAATC
                    ||| || || |||||||||
                    CTC CC  CC AGGGTCTTAG
                     _ TT  T        I
GAM546  PRSS8       AGAGGGAAGGATCCCAGAATCC    8611 TA  T T_  C      C
                     GAG GG  GG TCCCAGAATCC
                     ||| || || ||||||||||
                     CTC CC  CC AGGGTCTTAGG
                     __ _ TT  T       C
GAM546  RPP30       GTGGTGGCTCATGTAATCCC       8618        CCAG   I
                     TGGTGGCTC  AATCC
                     |||||||||  |||||
                     ACCACCGAG  TTAGG
                      TACA   I
GAM546  RPP30       GTGGTGGCTCATGTAATCCC       8618 TAGAGTGG    CCAG
                      TGGCTC  AATCC
                      ||||||  |||||
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                         ACCGAG   TTAGG
                    _____        TACA
GAM546 SMAC         TGGTGGCTCACGCCTGTAATCC   8710        ___ AG_  IIIG
                    TGGTGGCTC  CC  AATC
                    IIIIIIIII II  IIII
                    ACCACCGAG  GG  TTAG
                          TGC ACA   GIII
GAM546 SMAC         GAGTGGTGGCACGCTCCTGTAATCCC 8613 A      _    CAG   I
                    GTGGTG GCTCC  AATCC
                    IIIIII IIIII  IIIII
                    CACCGT CGAGG  TTAGG
                     _    G  ACA   I
GAM546 SMAC         GAGTGGTGGCACGCTCCTGTAATCCC 8613 TAGA      ____  CAG   II
                    GTGGTGGC  TCC  AATCCC
                    IIIIIIII  III  IIIIII
                    CACCACCG  AGG  TTAGGG
                    ____       TGCG  ACA   TC
GAM546 TBXAS1       AGAGTGGTGGTCTTCCAGA       8610       _ C  II
                    AGAGTGGTGG CT CCAG
                    IIIIIIIIII II IIII
                    TCTCACCACC GA GGTC
                         A A   TI
GAM546 TBXAS1       AGAGTGGTGGTCTTCCAGA       8610 TA      _ C   ATCC
                    GAGTGGTGG CT CCAGA
                    IIIIIIIII II IIIII
                    CTCACCACC GA GGTCT
                    __         A A   AIII
GAM546 TFCP2        AGTGGTGGCTTGCTGCTTCCC     8675        CCCAGAA I
                    GTGGTGGCT    TCC
                    IIIIIIIII    III
                    CACCACCGA    AGG
                    ACGACGA I
GAM546 TP53         GTGGTGGCTCACAATTGTAATCCC  8633 TGGT   C ____   I
                    GGCTC CAG   AATCC
                    IIIII III   IIIII
                    CCGAG GTT   TTAGG
                    ____    T  AACA   I
GAM547 ARNTL        TGACTTGTATCAATGGCT-CTGAG  8722       A    G AAGI
                    TGACTTGTA TGATGGCT CT
                    IIIIIIIII IIIIIIII II
                    ACTGAACAT GTTACCGA GA
                    A      _  CTCI
GAM547 COX11        GACTTGTAATGGTGATGCTTTGGCTAA8720 TG       A  C   AAGIII
                    ACTTGTAATG TGG TGCT
                    IIIIIIIIII III IIII
                    TGAACATTAC ACT ACGA
                    __        C  _  AACCGA
GAM547 FBN1         ACTTGTAAT-TTGGTTTCTAAG    8717 TGAC    GA  CTG
                    TTGTAAT TGG  CTAAG
                    IIIIIII III  IIIII
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                              AACATTA  ACC   GATTC
                              ____         A_   AAA
GAM547  GOLGA4           CTTAGTGATGAAATGGCTGCT    8718 TGACTT  A    __       AAG
                              GT ATGA  TGGCTGCT
                              || |||| ||||||||
                              CA TACT  ACCGACGA
                              T_____  C   TT      AGA
GAM547  MAP1A            TTATAAGCTGATGAGCTGCTAAG  8723 TGACTTGTAA    _      I
                              TGATG GCTGCTAAG
                              ||||| |||||||||
                              ACTAC CGACGATTC
                              TTCG_____   T    T
GAM547  PCDHA11          CTTGTTACTTTGGCTGCTA     8719 TGACTTGTAATGA      A
                              TGGCTGCTA
                              |||||||||
                              ACCGACGAT
                              CAATGAA_____        C
GAM547  PHKG1            TGACTTGTATTTCCATGGCT     8721        ATG__      GCTAA
                              TGACTTGTA  ATGGCT
                              ||||||||| ||||||
                              ACTGAACAT  TACCGA
                              AAAGG      IIIGA
GAM548  ARHGAP6          ACCTGGACGTGGGGCGTGC      8726 TGTACG C  A_ _ GA
                              AC TGG  CG GC  CGGG
                              || ||| || || ||||
                              TG ACC  GC CG  GTCC
                              _____   C  CC  A  AC
GAM548  SLC2A1           GTACG--CGGGT-GGCGACGGGC  8727 TG   ACC   AC
                              TACG  TGG  GGCGACGGG
                              ||||  |||  |||||||||
                              ATGC  GCC  CCGCTGCCC
                              __   ___   CA
GAM549  ASPA             GGAGTATAT--TTTAAT--TTTC  8741        AG     CA
                              GGAGTATAT TTTAGT TTTC
                              ||||||||| |||||| ||||
                              CCTCATATA AAATTA AAAG

                              __     __
GAM549  ASPA             GGAGTATAT--TTTAAT--TTTC  8741        AG     CAI
                              GGAGTATAT TTTAGT
                              ||||||||| ||||||
                              CCTCATATA AAATTA
                              __     AAA
GAM549  ATP6V1A1         ATAGAAATTGAGTCATTTCA     8733 ___ T  T        III
                              A AGTT AGTCATTTC
                              | |||| |||||||||
                              C TTAA TCAGTAAAG
                              TAT T  C       TII
GAM549  CCRL1            GTATATAGTTCTGTGTCATTT    8742          A__      III
                              GTATATAGTTT GTCATT
                              |||||||||| ||||||
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                    CATATATCAAG  CAGTAA
                       ACA      AII
GAM549  CCRL1      GTATATAGTTCTGTGTCATTT   8742 GGAGTA      A__      CA
                       TATAGTTT  GTCATTT
                       |||||||| |||||||
                       ATATCAAG  CAGTAAA
                    _____         ACA      AT
GAM549  CDH19      GAGGA-ATATTTAGTCAT    8736 _     ATAG      TT
                       GGAGTAT  TTTAGTCAT
                       ||||||| |||||||||
                       CCTTATA  AAATCAGTA
                    T       ____        TI
GAM549  CDH19      GAGGA-ATATTTAGTCAT    8736 ___     ATAG      I
                        GAGTAT  TTTAGTCA
                        |||||| ||||||||
                        CTTATA  AAATCAGT
                    CTC         ____         A
GAM549  FBXW7      GGAGTATATCGTCTACACAATT   8740     A   GT TTTCA
                       GGAGTATAT GTTTA  CA
                       ||||||||| |||||  ||
                       CCTCATATA CAGAT  GT
                          G    GT TAAII
GAM549  FBXW7      GGAGTATATCGTCTACACAATT   8740     A   GT TTI
                       GAGTATAT GTTTA  CA
                       |||||||| |||||  ||
                       CTCATATA CAGAT  GT
                          G    GT TAI
GAM549  GRM6       GAGAATA-AGTTAGTCCCTTTC  8734    TAT      A_   A
                       GGAGTA  AGTTAGTC  TTTC
                       ||||||  |||||||||  ||||
                       TCTTAT  TCAAATCAG  AAAG
                          ___        GG   A
GAM549  GRM6       GAGAATA-AGTTAGTCCCTTTC  8734    TAT      ATTI
                        GAGTA  AGTTAGTC
                        |||||  |||||||||
                        CTTAT  TCAAATCAG
                          ___        GGAA
GAM549  HIVEP2     GAGTATATAGATCA-ACATGTTCA  8737      T   T TTCI
                       AGTATATAG TTAG CAT
                       ||||||||| |||| |||
                       TCATATATC AGTT GTA
                       T    _   CAAG
GAM549  HIVEP2     GAGTATATAGATCA-ACATGTTCA  8737 GG      T   T _   I
                       AGTATATAG TTAG CAT TTCA
                       ||||||||| |||| ||| ||||
                       TCATATATC AGTT GTA AAGT
                         __     T  _  C  G
GAM549  HNRPH1     AGT-TATAGTTTACTCAGCTTCA   8732 GGAGTA       G  _
                       TATAGTTTA TCA TTTCA
                       ||||||||| ||| |||||
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                              ATATCAAAT AGT GAAGT
                              A_____        G  C
GAM549  HNRPH1        AGT-TATAGTTTACTCAGCTTCA  8732 GTA      G  _  I
                         TATAGTTTA TCA TTTC
                         ||||||||| ||| ||||
                         ATATCAAAT AGT GAAG
                              CA_        G  C  I
GAM549  LZTFL1        GAATTTATAGTTTA-TCAT     8735  A       G  I
                         GAGT TATAGTTTA TCA
                         |||| ||||||||| |||
                         CTTA ATATCAAAT AGT
                              A     _  A
GAM549  LZTFL1        GAATTTATAGTTTA-TCAT     8735 GGAGTA     G   T
                         TATAGTTTA TCATT
                         ||||||||| |||||
                         ATATCAAAT AGTAG
                              TTAA__     _  I
GAM549  MAP3K13       TATATAGTTCACTCTTTGCA     8743      G  ATTTCI
                         ATATAGTTTA TC
                         |||||||||| ||
                         TATATCAAGT AG
                              G AAACGI
GAM549  MAP4K5        GGAGTATATTCATTTCCTGTCATTT 8738      A_ A___    CAII
                         GGAGTATAT GTTT  GTCATTT
                         ||||||||| ||||  |||||||
                         CCTCATATA TAAA  CAGTAAA
                              AG  AGGA    IIIA
GAM549  RB1CC1        AGTATATAGTTAAAGAACATTT   8730 GGAG      T_ T_   CA
                         TATATAGTT AG CATTT
                         ||||||||| || |||||
                         ATATATCAA TC GTAAA
                              ____      TT TT   AA
GAM549  SLC6A12       GGAG-ATAAGGTTTTAGTCATATC 8739   T TAG_     T AI
                         GGAG ATA   TTTAGTCAT TC
                         |||| |||   ||||||||| ||
                         CCTC TAT   AAATCAGTA AG
                          _  TCCA       T II
GAM549  SLC6A12       GGAG-ATAAGGTTTTAGTCATATC 8739   T TAG_      TTI
                         GAG ATA   TTTAGTCAT
                         ||| |||   |||||||||
                         CTC TAT   AAATCAGTA
                          _  TCCA       TAI
GAM549  TCF2          AGTTTATAGTTTACAGCCATT    8731  A     __    III
                         AGT TATAGTT TAGTCAT
                         ||| |||||||  |||||||
                         TCA ATATCAA GTCGGTA
                              A  AT   AII
GAM549  TCF2          AGTTTATAGTTTACAGCCATT    8731 GGAGTA    __    TCA
                         TATAGTT TAGTCATT
                         ||||||| |||||||||
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                              ATATCAA GTCGGTAA
                        AA____      AT    CCI
GAM550 ACP5            AACTATTCTTTTATTGAACATCA  8746 TGAACATG        CCAI
                          TTTTTATTGAACA
                          IIIIIIIIIIIII
                          GAAAATAACTTGT
                        GATAA___         AGTC
GAM550 AR             TTCAGGAACATGTTCATG-ACA  8776 TT       _  GGT  TT
                        TCAGGAACAT TTCA  ACA
                        IIIIIIIIIII IIII  III
                        AGTCCTTGTA AAGT  TGT
                        __        C  AC_  CI
GAM550 BAZ1A          TTAAGGAACATTTTCCAGGTA   8777 TTTC      __       CATT
                        AGGAACAT TTCAGGTA
                        IIIIIIIII IIIIIIII
                        TCCTTGTA AGGTCCAT
                        AT__      AA    AIII
GAM550 CASP10        GAACGTGGTTTT--TGAACACCA  8762 TGAAC   TT  A
                         ATGT  TT TTGAACACCA
                         IIII  II IIIIIIIIII
                         TGCA  AA AACTTGTGGT
                        T____     CC  A
GAM550 CDC23         ACAT-TTTTTATTGAATTCCA    8752 TGAACATG       CA
                          TTTTTATTGAA CC
                          IIIIIIIIIII II
                          AAAAATAACTT GG
                        A_____        AA
GAM550 CDKN2B       TGAACATGTATTT-TTAAAC      8770     T  A    ACC
                        TGAACATGT TTT TTGAAC
                        IIIIIIIII III IIIIII
                        ACTTGTACA AAA AATTTG
                          T  _   III
GAM550 CEACAM5       GAGCAGATTTTTATTGAAC      8759 TGAA  T        ACC
                         CA GTTTTTATTGAAC
                         II IIIIIIIIIIII
                         GT TAAAAATAACTTG
                        TC__  C       AII
GAM550 COPG2         CAGGAGC-TTTCAGGTACA      8755 TTTCAGGAACA
                          TTTCAGGTACA
                          IIIIIIIIIII
                          AAAGTCCATGT
                        CTCG_____
GAM550 DDX11         CAGGATCTGCTTCAGGTACAT    8754 TTTCAGGAACA
                          TTTCAGGTACATT
                          IIIIIIIIIIII
                          GAAGTCCATGTAG
                        CTAGAC_____
GAM550 DIAPH2        TCAGGGTTAACATTTCAAGATCATT 8764 TTTC  ___       TA  II
                         AGG  AACATTTCAGG CATT
                         III  IIIIIIIIIII IIII
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                              TCC  TTGTAAAGTTC GTAA
                  ____     CAA        TA  GA
GAM550 DSG2       TCATGAAAAAT-CAGGTACATT   8766 TTTCA   CATT
                          GGAA   TCAGGTACATT
                          IIII   IIIIIIIIIII
                          CTTT  AGTCCATGTAA
                  TA___    TT__
GAM550 ED1        AGGAAACACATTTCAGGAACA   8753 TTTCAGGA     T TT
                          ACATTTCAGG ACA
                          IIIIIIIIII III
                          TGTAAAGTCC TGT
                  TTG_____        T  TC
GAM550 EIF2C1     TCAGAGAACAAATCAGGTACA   8763 TTTCA   TT      T
                          GGAACA TCAGGTACAT
                          IIIIII IIIIIIIIII
                          TCTTGT AGTCCATGTG
                  TC___    TT       T
GAM550 ELMO2      TGAAAGAGTATTTATTGAAAAC   8773   CAT T     C CA
                          TGAA  GT TTTATTGAA AC
                          IIII  II IIIIIIIII II
                          ACTT  CA AAATAACTT TG
                    TCT T      T II
GAM550 EYA1       TTCAGGAAACACATTTCAG       8775 TT   ___       GTACAT
                          TCAGGA  ACATTTCAG
                          IIIIII  IIIIIIIII
                          AGTCCT  TGTAAAGTC
                    __     TTG       AIIITT
GAM550 GAS1       TGTACATGTTTTAATAAAACA   8772  A      TATT   CCA
                          TG ACATGTTTT  GAACA
                          II IIIIIIIII  IIIII
                          AC TGTACAAAA  TTTGT
                          A     TTAT    III
GAM550 HMGB3      TTCAAAAACATTTCAG---CATT   8779 TT          GTACAT
                          TCAGGAACATTTCAG
                          IIIIIIIIIIIIIII
                          AGTTTTTGTAAAGTC
                          __        GTAAGI
GAM550 IDH3B      CATGTTCTTTATTGAACACC      8756 TGAACATG
                          TTTTTATTGAACACC
                          IIIIIIIIIIIIIII
                          AGAAATAACTTGTGG
                  A_____
GAM550 IFNA1      GAACATG-TTTTATT--ACAC   8761 TG      T GA
                          AACATGTTTT ATT ACAC
                          IIIIIIIIII III IIII
                          TTGTACAAAA TAA TGTG
                  __      _  __
GAM550 IFNA8      GAACATGTTTTTGTTACACA   8760 TG      A  A CC
                          AACATGTTTTT TTG ACA
                          IIIIIIIIII III III
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                        TTGTACAAAAA AAT TGT
                         __      C  G  TI
GAM550 IFNW1            TTTCTG-AACATTTCTCTGTACTTT 8784   AG      AG_  ATTI
                        TTTC GAACATTTC GTAC
                        |||| ||||||||| ||||
                        AAAG CTTGTAAAG CATG
                         A_      AGA  AAAI
GAM550 IFNW1            TGAACATGTTTTGTTATCTTAATAC 8768        TATTGAACACCAII
                        TGAACATGTTTT
                        ||||||||||||
                        ACTTGTACAAAA
                             CAATAGAATTATGI
GAM550 JUN           TCAGGTACAT--CAGGTACATT   8765 TTTC  A  TT
                        AGG ACA  TCAGGTACAT
                        ||| |||  ||||||||||
                        TCC TGT  AGTCCATGTA
                         ____    A  __
GAM550 KL           TTTCGAAAGGAACATTCCAG    8780  ___        GTACAT
                        TTTC AGGAACATTTCAG
                        |||| |||||||||||||
                        AAAG TCCTTGTAAGGTC
                         CTT        IIITTA
GAM550 KTN1            TGAACAA--TTTTATTGAGCA   8771    TGT      ACACC
                        TGAACA TTTTATTGA
                        |||||| |||||||||
                        ACTTGT AAAATAACT
                          T__      CGTII
GAM550 MAB21L1        TTTAAATAACATTTCAAGTATATT 8787 TTTCAGG       CATTI
                        AACATTTCAGGTA
                        |||||||||||||
                        TTGTAAAGTTCAT
                        AAATTTA       ATAAI
GAM550 MECP2        TTTTTGAAACGTATACAGGTACATT 8783 TTTCA    ATTT_     II
                        GGAAC   CAGGTACATT
                        |||||   ||||||||||
                        CTTTG   GTCCATGTAA
                        AAAAA   CATAT      II
GAM550 MKPX        TTTCAGAAAC--TTCAGGTACA   8786       AT      T
                        TTTCAGGAAC TTCAGGTACA
                        |||||||||| ||||||||||
                        AAAGTCTTG AAGTCCATGT
                              __        I
GAM550 MVK        TTCCACAAACCTCTCAGGTACA   8785   G  A      TT
                        TTTCA GAAC TTTCAGGTACA
                        ||||| |||| ||||||||||
                        AAGGT TTTG AGAGTCCATGT
                          G   G      II
GAM550 NCOA3        AACATTTCTGTTTTGAACACCA   8751 TGAACAT   A__
                        GTTTTT TTGAACACCA
                        |||||| ||||||||||
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                              TAAAGA  AACTTGTGGT
                         G_____        CAA
GAM550  NOVA1        GAACAGGTGCTTTTATTGA    8758 TG  __        ACACC
                         AACA TGTTTTTATTGA
                         IIII IIIIIIIIIIII
                         TTGT ACGAAAATAACT
                         __    CC       AIIIA
GAM550  NSMAF        AACATGTTTTTCCT-AACAC    8749 TGAA     ATTG   C
                         CATGTTTTT  AACAC
                         IIIIIIIII  IIIII
                         GTACAAAAA  TTGTG
                         ____        GGA_   T
GAM550  PRPS2        TTTTAGGATGCAGCATTTCAGGTA  8781 TTTC   A____        CATTI
                         AGGA   CATTTCAGGTA
                         IIII   IIIIIIIIIII
                         TCCT   GTAAAGTCCAT
                         AAAA  ACGTC      IIITT
GAM550  ROBO1        TGAACAAGTTTGGTTTTGGTGAACACCA8767    T  TTAT____       III
                         TGAACA GTTT    TGAACACCA
                         IIIIII IIII    IIIIIIIII
                         ACTTGT CAAA    ACTTGTGGT
                            T  CCAAAACC      III
GAM550  SCML1        TGAACATGTTTCCCTTGAA    8769        TA   CACC
                         TGAACATGTTTT TTGAA
                         IIIIIIIIIIII IIIII
                         ACTTGTACAAAG AACTT
                            GG  IIIA
GAM550  SPAG11       AACAAATATTTATTGAACACC    8750 TGAA T T        A
                         CA GT TTTATTGAACACC
                         II II IIIIIIIIIIII
                         GT TA AAATAACTTGTGG
                         ____   T T       A
GAM550  SPTBN1       TTGAGGAACATT--AGGCACA    8778 TTTC     TC    T
                         AGGAACATT AGGTACA
                         IIIIIIIII IIIIIII
                         TCCTTGTAA TCCGTGT
                         AC__       __    C
GAM550  SSA1         AACATGTTTTTGGTTGATCA    8748 TGAA     A_  A CC
                         CATGTTTTT TTGA CA
                         IIIIIIIII IIII II
                         GTACAAAAA AACT GT
                            ____     CC  A TC
GAM550  TFAP2C       TTTGGGGAACATTTACAGG    8782 TTTCA        _  TACAT
                         GGAACATTT CAGG
                         IIIIIIIII IIII
                         CCTTGTAAA GTCC
                         AAACC    T  IIITT
GAM550  TPTE         TTCAAGGGAACATTT-AGGATAGATT 8774 TT  __      C  TACATTII
                         TCA GGAACATTT AGG
                         III IIIIIIIII III
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                        AGT  CCTTGTAAA TCC
                        __   TC      _  TATCTAAA
GAM550  VAPA          GAACAGTTTGTTTTTATTG      8757 TG   ___           AACACC
                        AACA   TGTTTTTATTG
                        ||||  |||||||||||
                        TTGT  ACAAAAATAAC
                        __   CAA         AIIIAC
GAM550  VIP          AAAATATTTATTATTGAACA      8747 TGAAC    _        CC
                        ATGTTT TTATTGAACA
                        |||||| |||||||||||
                        TATAAA AATAACTTGT
                        T____    T      TG
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